



PvuI (7)
SgfI (6) **MfeI (82)**
1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203)
HindIII (245)
PvuII (239)
Bsu36I (291)
201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACCGCGCCCGCCGCCCTACCTGAGGCC
301 GCCATCCACGCGGTTGAGTCGCGTTCTGCCGCTCCCGCCTGTGGTGCCTCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCGGCGCTCCCTTGAGCCTACCTAGACTCAGCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

NcoI (560)
BstEII (555)
AgeI (552)
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCCCTACCTGAGATCACCGGTCACCATGGAGGGATCAGTATACACTTCAGATAACTACAC
601 CGAGGAAATGGGCTCAGGGGACTATGACTCCATGAAGGAACCTGTTTCCGTTGAAGAAAATGCTAATTTCAATAAAAATCTTCCGCCACCATCTACCC
13▶ E E M G S G D Y D S M K E P C F R E E N A N F N K I F L P T I Y S

BstEII (751)
701 ATCATCTTCTAACTGGCATTGTGGCAATGGATTGGTCATCCTGGTCATGGGTTACCAAGAAGAACTGAGAAGCATGACGGACAAGTACAGGCTGCACC
47▶ I I F L T G I V G N G L V I L V M G Y Q K K L R S M T D K Y R L H

BstAPI (844)
801 TGTCAGTGGCCGACCTCCTCTTTGTCATCAGCTTCCCTTCTGGGCGATTGATGCCGTGGCAAACCTGGTACTTTGGGAACCTCCTATGCAAGGCAGTCCA
80▶ L S V A D L L F V I T L P F W A V D A V A N W Y F G N F L C K A V H

MscI (968)
901 TGTCATCTACACAGTCAACCTCTACAGCAGTGTCTCATCCTGGCCTTATCAGTCTGGACCGTACCTGGCCATCGTCCACGCCACCAACAGTCAGAGG
113▶ V I Y T V N L Y S S V L I L A F I S L D R Y L A I V H A T N S Q R

BamHI (1043)
1001 CCAAGGAAGCTGTTGGCTGAAAAGGTGGTCTATGTTGGCGTCTGGATCCCTGCCTCCTGCTGACTATTTCCCGACTTCATCTTTGCCAACGTCAGTGAGG
147▶ P R K L L A E K V V Y V G V W I P A L L L T I P D F I F A N V S E
1101 CAGATGACAGATATATCTGTGACCGCTTACCCCAATGACTTGTGGGTGTTGATGTTCCAGTTTTCAGCACATCATGTTGGCCTTATCTGCCTGGTAT
180▶ A D D R Y I C D R F Y P N D L W V V V F Q F Q H I M V G L I L P G I

PshAI (1278)
1201 TGTCATCCTGCTGCTATTGCATTATCATCTCCAAGCTGTCACACTCCAAGGGCCACCAGAAGCGCAAGGCCCTCAAGACCACAGTCATCCTCATCCTG
213▶ V I L S C Y C I I I S K L S H S K G H Q K R K A L K T T V I L I L

BsaBI (1335)
ApaLI (1399)
1301 GCTTCTTCGCTGTTGGCTGCCTTACTACATTGGGATCAGCATCGACTCCTTATCCTCCTGAAATCATCAAGCAAGGGTGTGAGTTTGAGAACACTG
247▶ A F F A C W L P Y Y I G I S I D S F I L L E I I K Q G C E F E N T

BsaBI (1410)
1401 TGCACAAGTGGATTCCATCACCAGGCGCTTAGCTTTCTCCACTGTTGTCTGAACCCATCCTCTATGCTTTCTTGGAGCCAAATTTAAAACCTCTGC
280▶ V H K W I S I T E A L A F F H C C L N P I L Y A F L G A K F K T S A

BbsI (1596)
1501 CCAGCACGCACTCACCTCTGTGAGCAGAGGGTCCAGCCTCAAGATCCTCTCCAAGGAAAGCGAGGTGGACATTCATCTGTTTCCACTGAGTCTGAGTCT
313▶ Q H A L T S V S R G S S L K I L S K G K R G G H S S V S T E S E S

MscI (1635)
NheI (1629)
1601 TCAAGTTTTCACTCCAGCTAACACAGATGGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAAAAAA
347▶ S S F H S S •

HpaI (1767)
MfeI (1778)
1701 ATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGTGAATAAACAAGTTAACAACAACAAATGCATTCAATTTATGTTT

EcoRI (1863)
1801 CAGGTTCCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACTTTAACCTCC
1901 AAATCAAGCCTCTACTTGAATCCTTTTCTGAGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCT

SapI (2045)
2001 TTCATGGAGTTTAAAGATATAGTGTATTTTCCCAAGGTTTGAAGTCTTTCATTTCTTTATGTTTTAAATGCACTGACCTCCCACATTCCCTTTTATGTT

SspI (2102)
SwaI (2116)
2101 AAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAG
2201 TTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTAAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGTTGTAAGTGGGGGATG
141▶ N R T Y K L P I

SacI (2377)
2301 AGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGG
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 (2406)
2401 GGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCCCTGCTCACAGCAGACCC
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 (2541)

2501 AATGGCAATGGCTTCAGCACAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCAGTCTTGGTCCTGATGGCCGCCCG
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

BbsI (2687)

XmnI (2683)

2601 ACATGGTGCTTGTTCCTCATAGAGCATGGTGATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGGTGG
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 (2749)

2701 CCTCCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCA

Sacl (2806)

2801 CTAACGAGCTCTGCTTATATAGACCTCCACCCTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTG

SpeI (2904)

2901 ATTTACTAGTCAAAAACAACTCCCATTGACGTCAATGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCAGGCCATTGATGACTGCCAA

SnaBI (3032)

3001 AACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGACTGCCAAGTAGGAAAGTCCATAAGGTCATGACTGGGCATAATGCCAGGCGGGCC

NdeI (3137)

3101 ATTTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGATGACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACG
3201 TCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTGAGCCAGGCGGGCCATTTACC

PacI (3323)

PstI (3316)

SdaI (3315)

BspLU11I (3333)

3301 GTAAGTTATGTAACGCCTGCAGGTTAATTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCGTTTTTCCA
3401 TAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATACCAGGCGTTTCCCCCTGGA
3501 AGCTCCCTCGTGCCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGAAGCGTGGCGCTTCTCATAGCTCAGCT

ApaLI (3647)

3601 GTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCAAGCTGGGCTGTGTGCACGAACCCCGTTCCAGCCGACCCTGCGCCTTATCCGGTAACTATCG
3701 TCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGCTACAGAGTTC
3801 TTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTT
3901 GATCCGGCAAAACAAACCACCGCTGGTAGCGGTGGTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTT

EagI (4083)

PacI (4063) SwaI (4072) **NotI (4082)**

4001 TTCTACGGGTCTGACGCTCAGTGGAAACGAAAACCTCACGTTAAGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCCAATAAAATAT

4101 CTTTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACATAACGCTCTCCATCAAAAACAAACGAAACAAACAACTAGCAAATA
4201 GGCTGTCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA