



PvuI (7)
SgfI (6) 1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
MfeI (82)
101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGTCTGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)
Psp1406I (203) 201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACCGCGCCGCCCTACCTGAGGCC
PvuII (239)
Bsu36I (291)
301 GCCATCCACGCCGTTGAGTCGCGTTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAACTGCGTCCCGCTTAGGTAAGTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCTGCTTCTCAACTCTACGCTTTTGTTCGTTT

AgeI (552) **BspHI (560)**
501 TCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGGCGCTACCTGAGATCACCGGTATCATGACCATGACACTGAGACACTGCTGGACAGCAGGCCCCAGTTC
1▶ M T M R H C W T A G P S S

XcmI (697)
601 TTGGTGGTCTGCTTTTGTATGTCCATGTCATTTGGCCAGAGCCACATCTGCACCTCAGACAACTGCCACTGTCTTAACTGGAAGCTCAAAGACCCA
13▶ W W V L L L Y V H V I L A R A T S A P Q T T A T V L T G S S K D P
SapI (701) **Tth111I (792)**
701 TGCTCTTCTGGTCTCCAGCAGTCCCAACTAAGCAGTACCCAGCACTGGATGTGATTTGGCCAGAAAAGAAGTGCCACTGAATGGAAGTCTGACCTTGT
47▶ C S S W S P A V P T K Q Y P A L D V I W P E K E V P L N G T L T L

PstI (810) **NgoMIV (881)**
801 CCTGTACTGCCTGCAGCCGTTCCCTACTTCAGCATCTCTACTGGTGGGCAATGGTTCCTTCATTGAGCACCTTCCAGGCCGGCTGAAGGAGGGCCA
80▶ S C T A C S R F P Y F S I L Y W L G N G S F I E H L P G R L K E G H

NruI (906)
901 CACAAGTCGCGAGCACAGGAACACAAGCACCTGGTGCACAGGCGCTTGGTGTGGAAGAAGTGAAGCCACCCCTACGAAGTACCAACTTCTCCTGTTTG
113▶ T S R E H R N T S T W L H R A L V L E E L S P T L R S T N F S C L

BamHI (1005) **XcmI (1044)** **BbsI (1062)**
1001 TTTGTGGATCCTGGACAAGTGGCCAGTATCACATCATTCTGGCCAGCTCTGGGATGGTGAAGACAGCTCCGTCCTTCTCAAGAAACCTCTCTA
147▶ F V D P G Q V A Q Y H I I L A Q L W D G L K T A P S P S Q E T L S

NheI (1159)
1101 GCCACAGCCAGTATCCAGATCAGCAGGCCAGGGTTGCATAAAGCCAACCACCATGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTGG
180▶ S H S P V S R S A G P G V A •

HpaI (1297)
1201 ACAAACCACAAC TAGAATGCAGTGA AAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGTGAATAAACAAGTT

MfeI (1308) **EcoRI (1393)**
1301 AACAAACA AATTGCATTCATTTATGTTTCAGGTT CAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATCT
1401 AAAATACAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTACTGAATCCTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAAT

SapI (1575)
1501 GTGCATTAGCTGTTTGCAGCCTCACCTCTTTCATGGAGTTTAAAGATAGTGTATTTCCCAAGTTTGAAGTACTCTTTCATTTCTTTATGTTTTAAA

SspI (1632) **SwaI (1646)**
1601 TGCACTGACCTCCACATTCCCTTTTTAGTAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAG
1701 ATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAG

1801 CTTTAGTTCCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAAGCAGTCAGGAGCATAGT
141▶ • 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

SacI (1907) **BstXI (1936)**
1901 CAGAGATGAGCTCTGCACATGCCACAGGGGTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAA
108▶ S 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

StuI (2071)
2001 GTCCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATC
75▶ D 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
2101 TCCCCAGTCTTGGTCTGATGGCCGCCCGACATGGTCTTGTGTCCTCATAGAGCATGGTGTCTTCTCAGTGGCGACCTCCACAGCTCCAGATCCT
41▶ E 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

BbsI (2217)
2201 GCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCTATAGTGTGATGATTATACTATGCGGATATACTATGCGGATGATTAATTGTCAAACACGCGTG
8▶ Q S I N F T K M

XmnI (2213) **AseI (2279)**
2301 GATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGA

SacI (2336)

2401 GTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAACAAACTCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAAC
SpeI (2434)

2501 CGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGG
SnaBI (2562)

2601 TCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGTACTGCCAAGTGGGC
NdeI (2667)

2701 AGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGTCAATGGGCGGGGTCG

2801 TTGGGCGGTCAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCTGCAGGTTAATAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCG
PacI (2853)
PstI (2846)
SdaI (2845) BspLU11I (2863)

2901 TAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGA

3001 CTATAAGATAACCAGGCGTTTCCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCGACCCTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGG

3101 GAAGCGTGGCGCTTTTCCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTTCAGCC
ApaLI (3177)

3201 CGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGA

3301 GCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAG

3401 TTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAACCACCGCTGGTAGCGGTGTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAA

3501 AAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGGAAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTA
PacI (3593)

3601 ACATTTAAATCAGCGGCCGCAATAAAATATCTTTATTTTATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACATAACATACGCTCTCCATCAAAA
EagI (3613)
SwaI (3602) NotI (3612)

3701 CAAAACGAAACAAAACAAACTAGCAAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA