



PvuI (7)
SgfI (6) MfeI (82) EcoNI (96)
1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245) Bsu36I (291)
Psp1406I (203) **PvuII (239)** EcoNI (287)
201 GTGAACGTTCTTTTTTCGCAACGGGTTTGGCCGAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACAGCGCCCGCCCTACCTGAGGCC
301 GCCATCCACGCGGTTGAGTGCAGTTCGCCGCTCCCGCCTGTGGTGCCTCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCGGCTCTCCACGCTTGGCTGACCCTGCTTGTCTAACTCTACGCTTTTGTTCGTTT

BsaBI (570)
BspLU111 (560)
AgeI (552) **BsrGI (563)**
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCGCCTACCTGAGATCACCGGTCAACATGTACAAGATGAACATCTGCAACAAGCCCTCCAACAA
601 GACGCCCCCTGAGAAGAGTGTGTGGACGCCACCGCACAGCCAGCGGACCTCCCTGAGCTGCAGGGCCAGCGATCCCGCGAATGGGTGGAGCTGG
13▶ T A P E K S V W T A P A Q P S G P S P E L Q G Q R S R R N G W S W
701 CCCCCTACCCGCTCCAGATTGTGGCCTGGCTGTACCTCTTCTTGTGTGATCGGCTTTGGGATCCTTGTTCCTCCTGCCTCACCCTGAGGTC
47▶ P P H P L Q I V A W L L Y L F A V I G F G I L V P L L P H H W V
801 CCGCTGGCTACGCTTGCATGGGCGCCATCTTGTGTGGCCACCTGTGGTGCACCTGACCAGCGCTCCATCGATCCAGCAGATGCCAAGTGCAGGACAA
80▶ P A G Y A C M G A I F A G H L V V H L T A V S I D P A D A N V R D K
901 GAGCTATGCGGGGCCCTGCCATCTTCAACCGAAGCCAGCAGCACATGTCAATGAAGACCTGCACTGCAACTGTGCAACGTGGATGTGAGCGCTCGC
113▶ S Y A G P L P I F N R S Q H A H V I E D L H C N L C N V D V S A R
1001 TCCAAGCACTGCAGCGCTGCAACAAGTGCCTGTGGGTTTCGACCACCACTGCAAGTGGCTCAACAAGTGTGGGGGAGCGGAACTACCGGCTCTTC
147▶ S K H C S A C N K C V C G F D H H C K W L N N C V G E R N Y R L F

Eco47III (991)
1101 TACACAGTGTTCATCCGCTTTACTGGCGTCTGCTCCTGGTGTGGTGCACATATGCTTCTGAGGATTTTGTCAACCCCATGCGTCTGCAC
180▶ L H S V A S A L L G V L L L V L V A T Y V F V E F F V N P M R L R T
1201 CAACCGACTTTGAAGTCTGAAGAATCACACGGATGTGTGGTTCGTGTTCTGCTGCGCCCGCTGGAGACCCAGGCCCTGCCATCCTGGCCCTG
213▶ N R H F E V L K N H T D V W F V F L P A A P V E T Q A P A I L A L
1301 GCCGCCCTGCTATCCTTCTGGGCTCCTGTCCACAGCCCTCCTGGGACCTGCTGCTTCCACATTTATCTCATGTGGCACAAGCTCACCACCTATG
247▶ A A L L I L L G L L S T A L L G H L C F H I Y L M W H K L T T Y

XhoI (1453)
1401 AGTACATCGTGCAGCACCAGCCACAGGAGGCAAGGGGTTACAGGGAGCTCGAGTTCATGCTCCTCCAAGATGCGGCCATTACAGGAGATGGAGTT
280▶ E Y I V Q H R P P Q E A K G V H R E L E S C P P K M R P I Q E M E F
1501 CTACATCGGACCTTCAGACATATGCGCCAGAGCCCTGGCCAGCGGGCCAGCAGCAGTGAATGCCAAACTCTCGCCTGCCTCCCGGATCCG
313▶ Y M R T F R H M R P E P P G Q A G P A A V N A K H S R P A S P D P
1601 ACCCAGGTAGGAGGACTGTGCTGGGCTCCGGTCCAGTGGAGTGGGATAGAAAGAAGCTTACCCTGGCGCTCGCTCTGCTTCTTTGGCGATGT
347▶ T P G R R D C A G P P V Q V E W D R K K P L P W R S P L L L L A M

Bsu36I (1705) **AvrII (1794)**
1701 GGGGCCCTCAGGCTCCCGTGTCTCTGCAGAAAAAGAGAAGAGGCGGTGTATAAAGTGCAGACCTGAGACCTCGGATCCGGCGTGGGGCCTAGG
380▶ W G P Q A P P C L C R K R G R G A C I K C E R L R P R I R R R G L G

SalI (1823) **SacII (1834)** **NgoMIV (1869)**
1801 GCCCCAGCCGCTCCAGCTCGTGCAGCGATTCCGCGGACGCCAGCCCTGTGCAGCGCTGGCCCTGCCGGCGCCTACCCTCGGCGTGGCAGAGT
413▶ P P A A A P A R R R I P R T P A L C T P L A L P A P T T R R R Q S
1901 CCGTGACGAGATTCAGTGGCGCAGCGCCTGGGACGCGCTCTGGCCCGCCGGGGCCGGGCGGACAGCCAGCTGGCGGGCAGGCGCG
447▶ P W T R F Q W R R R A W A A P L W P P R G A G A D S P R W R G R R

NheI (2029)
2001 TGCGCCCGCTTTTCTGAGCCGAGCCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTGGACAAACCACAAGTGAATGCAGTAAAAAA
480▶ V R P P F S •

HpaI (2167) MfeI (2178)
2101 ATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAATTGCATTCATTTATGTTT

EcoRI (2263)
2201 CAGGTTCAAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACCTTAACTCC
2301 AAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCT

SapI (2445)
2401 TTCATGGAGTTTAAAGATATAGTGTATTTTCCCAAGTTTGAAGTACCTCTTCAATTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTATG

SspI (2502) **SwaI (2516)**
2501 AAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAATAAATGTTTTTATTAGCGAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAG
2601 TTTAGTAGTTGACTTAGGGAACAAAGGAACCTTAAATAGAAATGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTACTTGGGGGATG
141▶ • N R T Y K L P I

2701 AGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGG
131 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 G C P
BstXI (2806)
2801 GGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCCGTTGCTCACAGCAGACCC
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 (2941)
2901 AATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCAGTCTTGGTCTGATGGCCGCCCG
65 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
XmnI (3083)
3001 ACATGGTGTCTTGTGTCCTCATAGAGCATGGTGTCTTCTCAGTGGGACCTCCACCAGTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGGTGG
31 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 M
AseI (3149)
3101 CCCTCTATAGTGTGCTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCA
3201 CTAACGAGCTCTGCTTATATAGACCTCCACCCTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCGTTG
SpeI (3304)
3301 ATTTACTAGTCAAACAACAACTCCCACTGACGTCAATGGGGTGGAGACTTGAAATCCCGTGAGTCAAACCGCTATCCACGCCCACTGATGTACTGCCAA
SnaBI (3432)
3401 AACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCC
3501 ATTTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGATGACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACG
3601 TCAATGAAAAGTCCCTATTGGCGTACTATGGGAACATACGTCATTATTGACGTCAATGGGGCGGGGTCTGTTGGCGGTGAGCCAGGCGGGCCATTTACC
PacI (3723)
SdaI (3715) BspLUII (3733)
3701 GTAAGTTATGTAACGCTGCAGGTTAATTAAGAACATGTGAGCAAAAGCCAGCAAAAGGCCAGAAACCGTAAAAAGCCGCGTTGCTGGCGTTTTTCCA
3801 TAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCTGGA
3901 AGCTCCCTCGTGCCTCTCTGTCCGACCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGTTTTCTCATAGCTCAGCT
4001 GTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCAAGCTGGGCTGTGTGACGAACCCCGTTCCAGCCGACCGCTGCGCCTTATCCGGTAACTATCG
4101 TCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTC
4201 TTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTT
4301 GATCCGGCAAACAACACCCTGCTGAGCGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTT
EagI (4483)
PacI (4463) SmaI (4472) NotI (4482)
4401 TTCTACGGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAATAT
4501 CTTTATTTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAAACAAAACGAAAACAAAACAACTAGCAAATA
4601 GGCTGTCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA