



PvuI (7)
SgfI (6) **MfeI (82)**
1 GGATCTGCATCGCTCCGGTGCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
101 GAGAAAGTGGCGCGGGTAAACTGGAAAAGTATGTCGTGACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203)
HindIII (245)
Bsu36I (291)
201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACGCGCCGCCCTACCTGAGGCC
301 GCCATCCACGCCGGTTGAGTCGCGTTTCTGCCGCTCCCGCTGTGGTGCTCCTGAACTGCGTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

BstEII (555)
BssHII (567)
AgeI (552)
NcoI (560)
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCTACCTGAGATCACCGGTACCATGGAGCGCGCTCTGCTTGTGCTGCTGCTGCTGCC
601 GCTGGTGCACGTCTCTGCGACCACGCCAGAACCTTGAGCTGGACGATGAAGATTTCCGCTCGCTGCAACTTCTCGAACCTCAGCCCGACTGGTCC
13▶ L V H V S A T T P E P C E L D D E D F R C V C N F S E P Q P D W S

NgoMIV (742)
SacII (796)
701 GAAGCCTTCCAGTGTGTCTGCGAGTAGAGGTGGAGATCCATGCGCGGCTCAACCTAGAGCCGTTTCTAAAGCGCTCGATGCGGACGCCGACCCGC
47▶ E A F Q C V S A V E V E I H A G G L N L E P F L K R V D A D A D P

Tth11I (811)
NheI (897)
801 GGCAGTATGCTGACACGGTCAAGGCTCTCCGCTGCGCGGCTCACAGTGGGAGCCGACAGGTTCTGCTCAGTACTGGTAGGCGCCCTGCGTGTGCT
80▶ R Q Y A D T V K A L R V R R L T V G A A Q V P A Q L L V G A L R V L

XhoI (928)
901 AGCGTACTCCGCTCAAGGAAGTACGCTCGAGGACCTAAAGATAACCGGCACCATGCCTCCGCTGCCTCTGGAAGCCACAGGACTTGCACCTTCCAGC
113▶ A Y S R L K E L T L E D L K I T G T M P P L P L E A T G L A L S S

StuI (1071)
1001 TTGCGCTACGCAACGTGTCGTGGGCGACAGGGGCTTCTGGCTCGCCGAGCTGCAGCAGTGGCTCAAGCCAGGCCTCAAGGTAAGTACTGAGCATTGCCAAG
147▶ L R L R N V S W A T G R S W L A E L Q Q W L K P G L K V L S I A Q
1101 CACACTCGCTGCCTTTTCTGCGAACAGGTTCCGCGCTTCCCGCCCTTACCAGCCTAGACCTGTCTGACAATCCTGGACTGGGCGAACCGGGACTGAT
180▶ A H S P A F S C E Q V R A F P A L T S L D L S D N P G L G E R G L M

FspI (1247)
Eco47III (1242)
1201 GCGGCTCTGTGCCCCACAAGTCCCGGCCATCCAGAATCTAGCGTGCACAAACACAGGAATGGAGACGCCACAGGCGTGTGCGCCGACTGGCGGGC
213▶ A A L C P H K F P A I Q N L A L R N T G M E T P T G V C A A L A A

BssHII (1344)
Eco47III (1363)
NsiI (1374)
1301 GCAGGTGTGAGCCCCACAGCCTAGACCTCAGCCACAACCTCGTGCAGCCACCGTAAACCTAGCGCTCCGAGATGCATGTGGTCCAGCGCCCTGAACT
247▶ A G V Q P H S L D L S H N S L R A T V N P S A P R C M W S S A L N

PvuII (1473)
1401 CCCTAATCTGCTGTTGCTGGGCTGGAACAGGTGCCTAAAGGACTGCCAGCCAAAGCTCAGAGTGTCTGATCTCAGTGCACAGACTGAACAGGGCGCC
280▶ S L N L S F A G L E Q V P K G L P A K L R V L D L S C N R L N R A P
1501 GCAGCCTGACGAGTCCCGAGTGGATAACCTGACACTGGACGGGAATCCCTTCTGGTCCCTGGAAGTGCCTCCCCACAGGGCTCAATGAACTCC
313▶ Q P D E L P E V D N L T L D G N P F L V P G T A L P H E G S M N S

Tth11I (1626)
XmaI (1673)
NheI (1694)
Bsp120I (1670)
EcoRI (1688)
1601 GCGTGGTCCCAGCCTGTGACGTTCCGACCCTGTCGGTGGGGTGTGCGGAACCTGGTGTCTCCTCAAGGGGCCCCGGGCTTTGCTGAATTCGCTAGC
347▶ G V V P A C A R S T L S V G V S G T L V L L Q G A R G F A •
1701 TCGACATGATAAGATACATTGATGAGTTGGACAAACCACAACCTAGAATGCAGTGAAAAAATGCTTTATTGTGAAATTTGTGATGCTATTGCTTTATT

HpaI (1828)
MfeI (1839)
1801 TGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAACATTGCATTCAATTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGTTTTTAAAGCAAG

EcoRI (1924)
1901 TAAACCTCTACAAATGTGGTATGGAATCTAAATACAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAA
2001 TAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTTTGCAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGTATTTTCCAAGGTTT

SapI (2106)
SspI (2163)
Swal (2177)
2101 GAACTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTTAGTAAAATATTCAGAAATAATTTAAATACATCATTGCAATGA
2201 AAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTGTAGTGGACTTAGGGAACAAGGAACCTTTAATA
2301 GAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTTCATC

141 • N R T Y K L P I L E E I T T K V L K G N M

2401 TCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGT
 118 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 I S R D V E D S Y
 2501 AGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCCTTCTGCCCGTTGCTCACAGCAGACCCAAATGGCAATGGCTTACGACAGACAGTACCCTGCCAAT
 85 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 A C V T V R G I
 SacI (2438) BstXI (2467)
 2601 GTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCTGATGGCCGCCCGACATGGTGTGTTGTCTCATAGAGCATGGTGTCTTC
 52 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 D E Y L M T I K
 StuI (2602)
 2701 TCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATAC
 18 E T A V E V L E L D Q Q S I N F T K M
 BbsI (2748)
 2801 TATGCCGATGATTAATTGTCAAACACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACAC
 AseI (2810) SacI (2867)
 2901 GCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCCATGACGTCAATGGG
 SpeI (2965)
 3001 GTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAG
 SnaBI (3093)
 3101 ATGTACTGCCAAGTAGGAAAGTCCATAAAGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCA
 NdeI (3198)
 3201 TATGATACTTGTACTGCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATA
 PacI (3384)
 3301 CGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAATTAAGAACATGT
 SdaI (3376) BspLU11I (3394)
 3401 GAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCGTTTTTCCATAGGCTCCGCCCTGACGAGCATCACAAAATCGACG
 3501 CTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCCTGCCGCTT
 3601 ACCGATACCTGTCCGCTTTTCTCCCTCGGGAAGCGTGGCGTTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTGCTTCCGCTCAAGC
 3701 TGGGCTGTGTGCACGAACCCCGTTACGCCCACCGCTGCGCCTTATCCGGTAACTATCGTCTTGTAGTCCAACCCGTAAGACACGACTTATCGCCACT
 3801 GGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACA
 3901 GTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGTCCGCAACAAACCACCGCTGGTAGCGTGGTTTTT
 4001 TTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACG
 EagI (4144)
 4101 TTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGAATAAAATATCTTTATTTTATTACATCTGTGTGTTGGTTTTTGTGTG
 PacI (4124) SmaI (4133) NotI (4143)
 4201 AATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCAGTGCAAGTGCAGGTGCCAGAACATTTCT
 4301 CTATCGAA