



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

1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTCCGCAATTGAACGGGTGCCTA

101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGTGCTGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)

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

201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACCGCGCCGCCCTACCTGAGGGC

301 GCCATCCACGCCGGTTGAGTCGGCTTCTGCCGCTCCCGCCTGTGGTGCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

AgeI (552)
NcoI (560)
SacII (572)

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCGCTACCTGAGATCACCGGTCCCATGGGTGTCCCGCGGTCCAGAGGCCAGCAGCCCGG

601 CTGGGAAACCCTGCTCCTTGCTATTTTCTGGTGCATCCAGAGGCTGGTAGCAGCCTCAAGGTCACCACTCCATATTCTCTATGTGTGCCGAG

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

PstI (720)
SdaI (719)
Bsp120I (732)
DraIII (751)
Acc65I (776)

701 GGACAGAATGCCACCCTCACCTGCAGATTCTGGGCCCCGTGCCAAAGGGCCAGCATGTGACCATCTACAAGAGCTGGTACCTCAGCTCACGAGGCGAGG

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

801 TCCAGATGTCAAAGAACCAGCCCATACGAACTTACATTGCAGCACCTTCAGACCACGGAAGCCACCTGAAAGCCAACGCCAGCCATGACCAGCC

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

NheI (918)
FspI (956)

901 CCAGAAGCATGGGCTAGAGCTTAGCTTCTGACCACCAGGTAATTCTCTATCACCTGCGCAATGTGACCCCAAGGGACAGCGGCCTCTACTGCTGTCTA

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

NcoI (1046)
NsiI (1089)

1001 GTGATAGAATTA AAAAACACCACCCAGAACAACGGTCTACGGTCCATGGAGCTACAGGTACAGGCAGGCAAAGGCTCGGGGTCCACATGCATGGCGT

147▶ V I E L K N H H P E Q R F Y G S M E L Q V Q A G K G S G S T C M A

SgrAI (1143)

MscI (1139)

1101 CTAATGAGCAGGACAGTGACAGCATCACGGCTGCGGCCCTGGCCACCAGGCGCTGCATCGTGGGAATCCTCTGCCTCCCCTTATCTGCTGCTGGTCTA

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

1201 TAAGCAGAGACAGGTGGCTCTCACCGCGTCCAGGAGTTGGTGGAGATGGACAGCAGCAACACCAAGGAATCGAAAACCAGGCTTCGAGACCAT

213▶ K Q R Q V A S H R R A Q E L V R M D S S N T Q G I E N P G F E T T

Bsu36I (1318)
Acc65I (1382)

1301 CCACCTTCCAGGGGATGCTGAGGCCAAGACCAGGCCCACTGTCTATGTGGCCAGCGCAACCTTCGGAGTCAGGACGGTACCTGCTCTCTGACC

247▶ P P F Q G M P E A K T R P P L S Y V A Q R Q P S E S G R Y L L S D

PvuII (1494)

1401 CCAGCACACCTCTGTGCTCCAGGCCCTGGGACGTCTTTTTCCATCCCTAGATCCAGTCCCTGACTCCCCTAACTCTGAAGCCATCTAAACCAGCTG

280▶ P S T P L S P P G P G D V F F P S L D P V P D S P N S E A I •

AvrII (1509)
MscI (1521)

1501 GGAACCATCCTAGGACTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGACAAACCACAACCTAGAATGCAGTGAAAAAATGCTTTATTTGTG

HpaI (1653)
MfeI (1664)

1601 AAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAACATTCATTCTTTATGTTTCAGGTTACAGGGGA

EcoRI (1749)

1701 GGTGTGGGAGTTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACCTTAACTCCAATCAAGCCTCTA

1801 CTTGAATCCTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTTTTGACGCTCACCTTCTTTCATGGAGTTAA

SapI (1931)
SspI (1988)

1901 GATATAGTGTATTTTCCAAGGTTTGAAGTCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTTAGTAAAATATTCAGAAA

SwaI (2002)

2001 TAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGAC

2101 TTAGGGAACAAGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTACTTGAGGGGGATGAGTTCCTCAATGGT

141◀ • N R T Y K L P I L E E I T

SacI (2263)

2201 GGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCATGCCACAGGGGCTGACCACCCTG

127▶ T K 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

2301 ATGGATCTGCCACTCATCAGAGTAGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTT

93▶ I S 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

2401 CAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCCTGATGGCCGCCCCGACATGGTGCTTGTT
60 A C 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

2501 GTCCTCATAGAGCATGGTGATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGGTGGCCCTCTATAGTGA
27 D E 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

2601 GTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCATAAACGAGCTCTG
AseI (2635) SacI (2692)

2701 CTTATATAGACCTCCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCGTTGATTTACTAGTCAAA
SpeI (2790)

2801 ACAAACTCCCATTGACGTCAATGGGGTGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCAT

2901 GGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTG
SnaBI (2918)

3001 ACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCATTGACGTCAATGGAAAGTCC
NdeI (3023)

3101 CTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGCGGGGGTCTGTTGGCGGTGAGCCAGGCGGGCCATTTACCGTAAAGTTATGTAA
PstI (3202)
SdaI (3201) PacI (3209) BspLU11I (3219)

3201 GCCTGCAGGTTAATTAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAGGCCGCTTGTGGCGTTTTTCCATAGGCTCCGCCCCC
3301 CTGACGAGCATCAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCTGGAAGCTCCCTCGTGCG
3401 CTCTCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCCTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAGCTCACGCTGTAGGTATCTCAGT

3501 TCGGTGTAGGTCGTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTGAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACC
ApaLI (3533)

3601 CGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCC
3701 TAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAA
3801 ACCACCGCTGGTAGCGGTGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTG

3901 ACGCTCAGTGGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAATATCTTTATTTTCATTA
EagI (3969) PacI (3949) SmaI (3958) NotI (3968)

4001 CATCTGTGTGTTGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCCAGTG
4101 CAAGTGCAGGTGCCAGAACATTTCTCTATCGAA