



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

1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
 101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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

201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACAGCGCCCGCCGCCCTACCTGAGGCC
 301 GCCATCCACGCGGTTGAGTGCAGTTCGCCGCTCCCGCCTGTGGTGCCTCCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441) **NaeI (441)**

401 GGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCAACTCTACGTCTTTGTTTCGTTT

BstEII (555) **AgeI (552)** **Bsp120I**

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCCCTACCTGAGATCACCGGTACCATGTATAACATGATGGAGACGGAGCTGAAGCCGCCGGG
1▶ M Y N M M E T E L K P P G

HindIII (608)
RsrII (680)

601 CCCGAGCAAGCTTCGGGGGCGGCGGCGGAGGAGCAACGCCACGGCGCGGCGACCGGCGGCAACCAGAAGAACAGCCCGACCGCGTCAAGAGGCC
 13▶ P Q Q A S G G G G G G G N A T A A A T G G N Q K N S P D R V K R P

XmnI (702) **XmaI (722)**

701 ATGAACGCTTCATGGTATGGTCCCGGGGCGAGCGGCTAAGATGGCCAGGAGAACCCTAAGATGCACAACCTCGGAGATCAGCAAGCGCTGGGCGCGG
 47▶ M N A F M V W S R G Q R R K M A Q E N P K M H N S E I S K R L G A

BssHII (858)

801 AGTGGAACTTTTGTCCGAGACCGAGAAGCGCGGCTTCATCGACGAGGCCAAGCGGCTGCGCGCTCTGCACATGAAGGAGCACCCGGATTATAAATACCG
 80▶ E W K L L S E T E K R P F I D E A K R L R A L H M K E H P D Y K Y R

SacII (901) **BspHI (923)**
BsrBI (987)

901 GCCGCGCGGAAAACCAAGACGCTCATGAAGAAGATAAGTACACGCTTCCCGGAGGCTTGTGGCCCGGCGGGAACAGCATGGCGAGCGGGTTGGG
 113▶ P R R K T K T L M K K D K Y T L P G G L L A P G G N S M A S G V G

NgoMIV (1006) **NaeI (1006)**
PvuII (1096)

1001 GTGGCGCGCGCTGGGTGCGGGCGTGAACAGCGCATGGACAGTACGGCGACATGAACGGCTGGAGCAACGGCAGCTACAGCATGATGCAGGAGCAGC
 147▶ V G A G L G A G V N Q R M D S Y A H M N G W S N G S Y S M M Q E Q

XmaI (1116)
PstI (1180)

1101 TGGGTACCCGACGACCCCGGCTCAACGCTACGGCGCGGCACAGATGCAACCGATGACCGCTACGACGTGAGCGCCCTGCAGTACAACCTCCATGAC
 180▶ L G Y P Q H P G L N A H G A A Q M Q P M H R Y D V S A L Q Y N S M T

NcoI (1283) **XcmI (1283)**

1201 CAGCTCGACACCTACATGAACGGCTCGCCACCTACAGCATGTCTACTCGACGAGGGCACCCCGGTATGGCGCTGGGCTCCATGGGCTCTGTGGTC
 213▶ S S Q T Y M N G S P T Y S M S Y S Q Q G T P G M A L G S M G S V V

XcmI (1316) **BstEII (1329)**
EcoO109I (1370)

1301 AAGTCCGAGGCCAGCTCCAGCCCCCGTGGTTACCTTCTCTCCACTCCAGGGCGCCTGCCAGGCCGGGGACCTCCGGGACATGATCAGCATGTACC
 247▶ K S E A S S S P P V V T S S S H S R A P C Q A G D L R D M I S M Y

BsrBI (1464)

1401 TCCCCGGCGCGAGGTGCCGGAGCCGCTGCGCCAGTAGACTGCACATGGCCAGCACTACCAGAGCGCCCGGTGCCCGGCACGGCCATTAACGGCAC
 280▶ L P G A E V P E P A A P S R L H M A Q H Y Q S G P V P G T A I N G T

BspEI (1522)
Tth111I (1547) **BamHI (1579)** **MscI (1594)**

1501 ACTGCCCTGTGCGACATGAGTCCGGAGGGGTGGCTCTCTGGCAGACGTCGTGCGCCGAGACGAGGCGCCCGCGGATCCTGAGCTAGCTGGCCA
 313▶ L P L S H M E S G G G G S P G R R R R R R R R R R R R G S •

1601 GACATGATAAGATACATTGATGAGTTTGACAAACCAACTAGAATGCAGTGAATAAATGCTTTATTTGTGAATTTGTGATGCTATTGCTTTATTTG

HpaI (1726) **MfeI (1737)**

1701 TAACCATTATAAGCTGCAATAAACAAGTAAACAACAACATTGCATTCTTTATGTTTCAGGTTTCAGGGGAGGTGGGAGGTTTTTAAAGCAAGTA

EcoRI (1822)

1801 AAACCTCTACAAATGTGGTATGGAATTCATAAATACAGCATAGCAAACCTTTAACCTCCAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATA
 1901 AGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGACGCTCACCTTCTTTCATGGAGTTAAGATATAGTGTATTTCCAAGTGTGA

SspI (2061) **SwaI (2075)**

2001 ACTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTATGTAATAATTCAGAAATAATTTAAATACATCATTGCAATGAAA

EcoO109I (2136)

2101 ATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGACTTAGGGAACAAAGGAACCTTTAATAGA

SacI (2336) **BstXI (2365)**

2201 AATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTCATCTC
141▶ • N R T Y K L P I L E E I T T K V L K G N M E

2301 AATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAG
 118▶ I L V F C D 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

2401 GGGTGCCTGACAGCCACAATGGTGTCAAAGTCCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGT
84 P H R V A V 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
StuI (2500)
2501 AGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCTGTAGGCCGCCCGACATGGTGCTTGTTCCTCATAGAGCATGGTGATCTTCTC
51 A E I H V 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
BspHI (2650)
BbsI (2646)
XmnI (2642)
2601 AGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCATGATGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTA
18 T A V E V L E L D Q Q S I N F T K M
AseI (2708) SacI (2765)
2701 TGCCGATGATTAATTGTCAAACACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCACCCTACAG
SpeI (2863)
2800 CCTACCGCCATTTGCGTCAATGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCCTTGATTTACTAGTCAAAACAAACTCCCATTGACGTCAATGGG
SnaBI (2991)
2899 GTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAG
NdeI (3096)
2999 ATGTACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCTACTTGGCA
3099 TATGATACACTTGATGTACTGCCAAGTGGGCGAGTTTACCCTAAATACTCCACCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATA
PstI (3275) SdaI (3274) PacI (3282) BspLU11I
3199 CGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCTGCAGGTTAA TTAAGAACAT
3297 GTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGA
3397 CGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCCGACCCTGCCGC
3497 TTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCAA
ApaLI (3606)
3597 GCTGGGCTGTGTGCACGAACCCCCGTTAGCCCCGACCCTGCGCCTTATCCGGTAACATATCGTCTTGTAGTCCAAACCCGTAAGACACGACTTATCGCCA
3697 CTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAA
3797 CAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTT
3897 TTTTGTTCGAAAGCAGGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAAACGAAAACTCA
PacI (4022) SmaI (4031) NotI (4041)
3997 CGTTAAGGGATTTTGGTCAATGGCTAGTTAATTAACATTTAAATC AGCGGCCGCAATAAAAATATCTTTATTTTTCATTACATCTGTGTGTTGGTTTTTTGTG
4097 TGAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTT
4197 CTCTATCGAA