



PvuI (7) SgfI (6) MfeI (82) EcoNI (96)  
1 GGATCTGGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA  
101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGACTGGTCCGCCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245) Bsu36I (291)  
201 Psp1406I (203) PvuII (239) EcoNI (287)  
GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACCGCGCCCGCCCTACCTGAGGCC  
301 GCCATCCACGCGGTTGAGTGCAGTCTGCCGCTCCCGCTGTGGTGCCTCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)  
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

KasI (535) AgeI (552) BspLU11I (560)  
501 TCTGTTCTGCGCGGTTACAGATCCAAGCTGTGACCGCGCGCTACCTGAGATCACCGGTCAACATGTCAGAGTGGGAGTCTACTACAAAAGTGGGGCGA  
1 M S E W E S Y Y K T E G E  
601 GGAAGAGGAAGAGGAGGAGAGACCCCGACACAGGTGGAGAATATAAATATTCAGGAAGAGATAGCTTGATTTTTCTGGTTGATGCCTCCAGGGCTATG  
13 E E E E E E S P D T G G E Y K Y S G R D S L I F L V D A S R A M

BsaBI (790) BsrGI (764) PvuI (789)  
701 TTCGAATCTCAGGGTGAAGATGAAGTACACCTTTTATGATGAGCATCCAGTGTATCCAGAGTGTGTACACAGTAAGATCATAAGCAGCGATCGGGATC  
47 F E S Q G E D E L T P F D M S I Q C I Q S V Y T S K I I S S D R D  
801 TCCTGGCAGTGGTGTCTATGGAACCGAGAAAGATAAAAAATTCAGTGAATTTCAAAAATATTTATGCTTTACAAGATTTGGACAACCCAGGCGCTAAGCG  
80 L L A V V F Y G T E K D K N S V N F K N I Y V L Q D L D N P G A K R

XmnI (939) MscI (960) NcoI (963)  
901 AGTGTAGAGCTCGACAGTTTAAAGGACAACAGGGGAAAGCACTCCGAGACACGGTGGCCATGGGTCTGACTACTCTTTGAGTGAAGTGTCTCG  
113 V L E L D Q F K G Q Q G K K H F R D T V G H G S D Y S L S E V L W

NcoI (1080)  
1001 GTCTGTGCCAACCTTTCAGCGACGTCCAGTCAAGATGAGTCAAGAGGATCATGCTGTTACCAATGAAGACGACCCCATGGCCGTGACAGTGCTA  
147 V C A N L F S D V Q L K M S H K R I M L F T N E D D P H G R D S A

NsiI (1162)  
1101 AAGCCAGCCGGGCCAGGACCAAAGCCAGCGACCTCCGGGACACTGGGATCTTCTTGGACTTGATGCATCTGAAGAAGCCAGGAGGCTTTGATGTATCCGT  
180 K A S R A R T K A S D L R D T G I F L D L M H L K K P G G F D V S V  
1201 GTTCTACAGGGACATCATCACCACCGCTGAGGACGAGGACCTTGGGGTCACTTCGAGGAGTCAAGCAAGCTGGAAGACCTGTAAGGAAGTTTCGAGCC  
213 F Y R D I I T T A E D E D L G V H F E E S S K L E D L L R K V R A

ScaI (1356)  
1301 AAGGAGACAAAAAGCGAGTTCTGTCCAGGTTAAAGTTAAAGCTCGGTGAAGACGTAGTACTCATGGTGGGCATTTATAACTTGGTCCAGAAAGCTAACA  
247 K E T C K K R V L S R L K F K L G E D V V L M V G I Y N L V Q K A N  
1401 AGCCTTTTCCAGTGAAGTCTATCGGAAACAAATGAACCAAGTGAAGCAAGGACTTTTAAATGTAACACCGGCAGTCTACTCTGCCTAGTGA  
280 K P F P V R L Y R E T N E P V K T K T R T F N V N T G S L L L P S D  
1501 CACCAAGCGGTCTCTGACTTACGGGACACGTGAGATTGTGCTGGAGAAAGAGGAGACAGAGGAGTGAAGCGGTTTGTGAGCCAGGTTTGTCTCATG  
313 T K R S L T Y G T R Q I V L E K E E T E E L K R F D E P G L I L M

Bsu36I (1638)  
1601 GGCTTTAAGCCACGGTGATGCTGAAGAAGCAGCACTACTGAGGCCCTCTGTTGCTGTACCAAGAGGAGTCCCTGGTCAGTGGGAGCTCAACCTTGT  
347 G F K P T V M L K K Q H Y L R P S L F V Y P E E S L V S G S S T L

DraIII (1713) Eco47III (1702) BstXI (1715)  
1701 TCAGCGCTCTGCTCACCAGTGTGTGGAGAAGAAGGTCATAGCAGTGTGTAGATACACACCCCGGAAGAAGTCTCCCCGATTTTTGTGGCTTTGGTGCC  
380 F S A L L T K C V E K K V I A V C R Y T T P R K N V S P Y F V A L V P  
1801 CCAGGAAGAGGAGCTGGATGATCAGAACATTCAGGTGACTCCAGGAGGCTTCCAGCTTGTCTTCTCCCTTATGCCGATGACAAGCGGAAGGTGCCCTTT  
413 Q E E E L D D Q N I Q V T P G G F Q L V F L P Y A D D K R K V P F  
1901 ACTGAGAAGGTGACGGCAACAGGAGCAGATAGACAAGATGAAGGCCATTGTTCAAAAAGCTCCGCTTACATACAGGAGCGACAGTTTTGAGAATCCAG  
447 T E K V T A N Q E Q I D K M K A I V Q K L R F T Y R S D S F E N P

PstI (2002) BglII (2067)  
2001 TCCTGCAGCAGCACTTCCGCAACCTGGAGGCCCTAGCTTTGGACATGATGGAGTCCGAGCAAGTGGTAGACTGACACTACCCAAGGTTGAAGCCATAAA  
480 V L Q Q H F R N L E A L A L D M M E S E Q V V D L T L P K V E A I K  
2101 GAAAAGACTGGGTTCCCTGGCAGATGAGTTAAAGAAGTGTCTATCCTCCAGGTTATAATCCCGAGGGAAAAGTTGGCAAGGAAAACAAGATGATGAA  
513 K R L G S L A D E F K E L V Y P P G Y N P E G K V A K R K Q D D E  
2201 GGTCTACGAGTAAAAAGCCCAAGGTAGAGTTATCAGAAGAAGAGCTGAAGGCCATTTTCGTAAGGGCACACTGGGTAAGCTACTGTACTACCTACCTGA  
547 G S T S K K P K V E L S E E L K A H F R K G T L G K L T V P T L

NdeI (2304)  
2301 AGGACATATGCAAGGCTCATGGCTTAAAGAGTGGGCCGAAGAAGCAGGAAGTCTAGATGCTCTTATCAGACACTGGAGAAGAAGTACTAAAGCTCAG  
580 K D I C K A H G L K S G P K K Q E L L D A L I R H L E K N •

MscI (2412) NheI (2406)  
2401 AAGCCCGTACTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAACCAACTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTG

HpaI (2544) MfeI (2555)  
2501 ATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAACAACAATTGCATTCTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGA

2601 **EcoRI (2640)**  
GGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACTTTAACCTCCAATCAAGCCTCTACTTGAATCC

2701 TTTCTGAGGGATGAATAAGGCATAGGCATCAGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTAAGATATAGT

2801 **Swal (2893)**  
TATTTTCCAAGTTTGAAGTAGCTCTTCATTCTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTTAGTAAAATATTCAGAAATAATTTAAA

2901 TACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCCAGTTTAGTAGTTGGACTTAGGGAAC

3001 **BstXI (3183)**  
AAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGAC  
141 • N R T Y K L P I L E E I T T K V

3101 **StuI (3318)**  
CAGCTTGCCATTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGTGACCACCCTGATGGATCTG  
124 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 V V R I S R

3201 TCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGA  
90 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 A I A E A C V

3301 **BspHI (3468)**  
CAGTGACCCTGCCAATGTAGGCCCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCTGATGGCCGCCCGACATGGTGCTTGTTCCTCATA  
57 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 H H K N D E Y

3401 **XmnI (3460)**  
GAGCATGGTATCTTCTCAGTGGCGACCTCCACCAGTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGATGGCCCTCTATAGTGAGTCGTATTA  
24 L M T I K E T A V E V L E L D Q Q S I N F T K M

3501 **AseI (3526)**  
TACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCCTAAACGAGCTCTGCTTATATAG

3601 **SpeI (3681)**  
ACCTCCCACGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCGTTGATTTACTAGTCAAAACAAACTC

3700 CCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTAAGTCCAAAACCGCATCATCATGGTAATAG

3800 **SnaBI (3809)**  
CGATGACTAATACGTAGATGTAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCAATGACGTCAAT

3900 **NdeI (3914)**  
AGGGGGCTACTTGGCATATGATACACTTGTACTGCAAGTGGGCAGTTTACCCTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGC

4000 **PstI (4093)** **SdaI (4092)**  
GTTACTATGGAAACATACGTCAATATTGACGTCAATGGGGCGGGTCTTGGCGGTCAGCCAGGCGGGCCATTTACCCTAAGTTATGTAACGCCTGCA

4099 **PacI (4100)** **BspLU11I (4110)**  
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 A A C C G T A A A A G G C C G T T G C T G G C G T T T T C C A T A G G C T C G C C C C C T G A C C

4198 A G C A T C A C A A A A T C G A C G C T C A A G T C A G A G G T G G C G A A A C C G A C A G G A C T A T A A G A T A C C A G G C G T T T C C C C T G G A A G C T C C T C G T G C G C T C C C

4298 T G T T C C G A C C C T G C C G T T A C C G G A T A C C T G T C C G C T T T C T C C T T C G G A A G C G T G G C G C T T T C T C A T A G C T C A C G C T G T A G G T A T C T C A G T T C G G T G

4398 **ApaLI (4424)**  
TAGGTCGTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTAGCCGACCGCTGCGCCTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAA

4498 G A C A C G A C T T A T C G C C A C T G G C A G C A G C C A C T G G T A A C A G G A T T A G C A G A G C G A G G T A T G T A G G C G G T G C T A C A G A G T T C T T G A A G T G G T G G C C T A A C T A

4598 C G G C T A C T A G A A G A A C A G T A T T T G G T A T C T G C G C T G T G T G A A G C A G T T A C C T T C G G A A A A G A G T T G G T A G C T T T G A T C C G G C A A A C A A C C A C C

4698 G C T G G T A G C G G T G G T T T T T T G T T T G C A A G C A G A T T A C G C G A G A A A A A A G G A T C T C A A G A A G A T C C T T T G A T C T T T T C T A C G G G T C T G A C G C T C

4798 **EagI (4860)** **PacI (4840)** **Swal (4849)** **NotI (4859)**  
A G T G G A A C G A A A A C T C A C G T T A A G G G A T T T T G G T C A T G G C T A G T T A A T T A A C A T T T A A A T C A G C G C C G C A A T A A A A T A T C T T T A T T T T C A T T A C A T C T G

4898 T G T G T T G G T T T T T T G T G T A A T C G T A A C A T A C G C T C C A T C A A A A C A A A A C G A A A C A A A A C A A A C T A G C A A A A T A G G C T G T C C C C A G T G C A A G T G

4998 C A G G T G C C A G A A C A T T T C T A T C G A A