



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

1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
 101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGCTCCGCCTTTTCCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203)
HindIII (245) **Bsu36I (291)**

201 GTGAACGTTCTTTTTTCGCAACGGGTTTGGCCGACAGTGAAGCTTCGAGGGGCTCGCATCTCTCTTACAGCGCCCGCCGCTACCTGAGGGCC
 301 GCCATCCACGCGGTTGAGTGCAGTCTGCCGCTCCCGCCTGTGGTGCCTCCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)

401 GGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

BspHI (560)

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGGCTACCTGAGATCACCGGTCATCATGAAGATCCTCTGCTACTGCTGACCTTGTCTCTGGC
AgeI (552) **Tth111I (585)**

601 CTCCAGGACAAAAGCAGGGGAGATCATCGGGGACATGAAGTCAAGCCCACTCTCGACCCTACATGGCCTTACTTTTCATCAAGGATCAGCAGCCTGAG
 13▶ S R T K A G E I I G G H E V K P H S R P Y M A L L S I K D Q Q P E **Bsu36I (694)**

Bsp120I (785)

701 GCGATATGTGGGGCTTCTTATTTCGAGAGGACTTTGTGCTGACTGCTGCTCACTGTGAAGGAAGTATAATAAATGCACTTTGGGGGCCACAAATCA
 47▶ A I C G G F L I R E D F V L T A A H C E G S I I N V T L G A H N I

BbsI (810)
NsiI (840)

801 AAGAACAGGAGAAGACCCAGCAAGTCATCCCTATGGTAAAATGCATTCACCCAGACTATAATCCTAAGACATTCTCCAATGACATCATGCTGCTAAA
 80▶ K E Q E K T Q Q V I P M V K C I P H P D Y N P K T F S N D I M L L K
 901 GCTGAAGAGTAAGGCCAAGAGGACTAGAGCTGTGAGGCCCTCAACCTGCCAGGCGCAATGTCAATGTGAAGCCAGGAGATGTGTGCTATGTGGCTGGT
 113▶ L K S K A K R T R A V R P L N L P R R N V N V K P G D V K P G D V C Y V A G
 1001 TGGGAAGGATGGCCCAATGGGCAAACTCAAACACGCTACAAGAGTTGAGCTGACAGTACAGAAGGATCGGGAGTGTGAGTCTACTTTAAAAATC
 147▶ W G R M A P M G K Y S N T L Q E V E L T V Q K D R E C E S Y F K N

SandI (1130) **PstI (1199)**

1101 GTTACAACAAAACCAATCAGATATGTGCGGGGGACCCAAAGACCAACGCTTCTCTTTCCGGGGGATTCTGGAGGCCGCTTGTGTGTAATAAAAGTGGC
 180▶ R Y N K T N Q I C A G D P K T K R A S F R G D S G G P L V C K K V A

BbrPI (1241)
XhoI (1260)

1201 TGCAGGCATAGTTTCTATGGATATAAGGATGGTTACCTCCACGTGCTTTCCACAAAGTCTCGAGTTTCTTATCCTGGATAAAGAAAACCAATGAAAAGC
 213▶ A G I V S Y G Y K D G S P P R A F T K V S S F L S W I K K T M K S

NheI (1328)

BamHI (1322) **MscI (1334)**

1301 AGCTAACTACAGAAGCAACATCGGATCCGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAACCACAAGTGAATGCAGTGAATAA
 247▶ S •

HpaI (1466) **MfeI (1477)**

1401 TGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAAGTTAACAAACAACATTGCATTTTATGTTTC

EcoRI (1562)

1501 AGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTTAAAATACAGCATAGCAAACTTTAACCTCCA
 1601 AATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGACGCCTCACCTTCTT

SapI (1744)

1701 TCATGGAGTTTAAGATATAGTGTATTTTCCAAGGTTTGAAGTACTCTTCTATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTATGA

SspI (1801)
SwaI (1815)

1801 AAATATTCAGAAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGT
 1901 TTAGTAGTTGGACTTAGGGAACAAAGAACCTTTAATAGAAATGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTACTTGAGGGGGATGA
141▶ • N R T Y K L P I L

SacI (2076)

2001 GTTCTCAATGGTGGTTTTGACCAGCTTGCATTCAATGAGCACAAGCAGTCAAGGAGCATAGTCAAGATGAGTCTCTGCACATGCCACAGGG
 131▶ 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

BstXI (2105)

2101 GCTGACCAACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCA
 98▶ 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 S G

StuI (2240)

2201 ATGGCAATGGCTTCAACAGACAGTACCTGCAATGTAGGCTCAATGTGGACAGCAGAGATGATCTCCCAGTCTTGGTCTGATGGCCGCCCCGA
 64▶ 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 A G V

BbsI (2386)

XmnI (2382)

2301 CATGGTGCTTGTGCTCATAGAGCATGGTATCTTCTCAGTGGCGACCTCCACAGCTCCAGATCCTGCTGAGAGATGTTGAAGGCTTTCATGGTGGC
 31▶ 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 (2448)

2401 CCTCTATAGTGAAGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCAC

SacI (2505)
 2501 TAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCGTTGA

SpeI (2603)
 2601 TTTACTAGTCAAACAAACTCCCATTGACGTCAATGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTA CTGCCAAA

SnaBI (2731)
 2701 ACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGACTGCCAAGTAGGAAAGTCCCAT AAGGTCATGTACTGGGCATAATGCCAGGCGGGCCA

NdeI (2836)
 2801 TTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGT

2901 CAATGGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGT CAGCCAGGCGGGCCATTACCG

PacI (3022)
 PstI (3015)
 SdaI (3014) BspLU11I (3032)
 3001 TAAGTTATGTAACGCTGCAGGTTAATTAAGAACATGTGAGCAAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCAT

3101 AGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCTGGAA

3201 GCTCCCTCGTGGCTCTCTGTCCGACCTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAGCTCACGCTG

ApaLI (3346)
 3301 TAGGTATCTCAGTTCGGTGTAGGTGCTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTT CAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGT

3401 CTTGAGTCCAACCCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGTACAGAGTTCT

3501 TGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTG

3601 ATCCGGCAAACAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTT

EagI (3782)
 PacI (3762) SmaI (3771) NotI (3781)
 3701 TCTACGGGGTCTGACGCTCAGTGAACGAAAAC TACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCGCAATAAAATATC

3801 TTTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAG

3901 GCTGTCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA