



PvuI (7)
SgfI (6) 1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA **MfeI (82)**
101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)
Psp1406I (203) 201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACAGCGCCCGCCGCCCTACCTGAGGCC
PvuII (239)
Bsu36I (291)
301 GCCATCCACGCGGTTGAGTCGCGTTCTGCCGCTCCCGCCTGTGGTGCCTCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
NaeI (441) 401 GGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTCTCAACTCTACGTCTTTGTTTCGTTT

NcoI (560)
BstEII (555)
KasI (535) 501 TCTGTTCTGCGCGGTTACAGATCCAAGCTGTGACCGCGGCTACCTGAGATCACCGGTACCATTGGGTAAGGAGACCCCAACAAGCCGGGGCAAAT
AgeI (552) 1▶ M G K G D P N K P R G K M
SacII (586)

BsiWI (605) 601 GTCCTCGTACGCCTTCTTCTGTCAGACCTGCCGGAAGAGCACAAGAAGAAACACCCGGACTTCTCCGTCAATTTCCGCGGAATTTCCCAAGAAGTGTTCG
13▶ S S Y A F F V Q T C R E E H K K K H P D S S V N F A E F S K K C S
EcoRI (679)
Tth111I (711)
BbsI (708) 701 GAGAGATGGAAGACCATGCTGCAAAGGAGAAGTGAAGTTTGAAGATATGGCAAAAAGTGACAAAGCTCGCTATGACAGGGAGATGAAAAATTACGTTT
47▶ E R W K T M S A K E K S K F E D M A K S D K A R Y D R E M K N Y V
801 CTCCAAAGGTGATAAGAAGGGGAAAGAAAGGACCCCAATGCTCCTAAAAGGCCACCATCTGCCTTCTTCTGTTTTGCTCTGAACATCGCCCAAAGAT
80▶ P P K G D K K G K K K D P N A P K R P P S A F F L F C S E H R P K I

NdeI (989) 901 CAAAAGTGAACACCTGGCCTATCCATTGGGATACTGCAAAGAAATTGGGTAAATGTGGTCTGAGCAGTCAGCCAAAGATAAACAACCATATGAACAG
113▶ K S E H P G L S I G D T A K K L G E M W S E Q S A K D K Q P Y E Q
Bsp120I (1080)
1001 AAAGCAGCTAAGCTAAAGGAGAAATATGAAAAGGATATTGCTGCATATCGTGCCAAGGGCAAAAGTGAAGCAGGAAAGAGGGCCCTGGCAGGCCAACAG
147▶ K A A K L K E K Y E K D I A A Y R A K G K S E A G K K G P G R P T
1101 GCTCAAAGAAAGAACGAACAGAGAAGATGAGGAGGAGGAGGAGGAAGAAGAAGATGAAGATGAGGAGGAAGAGGATGAAGATGAAGAATAAATGGCTAT
180▶ G S K K K N E P E D E E E E E E D E D E E E D E D E E •

MscI (1232)
NheI (1226) 1201 CCTTAATGATGCGTGTGAATGTGTGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGCAAAACCAACTAGAATGCAGTGAAAAAATG

HpaI (1364) 1301 CTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAATTCATTTCATTTTATGTTTCAG
MfeI (1375)

EcoRI (1460) 1401 GTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCATAAATACAGCATAGCAAACCTTAACTCCTCAA
1501 TCAAGCCTCTACTGAACTCTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTGCAATGTGCATTAGCTGTTTGCAGCCTCACCTCTTTC

SspI (1699) 1601 ATGGAGTTAAGATATAGTGTATTTTCCAAGGTTTGAAGTACCTCTTCAATTTCTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTAGTAAA

Swal (1713) 1701 ATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTT
1801 AGTAGTTGGAAGTACAGGAAACAAAGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGGGGGATGAGT
141▶ • N R T Y K L P I L

SacI (1974) 1901 TCCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGC
130▶ 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 G C P S
BstXI (2003) 2001 TGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAAT
97▶ 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 S G I

StuI (2138) 2101 GGCAATGGCTTCAGCACAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCAGTCTTGGTCTGATGGCCGCCCGACA
64▶ 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 A G V
BspHI (2288)
BbsI (2284)
XmnI (2280) 2201 TGGTGCTTGTGCTCATAGAGCATGGTATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGCTTTCATGATGGCCC
30▶ 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 M

AseI (2346) 2301 TCCTATAGTGAAGTCTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTATCTGACGGTTCACTA

2401 SacI (2403) AACGAGCTCTGCTTATATAGACCTCCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATT

2501 SpeI (2501) TACTAGTCAAAACAAACTCCATTGACGTCAATGGGGTGGAGACTTGGAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTIONGCAAAA

2600 SnaBI (2629) CCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAAGTCATGTACTGGGCATAATGCCAGGCGGGCCAT

2700 NdeI (2734) TTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTC

2800 AATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGGCGGGTTCGTTGGCGGTCAGCCAGGCGGGCCATTACCGT

2900 PstI (2913) SdaI (2912) PacI (2920) BspLU11I (2930) AAGTTATGTAACGCTGCAGGTTAA TTAAGAACATGTGAGCAAAAGGCCAGGAACCGTAAAAAGCCGCTTGCTGGCGTTTTTCCA

2998 TAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATACCAGGCGTTTCCCCTGGA

3098 AGCTCCCTCGTGGCTCTCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCAGCT

3198 ApaLI (3244) GTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCAAGCTGGGCTGTGTGCACGAACCCCGTTCCAGCCGACCGCTGCGCCTTATCCGGTAACTATCG

3298 TCTTGAGTCCAACCCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGCTACAGAGTTC

3398 TTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGATTGGTAGCTCTT

3498 GATCCGGCAAACAAACCAGCTGGTAGCGGTGGTTTTTTTGTGTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTT

3598 PacI (3660) SwaI (3669) EagI (3680) NotI (3679) TTCTACGGGTCTGACGCTCAGTGAACGAAACTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCCAATAAATAT

3698 CTTTATTTTATTACATCTGTGTGTTGGTTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAAACAAAACGAAACAAAACAACTAGCAAAATA

3798 GGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA