



PvuI (7)
SgfI (6)
 1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTCGGCAATTGAACGGGTGCCTA
 101 GAGAAAGTGGCGCGGGTAAACTGGAAAAGTGTCTGTACTGGCTCCGCTTTTTCCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)
Psp1406I (203) **PvuII (239)** **Bsu36I (291)**
 201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACGCGCCGCGCCCTACCTGAGGCC
 301 GCCATCCACGCCGGTTGAGTCGCGTTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAAGTGCCTCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMI (441)
 401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

KasI (535) **SgrAI (551)**
 501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGCGAAGGAGGGCCACCATGACTCCCTGGCTTGGGCTTGTCTGTC
 1▶ M T P W L G L V V

ApaLI (640)
 601 TCCTGAGCTGCTGGAGCCTTGGGCACTGGGGCGGGAAGCGTGCACATGCTCTCCAGCCATCCCAGGATGCCTTCTGCAACTCCGACATCGTGATCCG
 10▶ L L S C W S L G H W G A E A C T C S P S H P Q D A F C N S D I V I R

BstXI (702) **Bsp120I (734)**
 701 GGCCAAAGTGGTGGGAAAGAAGCTGGTGAAGGAGGGCCCTTTGGCACTCTGGTCTACACTATTAAGCAGATGAAGATGTACCAGGCTTTCAGTAAGATG
 43▶ A K V V G K K L V K E G P F G T L V Y T I K Q M K M Y R G F S K M

BbrPI (803)
 801 CCCACGTGCAGTACATTACACGGAAGCCTCTGAAAGTCTTTGTGGCCTCAAGCTAGAAGTCAACAAATACCAGTACCTGCTGACAGGGCGCGTGTATG
 77▶ P H V Q Y I H T E A S E S L C G L K L E V N K Y Q Y L L T G R V Y

BsrGI (909)
 901 AAGGCAAGATGTACACAGGACTGTGCAACTTTGTGGAGAGGTGGGACCACCTCACACTGTCCAGCGCAAGGGCCTCAATTACCGCTACCACCTGGGTTG
 110▶ E G K M Y T G L C N F V E R W D H L T L S Q R K G L N Y R Y H L G C
 1001 CAATTGCAAGATCAAGTCTGCTACTACTTGCCTTGTGTTTGTGACCTCAAGAATGAGTGTCTCTGGACCGACATGCTCTCAATTTTGGGTACCCTGGC
 143▶ N C K I K S C Y Y L P C F V T S K N E C L W T D M L S N F G Y P G

PvuII (1147) **PstI (1144)**
 1101 TATCAGTCCAACACTACGCCTGCATCCGGCAGAAGGGTGGCTACTGCAGCTGGTACCGAGGATGGGCTCCCCAGACAAGAGCATCAGCAACGCCACAG
 177▶ Y Q S K H Y A C I R Q K G G Y C S W Y R G W A P P D K S I S N A T

MscI (1232) **NheI (1226)**
 1201 ACCCTGAACCCAGACCTTCCCCACCGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAAGTGAATGCAGTGAAAAAATG
 210▶ D P •

HpaI (1364)
 1301 CTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAG

EcoRI (1460)
 1401 GTTCAGGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACTTTAACCTCCAAA
 1501 TCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTC

SapI (1642) **SspI (1699)**
 1601 ATGGAGTTTAAGATATAGTGTATTTTCCCAAGTTTGAAGTCTTTCATTTCTTTATGTTTAAATGCACTGACCTCCACATTCCCTTTTATAGTAAA

SwaI (1713)
 1701 ATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTT

1801 AGTAGTTGGACTTAGGGAACAAAGAACCTTTAATAGAAATGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTACTTGGAGGGGATGAGT
 141▶ • N R T Y K L P I L

SacI (1974)
 1901 TCCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGC
 130▶ 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 S

BstXI (2003)
 2001 TGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAAT
 97▶ 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 I

StuI (2138)
 2101 GGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCTGATGGCCGCCCCGACA
 64▶ 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 V

BspHI (2288)
BbsI (2284)
XmnI (2280)

2201 TGGTGCTTGTTCCTCATAGAGCATGGTGATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGATGGCCC
 30 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 (2346)

2301 TCCTATAGTGAGTCGTATTATACTATGCGGATATACTATGCGGATGATTAATTGTCAAACACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCATA

SacI (2403)

2401 AACGAGCTCTGCTTATATAGACCTCCACCCTACACGCCTACCGCCATTGCGTCAATGGGCGGAGTTGTTACGACATTTTGAAAGTCCCCTTGATT

SpeI (2501)

2501 TACTAGTCAAAACAACTCCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTAAGTCCAAAC

SnaBI (2629)

2601 CGCATCATCATGGTAATAGCGATGACTAATACGTAGATGACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATT

NdeI (2734)

2701 TACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGTACTGCCAAGTGGGCAGTTTACCCTAAATACTCCACCCATTGACGTCA

2801 ATGGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTACGCCAGGCGGGCCATTACCCTA

PacI (2920)
PstI (2913)
SdaI (2912) **BspLU11I (2930)**

2901 AGTTATGTAACGCCTGCAGGTTAATTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCCTTTTCCATAG

3001 GCTCCGCCCCCTGACGAGCATCAGAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTCCCCCTGGAAGC

3101 TCCCTCGTGCCTCTCCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCAGCTGTA

ApaLI (3244)

3201 GGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTCAGCCGACCGCTGCGCTTATCCGGTAACTATCGTCT

3301 TGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGATTCTTG

3401 AAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGAT

3501 CCGCAACAACACCCTGCTAGCGGTGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTC

EagI (3680)
PacI (3660) SwaI (3669) NotI (3679)

3601 TACGGGGTCTGACGCTCAGTGGAACGAAACTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAATATCTT

3701 TATTTTCATTACATCTGTGTGTTGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAAATAGGC

3801 TGTCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA