



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

101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGACTGGCTCCGCCTTTTTCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCC

**HindIII (245)**  
**Psp1406I (203)** 201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACCGCCGCCGCCCTACCTGAGGCC **PvuII (239)** **Bsu36I (291)**

301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCCTGTGGTGCTCTCTGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCGCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTAACTCTACGCTTTTGTTCGTTT **NgoMIV (441)**

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCCCTACCTGAGATCACCGGTCACCATGGCATCAGGCAGGGCACGCTGCACCCGAAAACCTCCG **NcoI (560)** **BstEII (555)** **BspEI (596)**  
1 M A S G R A R C T R K L R **BspEI (674)**

601 GAACTGGGTGGTGGAGCAAGTGGAGAGTGGGCAGTTTCCGGAGTGTGCTGGGATGATACAGCTAAGACCATGTTCCGGATTCCCTGAAACATGCAGGC **PvuII (791)** **BstXI (790)**  
13 N W V V E Q V E S G Q F P G V C W D D T A K T M F R I P W K H A G

701 AAGCAGGACTTCCGGGAGGACCAGGATGCTGCCTTCTCAAGGCTGGCAATATTTAAGGGAAAGTATAAGGAGGGGACACAGGAGGTCCAGCTGTCT **SspI (750)**  
47 K Q D F R E D Q D A A F F K A W A I F K G K Y K E G D T G G P A V

801 GGAAGACTCGCCTGCGTGTGCACTCAACAAGAGTTCTGAATTTAAGGAGTTCTGAGAGGGGCCGATGGATGTTGCTGAGCCCTACAAGGTGTATCA **BbsI (801)** **ApaLI (818)**  
80 W K T R L R C A L N K S S E F K E V P E R G R M D V A E P Y K V Y Q

901 GTTGCTGCCACCAGGAATCGTCTCTGGCCAGCCAGGACTCAGAAAGTACCATCAAAGCGACAGCACAGTTCTGTCTCTGAGAGGAAGGAGGAAGAG **XcmI (1086)**  
113 L L P P G I V S G Q P G T Q K V P S K R Q H S S V S S E R K E E E

1001 GATGCCATGCAGAAGTGCACACTCAGTCCCTCTGTGCTCCAGGACTCCCTCAATAATGAGGAGGAGGGGCCAGTGGGGGAGCAGTCCATTGAGCATTTG **Bsu36I (1301)**  
147 D A M Q N C T L S P S V L Q D S L N N E E E G A S G G A V H S D I

1101 GGAGCAGCAGCAGCAGCAGCCCTGAGCCACAGGAAGTTACAGACACAAGTGGAGGGCCCTTTCAAGGGGATCAGAGGTTCCCTGGAGTTTCTGCTTCC **XcmI (1470)**  
180 G S S S S S S P E P Q E V T D T T E A P F Q G D Q R S L E F L L P

1201 TCCAGAGCCAGACTACTCACTGCTCACCTTCACTACAACGGGCGGTGGTGGGCGAGGCCAGGTGCAAAGCCTGGATTGCCGCTTGTGGCTGAG **XcmI (1470)**  
213 P E P D Y S L L L T F I Y N G R V V G E A Q V Q S L D C R L V A E

1301 CCCTCAGGCTCTGAGAGCAGCATGGAGCAGGTGCTGTTCCCAAGCCTGGCCACTGGAGCCACGCAGCGCCTGCTGAGCCAGCTTGAAGGGGCATCC **XcmI (1470)**  
247 P S G S E S S M E Q V L F P K P G P L E P T Q R L L S Q L E R G I

1401 TAGTGCCAGCAACCCCGAGGCCTCTTCTGTCAGCGCCTTTGCCCATCCCATCTCTGGAATGCACCCGAGCTCCAGTGGCCAGGCCGCATCT **Tth111I (1552)**  
280 L V A S N P R G L F V Q R L C P I P I S W N A P Q A P P G P G P H L

1501 GCTGCCAGCAACGAGTGCCTTTCAGAACCCCTACTTCTGAGAGACTTGGTCAGGACTTTTTCAGGGCCTGGGCCCCACCGAAGTTCCAG **SapI (1524)** **PstI (1545)** **Bsp120I (1578)**  
313 L P S N E C V E L F R T A Y F C R D L V R Y F Q G L G P P P K F Q

1601 GTAACACTGAATTTCTGGAAAGAGGCCATGGCTCCAGCCATACTCCACAGAATCTTATCACAGTGAAGATGGAGCAGGCCTTTGCCGATACTTGTGG **NcoI (1626)**  
347 V T L N F W E E S H G S S H T P Q N L I T V K M E Q A F A R Y L L

1701 AGCAGACTCCAGAGCAGCAGGCAGCCATCTGTCCCTG TGTAGAGCCTGC GGATCCTATCCCTATGATGTGCCAGACTATGCTGGCTATCCATATGATGT **BamHI (1750)** **NdeI (1790)**  
380 E Q T P E Q Q A A I L S L C R A C G S Y P Y D V P D Y A G Y P Y D V

1801 TCCTGATTATGCTGGATACCCTTATGATGTGCCAGACTATGCCTAAAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGACAAACCACAAC **NheI (1847)**  
413 P D Y A G Y P Y D V P D Y A •

1901 TAGAATGCAGTGAATAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAACAACAAT **HpaI (1985)** **MfeI (1996)**

2001 TGCATTCATTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAATGTGGTATGGAATCTAAAATACAGCAT **EcoRI (2081)**

2101 AGCAAACTTTAACCTCCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTG

2201 TTTGAGCCTCACCTTCTTCATGGAGTTAAGATATAGTGTATTTTCCCAAGTTTGAAGTACTCTTCAATTTCTTTATGTTTTAAATGCAGTACCTC **SapI (2263)**

2301 CCACATTCCTTTTTAGTAAAATATTAGAAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCC **SspI (2320)** **SwaI (2334)**

2401 CTTATAATATCCCCAGTTTAGTAGTTGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTCTG **SspI (2320)** **SwaI (2334)**  
141 • N R

2501 GTGTA<sup>137</sup>CTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCT  
137 T 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

BstXI (2624)

2601 CTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCCTTCTGCCC  
104 R 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

2701 GTTGCTCACAGCAGACCAATGGCAATGGCTTCAGCACAGACAGTGACCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTG  
71 N 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

2801 GTCCTGATGGCCCGCCGACATGGTGTGTTGCCTCATAGAGCATGGTGATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGT  
37 T 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

BspHI (2909)

BbsI (2905)

XmnI (2901)

AseI (2967)

2901 TGAAGTCTTCATGATGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCC  
4 F T K M

3001 AGC TTATCTGACGGTTCAC<sup>137</sup>TAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACA

SpeI (3122)

3101 TTTTGAAAGTCCCCTGTTGATTACTAGTCAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACG

SnaBI (3250)

3200 CCCATTGATGTA<sup>137</sup>CTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTA<sup>137</sup>CTGCCAAGTAGGAAAGTCCCATAAGGTCTACTG

NdeI (3355)

3300 GCATAATGCCAGGCGGGCCATTTACCGTCAATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGATGTA<sup>137</sup>CTGCCAAGTGGGAGTTTACCGTA

3400 AATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCAATTATTGACGTCAATGGGCGGGGTCGTTGGCGGTCA

PstI (3534)

SdaI (3533)

PacI (3541)

BspLU11I (3551)

3500 GCCAGGCGGGCCATTTACCGTAAGTTATGTAACCTCTG C A G G T T A A T T A A G A A C A T G T G A G C A A A A G G C C A G C A A A A G G C C A G G A A C C G T A A A A A G G C  
3598 CGCGTTGTGCGGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGA

3698 TACCAGGCGTTTTCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGG

ApaLI (3865)

3798 CGCTTTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTGCTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTACGCCGACCGCTG

3898 CGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTAT

3998 GTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCG

4098 GAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGTGGTAGCGGTGTTTTTTTTGTTTGAAGCAGCAGATTACGCCGAGAAAAAAGGATC

PacI (4281) SwaI (4290)

4198 TCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAA

EagI (4301)

NotI (4300)

4298 TC AGCGCCGCAATAAAATATCTTTATTTTCATTACATCTGTGTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAA

4398 ACAAACAAACTAGCAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA