



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

1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
 101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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

201 GTGAACGTTCTTTTTTCGCAACGGGTTTGGCCGAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACAGCGCCCGCCGCTACCTGAGGGCC
 301 GCCATCCACGCGGTTGAGTGCAGTTCGCCGCTCCCGCCTGTGGTGCCTCCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)

401 GGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCGGCTCTCCACGCTTGGCTGACCCTGCTTGTCTCAACTCTACGTCTTTGTTTCGTTT

BspHI (560)

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCCTACCTGAGATCACCGGTCATCATGAACACCCGTAACGCTGGAAATGGACCTCGAGAA
AgeI (552) **XhoI (592)**

Bsp120I (688)

601 CCTGGAGGACCTGTTCTGGAACTGGACAGATTGGACAATAACGACACCTCCCTGGTGGAAAATCATCTCTGCCCTGCCACAGAGGGCCCTCATG
 13▶ L E D L F W E L D R L D N Y N D T S L V E N H L C P A T E G P L M

BsrBI (790)

701 GCCTCCTTCAAGGCCGTGTTCTGCCCCGTGGCCTACAGCCTCATCTTCTCCTGGCGTGATCGGCAACGTCCTGGTGTGGTGTATCCTGGAGCGGCACC
 47▶ A S F K A V F V P V A Y S L I F L L G V I G N V L V L V I L E R H

BbsI (862)

801 GGCAGACACGAGTTCCACGGAGACCTTCTGTTCCACCTGGCCGTGGCCGACCTCCTGCTGTTTCTTCTTCCCTTTGCCGTTGGCCGAGGGCTCTGT
 80▶ R Q T R S S T E T F L F H L A V A D L L L V F I L P F A V A E G S V

PstI (963)

901 GGGCTGGGTCCTGGGACCTTCCCTGCAAACTGTGATTGCCCTGCACAAAGTCAACTTCTACTGCAGCAGCCTGCTCCTGGCTGCATCGCGTGGAC
 113▶ G W V L G T F L C K T V I A L H K V N F Y C S S L L L A C I A V D

BstXI (1076)

1001 CGCTACCTGGCCATTGTCCACGCGTCCATGCCTACCGCCACCGCCGCTCCTCTCCATCCACATCACCTGTGGGACCATCTGGCTGGTGGGCTTCTCC
 147▶ R Y L A I V H A V H A Y R H R R L L S I H I T C G T I W L V G F L

SphI (1197)

1101 TTGCCTTGCAGAGATTCTCTTCCGCAAAAGTCAGCCAAGGCCATCACAACAACTCCCTGCCACGTTGCACCTTCTCCCAAGAGAACCAAGCAGAAACGCA
 180▶ L A L P E I L F A K V S Q G H H N N S L P R C T F S Q E N Q A E T H

BstAPI (1287)

1201 TGCCTGGTTCACCTCCCGATTCTCTACCATGTGGCGGATTCTGCTGCCATGCTGGTGTGGGCTGGTGTACTGTTGGGGTAGTGACAGGTTGGCG
 213▶ A W F T S R F L Y H V A G F L L P M L V M G W C Y V G V V H R L R

BstEII (1376)

1301 CAGGCCAGCGGCGCCCTCAGCGGAGAAAGCAGTCAGGGTGGCCATCCTGGTGAACATCTTCTCCTCTGCTGGTACCCTACCACATCGTCATCT
 247▶ Q A Q R R P Q R Q K A V R V A I L V T S I F F L C W S P Y H I V I

DraIII (1473)

1401 TCCTGGACACCCTGGCGAGGCTGAAGGCCGTGGACAATACCTGCAAGCTGAATGGCTCTCTCCCGTGGCCATCACCATGTGTGAGTTCTGGGCTGGC
 280▶ F L D T L A R L K A V D N T C K L N G S L P V A I T M C E F L G L A

NgoMIV (1534)

SgrAI (1533)

1501 CCACTGCTGCCTCAACCCATGCTCTACTTTTCGCCGGCGTGAAGTTCGCGAGTGACCTGTGCGGGCTCTGACGAAGCTGGGCTGTACCGGCCCTGCC
 313▶ H C C L N P M L Y T F A G V K F R S D L S R L L T K L G C T G P A

SapI (1611)

1601 TCCCTGTGCCAGCTTCCCTAGCTGGCGCAGGAGCAGTCTCTGAGTCAGAGAATGCCACCTCTCTCACCAGTTCTAGGTCACAGTGTCCCTTTTA
 347▶ S L C Q L F P S W R R S S L S E S E N A T S L T T F •

NheI (1744)

1701 TTGCTGCTTTTCTTGGGCGAGGAGTGATGCTGGATGCTCCTTCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTGGACAAACCACAACCTAG

HpaI (1882) **MfeI (1893)**

1801 AATGCAGTAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACATTATAAGCTGCAATAAACAAGTTAACACAACAATTGC

EcoRI (1978)

1901 ATTCAATTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATCTAAAATACAGCATAGC
 2001 AAAACTTTAACCTCCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTT

SapI (2160)

2101 GCAGCCTCACCTTCTTTCATGGAGTTTAAAGATAGTGTATTTTCCCAAGTTTGAAGTCTTCTTCTTTTATGTTTTAAATGCACTGACCTCCCA

SspI (2217) **SwaI (2231)**

2201 CATTCCCTTTTAGTAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAAATCCAGATGCTCAAGGCCCTT

2301 CATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGAACCTTAAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTCTGGTG
141◀ • N R T

2401 TACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTC
136 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 P A Y D S I L E R SacI (2492)

2501 TGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCCGTT
103 C M G C P 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 BstXI (2521)

2601 GCTCACAGCAGACCAATGGCAATGGCTTCAGCACAGACAGTACCCTGCCAATGTGGACAGCAGAGATGATCTCCCAGTCTTGTC
70 S V A S G 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 StuI (2656)

2701 CTGATGGCCGCCCCGACATGGTGTGTTGTCTCATAGAGCATGGTGTCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGA
36 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 E L D Q Q S I N F XmnI (2798)

2801 AGGTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGC
34 T K M BbsI (2802) AseI (2864)

2901 TTATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTT
SacI (2921)

3001 TGGAAAGTCCCGTTGATTTACTAGTCAAACAAACTCCCAATTGACGTCAATGGGGTGGAGACTTGAAATCCCGTGAGTCAAACCGCTATCCACGCCCA
SpeI (3019)

3101 TTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCAT
SnaBI (3147)

3201 AATGCCAGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAATA
NdeI (3252)

3301 CTCCACCCATTGACGTCAATGAAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGTCAATGGGGGGGGTCTTGGCGGGTCAGCCA

3401 GCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAAATAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGCCGCGTT
PacI (3438) PstI (3431) SdaI (3430) BspLU11I (3448)

3501 GCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATACCG
3601 GCGTTTTCCCCTGGAAGCTCCCTCGTGCCTCTCTGTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTT

3701 CTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTTCAGCCCAGCCGCTGCGCCTT
ApaLI (3762)

3801 ATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGC

3901 GGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAA

4001 GAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGA

4101 AGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCG
PacI (4178) SmaI (4187) EagI (4198) NotI (4197)

4201 GCCGCAATAAAATATCTTTATTTTACATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACATAACATACGCTCTCCATCAAAAACAAAACGAAACAAAA
4301 CAAACTAGCAAAATAGGCTGTCCCCAGTGAAGTGCAGGTGCCAGAACATTTCTCTATCGAA