



PvuI (7)
SgfI (6) **EcoNI (96)**
1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGCAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTCGGCAATTGAACGGGTGCCTA
101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGCTCCGCCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203) **HindIII (245)** **Bsu36I (291)**
201 GTGAACGTTCTTTTTTCGCAACGGGTTTGGCCGACAGTGAAGCTTCAGAGGGCTCGCATCTCTCTTACAGCGCCCGCCGCTACCTGAGGCC
301 GCCATCCACGCGGTTGAGTGCCTTCTGCCGCTCCCGCCTGTGGTGCCTCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441) **NaeI (441)**
401 GGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCAACTCTACGTCTTTGTTTCGTTT

NcoI (560) **BstEII (555)**
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCCTACCTGAGATCACCGGTACCATTGGAGTCAGTTATGTCCAAGTATGAAAACAGATTCT
601 TATTTTCCCTGACTACCTGGAAGAATCCCGGATACAGATGAGCTGGTATGGATTCTGGGAAGCAGCACCCCTTAAGACAGAAAACTAAGCTGTG
13▶ I F P D Y L E E F P D T D E L V W I L G K Q H P L K T E K S K L L

EcoO109I (762)
701 TCTGATATAAGTGCCTGCTATGGTTACATACAGAAGGAAGTTTTCCCGATTGGGGGAAACAGGCCCTCATCTGATGCTGGATGGGATGTATGCTGC
47▶ S D I S A R L W F T Y R R K F S P I G G T G P S S D A G W G C M L
801 GCTGTGGGAGATGATGCTGGCTCAAGCCCTCATCTGCAGACACTTGGGAAGGATTGGAAGTGGGAGAGACAAAAAGAACACCCAAAGAATACCAAG
80▶ R C G Q M M L A Q A L I C R H L G R D W N W E R Q K E Q P K E Y Q R
901 GATACTGCAGTGTTCCTAGATAGAAAAGACTGTTGCTATTCAATCCATCAGATGGCACAATGGGTGTAGGAGAAGGAAATCAATTGGCGAATGGTTT
113▶ I L Q C F L D R K D C C Y S I H Q M A Q M G V G E G K S I G E W F

NcoI (1076)
1001 GGACCAACACAGTTGCACAGGTGATAAAAAACTCGCTTATTTGATGAATGGAATTCCTTGGCTGTTTATGTTTCCATGGATAACACAGTGGTCATTG
147▶ G P N T V A Q V I K K L A L F D E W N S L A V Y V S M D N T V V I

EcoRV (1102) **PvuII (1148)**
1101 AAGATATCAAGAAAATGCTGTGTTCTTCTGTGGTGTGCTGACCCAGCTGGTGATTTTCTGACTGCATCCAATCAGAGTAGAGACCTCTGTCCC
180▶ E D I K K M C C V L P V G A A D P A G D F L T A S N Q S R D T S V P
1201 GTGCTCAGCTGAAACCCCTGCTGCTATTGTGCCCTTCGCTGGGATAAACCAATCAATCCTGTGTATGTTGAAGCATTCAAAGAGTGTTTAAG
213▶ C S A W K P L L L I V P L R L G I N Q I N P V Y V E A F K E C F K
1301 ATGCCACAGTCTTTAGGGGCTTTAGGAGGAAAGCAATAACGCCTATTATTTTATAGGATTCCTAGGAGATGAGCTCATTTTTTGGACCCTCACAAA
247▶ M P Q S L G A L G G K P N N A Y Y F I G F L G D E L I F L D P H T

SpeI (1431) **BsaBI (1476)** **BamHI (1494)**
1401 CCCAGACTTTTGTGACATTGAAGAGAGTGGACTAGTAGACGACCAGACTTTTTCATTGCTGCAGTCTCCACAGCGGATGAGTATCCTGAACCTGGATCC
280▶ T Q T F V D I E E S G L V D D Q T F H C L Q S P Q R M S I L N L D P
1501 TTCTGTGGCCTTGGGATTTTTCTGCAAGAAGAGAAAGACTTTGATAATTGGTGTAGCCTTGTTCAGAAGGAAATCTAAAGGAGAATTTGAGGATGTT
313▶ S V A L G F F C K E E K D F D N W C S L V Q K E I L K E N L R M F

XmnI (1600) **BstXI (1618)** **SaII (1689)**
1601 GAATTGGTTCAGAAGCACCCATCACACTGGCCTCCCTTTGTACCTCCAGCCAAGCCAGAAGTGACAACCACAGGGGCAGAATTCATAGAGTCTGACTGAAC
347▶ E L V Q K H P S H W P P F V P P A K P E V T T T G A E F I E S T E

MscI (1777) **NheI (1771)**
1701 AACTGGAGACTTTGAGCTGGAGGAAGATTTTGAATTCTGAGTGTAGCTAGTTAGAATCAGTGGTGGCTAGCTGGCCAGACATGATAAGATACAT
380▶ Q L E D F E L E E D F E I L S V G •
1801 TGATGAGTTTGGACAAACCAACTAGAATGCAGTGAATAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGC

HpaI (1909)
1901 AATAACAAGTTAAACAACAATTCATTCTTTTATGTTTCAGGTTTCAAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTTACAAATGTG
2001 GTATGGAATCTAAAATACAGCATAGCAAACTTAACTCCAATCAAGCCTTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGG
2101 GCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTCTTTCATGGAGTTAAGATATAGTGATTTTCCCAAGGTTTGAAGTGCCTTCTCATTCT

SspI (2244) **Swal (2258)**
2201 TTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTTAGTAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTA

EcoO109I (2319)
2301 GGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTGTGACTTAGGGAACAAAGAACCTTTAATAGAAATGGACAGCAAGAAA
2401 GCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAAGCAGT
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

BstXI (2548)
2501 CAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCAC
112▶ 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 P H R V A V

StuI (2683)
2601 AATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCAGCACAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACA
79▶ 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 Y A E I H V

2701 GCAGAGATGATCTCCCAGTCTTGGTCCTGATGGCCGCCCGACATGGTGCTTGTTCCTCATAGAGCATGGTGATCTTCTCAGTGGCGACCTCCACCA
45 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 E T A V E V L

BspHI (2833)

XmnI (2825) **BbsI (2829)** AseI (2891)

2801 GCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGATGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGT
12 E L D Q Q S I N F T K M

2901 CAAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGT

SpeI (3046)

3001 CAATGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCCTTGATTTACTAGTCAAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGAAATCC

SnaBI (3174)

3100 CCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGA

NdeI (3279)

3200 AAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTA

3300 CTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCATTATTGACGTCAA

SdaI (3457) **PacI (3465)** **BspLU11I (3475)**

3400 TGGGCGGGGTCGTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCTGCAGGTTAA TTAAGAACATGTGAGCAAAAGGCCAGCA

3498 AAAGGCCAGGAACCGTAAAAAGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGG

3598 CGAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCG

ApaLI (3789)

3698 CCTTTCTCCCTTCGGAAGCGTGGCGCTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTGCTCCAAGCTGGGCTGTGTGCACGA

3798 ACCCCCGTTCAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGT

3898 AACAGATTAGCAGAGCGAGGTATGTAGCGGTGTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCG

3998 CTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGTTTTTTGTTTGAAGCAGCA

4098 GATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTC

EagI (4225)

PacI (4205) SmaI (4214) **NotI (4224)**

4198 ATGGCTAGTTAATTAACATTTAAATC AGCGGCCGCAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGTTTTTTGTGTAATCGTAACTAACATA

4298 CGCTCTCCATCAAACAAACGAAACAAACAAACTAGCAAAATAGGCTGTCCCAGTGCAAGTGACAGGTGCCAGAACATTTCTCTATCGAA