



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

1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGCAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
 101 GAGAAGGTGGCGGGGTAACCTGGAAAGTGATGTCGTGTAAGTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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

201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACCGCCGCCCGCCCTACCTGAGGCC
 301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCCTCCCGCCTGTGGTGCCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

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

401 GGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGTCTTTGTTTCGTTT

BspHI (560)

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCGCTACCTGAGATCACCGGTCATCATGAGCAGAAGCAAACGTGACAACAATTTTTATAGTGT
 601 AGAGATTGGAGATTCTACATTCACAGTCTAAAACGATACCAGAATTTAAAGCCTATAGGCTCAGGAGCTCAAGGAATAGTGTGTGCAGTCTATGATGCC
 13▶ E I G D S T F T V L K R Y Q N L K P I G S G A Q G I V C A A Y D A

KasI (535) **AgeI (552)**
BspIII (765) **SpeI (780)**

701 ATTCTTGAAGAAATGTTGCAATCAAGAAGCTCAGCCGGCCATTTGAAATCAGACCCATGCTAAGCGCGCCTACCGAGAAGTCTTATGAAGTGTG
 47▶ I L E R N V A I K K L S R P F Q N Q T H A K R A Y R E L V L M K C

BsaBI (895)

801 TTAATCACAAAAATATAATTGGCCTTTTGAATGTTTTACACCCACAGAAATCCCTAGAAGAATTTCAAGATGTTTACATAGTCATGGAGCTCATGGATGC
 80▶ V N H K N I I G L L N V F T P Q K S L E E F Q D V Y I V M E L M D A

BspHI [m] (931)

901 AAATCTTTGCCAAGTGATTCAGATGGAGTTAGATCATGAAAGAATGTCCTACCTTCTCTATCAAATGCTGTGTGGAATCAAGCACCTTCACTCTGCTGGA
 113▶ N L C Q V I Q M E L D H E R M S Y L L Y Q M L C G I K H L H S A G

PstI (1085)

1001 ATTATTCATCGGGACTTAAAGCCTAGTAATATAGTAGTCAAATCAGACTGCACCTTGAAGATTCTTGATTTGGACTGGCGAGGACTCGAGGAACAGGTT
 147▶ I I H R D L K P S N I V V K S D C T L K I L D F G L A R T A G T S

Psp1406I (1174)

1101 TTATGATGACGCCTTATGTGGTACTCGTACTACAGAGCACCAGAGGTCATTCTCGGCATGGGCTACAAGGAGAACGTTGACATTTGGTCAGTTGGGTG
 180▶ F M M T P Y V V T R Y Y R A P E V I L G M G Y K E N V D I W S V G C
 1201 CATCATGGGAGAAATGATCAAAGGTGGTGTGTTTCCAGGTACAGATCATAATTGATCAGTGGAAATAAGTTATTGAACAGCTCGGAACACCTTGTCTC
 213▶ I M G E M I K G G V L F P G T D H I D Q W N K V I E Q L G T P C P

BspHI (1304)

EcoRI (1300)
StuI (1348)

1301 GAATTCATGAAGAACTACAACCAACAGTAAGGACTTATGTTGAAAACAGGCCTAAATACGCTGGATATAGCTTTGAGAAACTGTTCCCGATGTGCTTT
 247▶ E F M K K L Q P T V R T Y V E N R P K Y A G Y S F E K L F P D V L

Ppu10I (1475) **NsiI (1475)**

1401 TCCAGCTGACTCAGAGCATAACAACTTAAAGCCAGTCAGGCAAGAGATTTGTTATCCAAAATGCTAGTAATAGATGCATCCAAAAGGATCTCCGTAGA
 280▶ F P A D S E H N K L K A S Q A R D L L S K M L V I D A S K R I S V D
 1501 TGAAGCTCTCCAGCACCCATACATCAACGTCCTGGTATGATCCTTCAGAAGCAGAAGCCCAACCAAGATCCCGGACAAGCAGTTAGATGAGAGGGAG
 313▶ E A L Q H P Y I N V W Y D P S E A E A P P P K I P D K Q L D E R E
 1601 CACACAATAGAGGAGTGGAAAGAAGTATATACAAGGAGGTAATGGATTTGGAGGAACGAAGTAAAGATGGAGTCATAAGAGGGCAGCCGTCTCCTTTAG
 347▶ H T I E E W K E L I Y K E V M D L E E R T K N G V I R G Q P S P L

MseI (1745)

NheI (1739)

1701 CACAGGTGCAGCAATGATCAATGGCTCTCAGCATCCATCGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGC
 380▶ A Q V Q Q •

HpaI (1877) **MfeI (1888)**

1801 AGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAAACAATTCATTCA

EcoRI (1973)

1901 TTTTATGTTTCAGGTTGAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAATGTGGTATGGAATTTAAATAACAGCATAGCAAAC
 2001 TTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGC
 2101 CTCACCTTCTTCATGGAGTTTAAAGATATAGTGTATTTTCCCAAGGTTTGAAGTACTGCTCTTCTTTTATGTTTTAAATGCACTGACCTCCACATTC

SspI (2212) **SwaI (2226)**
EcoO109I (2287)

2201 CCTTTTTAGTAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAA
 2301 TATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGCTGTTACTT
 2401 GAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCAC
 135▶ 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 C

2501 **BstXI (2516)** ATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCCGTTGCTCA
101 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 S V

2601 CAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCAGTCTTGGTCTGAT
68 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 R I

2701 GGCCGCCCGACATGGTGTCTTGTTCCTCATAGAGCATGGTGTCTTCTCAGTGGGACCTCCACCAGTCCAGATCCTGCTGAGAGATGTTGAAGGTC
35 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 T

BbsI (2797)
BspHI (2801) **AseI (2859)**
2801 TTCATGATGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTATC
1 K M

2901 TGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAA

3001 **SpeI (3014)** AGTCCCGTTGATTACTAGTCAAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGA

3100 **SnaBI (3142)** TGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAATG

3200 **NdeI (3247)** CCAGGCGGGCCATTACCCTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGTACTGCCAAGTGGGCGAGTTTACCGTAAATACTCC

3300 ACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTGAGCCAGGCG

3400 **PstI (3426)** **SdaI (3425)** **PacI (3433)** **BspLU111 (3443)** GGCCATTTACCGTAAGTTATGTAACGCTG CAG G TT AA TTAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGCTTGC
3498 TGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGC
3598 GTTCCCCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTCT

3698 **ApaLI (3757)** CATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTGTTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTACGCCGACCGCTGCGCCTTAT

3798 CCGGTAACATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGG

3898 TGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGA

3998 GTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAG

4098 **EagI (4193)** **PacI (4173)** **SwaI (4182)** **NotI (4192)** ATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGGC

4198 CGCAATAAAATATCTTTATTTTTCATTACATCTGTGTGGTTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAAAACGAAACAAAAACA

4298 AACTAGCAAAATAGGCTGTCCCCAGTGAAGTGCAAGTGCCAGAACATTTCTCTATCGAA