

PvuI (7)
SgfI (6)
MfeI (82) **EcoNI (96)**

1 GGATCTGGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

101 GAGAAGGTGGCGGGGTAAACTGGGAAAGTGATGTCGTGACTGGCTCCGCCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTCAGTAGTCGCC

Psp1406I (203)
HindIII (245)
Bsu36I (291)
EcoNI (287)

201 GTGAACGTTCTTTTTTCGCAACGGGTTTGGCCGAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCCTTACGCGCCCGCCGCTACCTGAGGGCC

301 GCCATCCACGCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCTCTGAAGTGCCTCGCGCTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
NaeI (441)

401 GGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTCTCAACTCTACGTCTTTGTTTCGTTT

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

501 TCTGTTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCGCTACCTGAGATCACCGTTCAGCATGCCTGTCCAGCCTCTGGCCCCATCCTCTGGTCC

601 TTTCTGCTTCTGACTCTACTGCTGGGACTTACAGAAGTGGCAGGTGAGGAGGAGCTACAGATGATTCAGCCTGAGAAGCTCCTGTTGGTCACAGTTGGA

13▶ F L L L T L L L G L T E V A G E E E L Q M I Q P E K L L L V T V G

701 AAGACAGCCACTCTGCACTGCACTGTGACCTCCCTGCTTCCCGTGGACCCGCTCTGTGGTTCAGAGGAGTTGGACCAGGCCGGAATTAACTTACAATC

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

801 AAAAAAGAGGCCACTTCCCGAGGTAACAACAGTTTCAGACCTCACAAGAGAAAACAATGGACTTTTCCATCCGCATCAGTAGCATCACCCAGCAGA

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

SandI (744)
AseI (786)

901 TGTCGGCACATACTACTGTGTAAGTTTCGAAAAGGGAGCCCTGAGAAGCTGGAGTTTAAAGTCTGGACCAGGCACTGAGATGGCTTTGGGTGCCAAACC

113▶ V G T Y Y C V K F R K G S P E N V E F K S G P G T E M A L G A K P

1001 TCTGCCCCGTGGTATTGGCCCTGCGGCGAGGACCACACCTGAGCATACAGTGAAGTTTACCTGTGAGTCCCATGGCTTCTCTCCAGAGACATCACCC

147▶ S A P V V L G P A A R T T P E H T V S F T C E S H G F S P R D I T

XmnI (1101)
NcoI (1071)
XcmI (1193)

1101 TGAAATGGTTCAAAAATGGGAATGAGCTCTCAGACTTCCAGACCAACCTGGACCCACAGGACAGAGTGTGGCCTACAGCATCCCGAGCACAGCCAGGGT

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

1201 GGTACTGGACCCCTGGGACGTTTCGCTCTCAGGTCATCTGCGAGGTGGCCATGTACCTTGCAGGGGGACCCCTTCTGTTGGGACTGCCAACTTGTCTGAG

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

1301 GCCATCCGAGTTCACCCACCTTGGAGGTTACTCAACAGCCCATGAGGGCGGGGAACAGGTAACAGTCACTGCCAGGTGAGGAAGTTCTACCCCCAGA

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

Asp718I (1477)
Acc65I (1477)

1401 GCCTACAGCTGACCTGGTTGGAGAATGGAACGTGTGCCAGAGAGAAACAGCCTCGACCCTTACAGAGAACAAGGATGGTACCTACAACCTGGACAAGCTG

280▶ S L Q L T W L E N G N V C Q R E T A S T L T E N K D G T Y N W T S W

1501 GTTCTGGTGAACATATCTGACCAAAGGATGATGTGGTCTCACCTGCAGGTGAAGCATGATGGCAGCTGGCGGTGAGCAACGCCTTGGCCTGGAG

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

Bsp120I (1689)

1601 GTCACAGTCCACCAGAAGGACCAGAGCTCAGATGCTACCCCTGGCCCGGCATCATCTTACTGCGCTGCTCCTCATAGCTGTCCCTCTGGGCCCATCT

347▶ V T V H Q K D Q S S D A T P G P A S S L T A L L L I A V L L G P I

MscI (1742)
NheI (1736)

1701 ATGTCCTGGAAGCAGAAGACCTGACTCTCCTCCGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAACCACTAGAATGCAGT

380▶ Y V P W K Q K T •

HpaI (1874)
MfeI (1885)

1801 GAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAATTGCATTCAATT

EcoRI (1970)

1901 TATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAATGTGGTATGGAATCTAAATACAGCATAGCAAACTTT

2001 AACCTCCAATCAAGCCTCTACTTGAATCCTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTTGGCAATGTGCATTAGCTGTTTGCAGCCTC

2101 ACCTTCTTTCATGGAGTTAAGATATAGTATTTTCCCAAGGTTTGAAGTACTCTTCAATTTCTTTATGTTTAAATGCACTGACCTCCACATTCCCT

SspI (2209)
Swal (2223)

2201 TTTTAGTAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATAT

2301 CCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGAACCTTAAATAGAAATGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTACTTGAG

2401 GGGGATGAGTTCTCAATGGTGGTTTTGACCAGCTTGCATTCTCAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGCACATG

134▶ 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 L E R C M

2501 CCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAG

100▶ 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 Q G N S V A

StuI (2648)

2601 CAGACCCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCCTGATGGC
67 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 K T R I A **BspHI (2798)**

XmnI (2790)

2701 CGCCCCGACATGGTGCTTGTTCCTCATAGAGCATGGTGATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTC
34 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 I N F T K

AseI (2856)

2801 ATGATGGCCCTCTATAGTGAGTCGATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACAGCGTGGATGGCGTCTCCAGCTTATCTGA
0 M ←

2901 CGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCACCCTACACGCCTACCGCCATTTGGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGT

SpeI (3011)

3001 CCCGTTGATTTACTAGTCAAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGT

SnaBI (3139)

3100 ACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCA

NdeI (3244)

3200 GCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACC

3300 CATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGCGGGGGTCTGTTGGCGGTCAGCCAGGCGGGC

PstI (3423)
SdaI (3422)**PaeI (3430)**
BspLU11I (3440)

3400 CATTACCCTAAGTTATGTAACGCTG C A G G T T A A T T A A G A A C A T G T G A G C A A A A G G C C A G A A A A G G C C A G A A C C G T A A A A A G G C C G T T G C T G G
←

3498 CGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATACCAGGCGTT

3598 TCCCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCAT

ApaLI (3754)

3698 AGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTAGCCGACCGCTGCGCCTTATCCG

3798 GTAACATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGC

3898 TACAGAGTCTTGAAGTGGTGGCCTAACACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGGTT

3998 GGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATC

EagI (4190)

PaeI (4170) SwaI (4179) **NotI (4189)**

4098 CTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCGC

4198 AATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAAACAAAACGAAAACAAAACAAC

4298 TAGCAAAATAGGCTGTCCCAAGTGCAGGTGCCAGAACATTTCTATCGAA