



PvuI (7)  
SgfI (6)  
1 GGATCTGGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTCGGCAATTGAACGGGTGCCTA  
101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGCTCCGCCTTTTCCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203) PvuII (239) Bsu36I (291)  
201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTTCACGCGCCCGCCCTACCTGAGGCC  
301 GCCATCCACGCGGGTTGAGTCGCGTTTCTGCCGCCTCCCGCTGTGGTGCCTCCTGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)  
NaeI (441)  
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCAACTCTACGTCTTTGTTTCGTTT

NcoI (560)  
BstEII (555)  
KasI (535) AgeI (552) BamHI (579)  
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCGCTACCTGAGATCACCGGTCACCATGGCGGCAGCTACGGGGGATCCTGGACTCTCTAAACT  
601 GCAGTTTGCCCTTTTAGTAGTGCCTTGGATGTTGGGTTTTGGCATGAGTTGACCCAGAAGAAGCTGAACGAGTATCGGCTGGATGAAGTCCCAAGGAC  
13> Q F A P F S S A L D V G F W H E L T Q K K L N E Y R L D E A P K D  
701 ATTAAGGGTTATTACTACAATGGTGACTCTGCTGGGCTGCCAGCTCGCTTAACATTGGAGTTCAGTGCCTTTGACATGAGTGCCTCCACCCAGCCCGTT  
47> I K G Y Y Y N G D S A G L P A R L T L E F S A F D M S A P T P A R

XhoI (838)  
801 GCTGCCAGCTATTGGAACACTGTATAACCAACACACTCGAGTCTTTCAAGACTGCAGATAAGAAGCTCCTTTTGGAAACAGCAGCAAATGAGATATG  
80> C C P A I G T L Y N T N T L E S F K T A D K K L L L E Q A A N E I W  
901 GGAATCCATAAAATCAGGCACTGCTCTTGAACCCCTGTACTCCTCAACAAGTTCCTCCTTGGACATTTGCAGATCTAAAGAAGTACCCTTCTACTAT  
113> E S I K S G T A L E N P V L L N K F L L L T F A D L K K Y H F Y Y  
1001 TGGTTTTGCTATCCTGCCCTCTGCTTCCAGAGAGTTTACCTCTATTGAGGGCCAGTGGGTTTGGATCAAAGGTTTCACTAAAACAGATTGAAGCAC  
147> W F C Y P A L C L P E S L P L I Q G P V G L D Q R F S L K Q I E A

NdeI (1109)  
1101 TAGAGTGTGCATATGATAATCTTTGTCAAACAGAGGAGTCCACAGCTCTTCTTACTTCTTAATCAAGTATGATGAGAACATGGTGTGTTTCCCTTGC  
180> L E C A Y D N L C Q T E G V T A L P Y F L I K Y D E N M V L V S L L  
1201 TAAACTACAGTGATTTTCCAAGTCAAAGGACGAAGATAACAATTGGTGTATATGATGATCCCTGTAACCTAGCCAGTACCCTGGATGGCCTTTGAGG  
213> K H Y S D F F Q G Q R T K I T I G V Y D P C N L A Q Y P G W P L R  
1301 AATTTTTTGGTCTAGCAGCCACAGATGGAGTAGCAGTTTCCAGTCTGTTGAAGTTGTTTGTCTCCGTGACCGTACCATGCAGGGGGCAGAGACGTTG  
247> N F L V L A A H R W S S S F Q S V E V V C F R D R T M Q G A R D V

BstBI (1414)  
1401 CCCACAGCATCATCTTGAAGTGAAGCTTCCAGAAATGGCATTAGCCAGATTGTCTAAAGCAGTTGGATGGAAAAAGAACCAGAAAGGAGGCATGGG  
280> A H S I I F E V K L P E M A F S P D C P K A V G W E K N Q K G G M G

BsaBI (1561)  
1501 ACCAAGGATGGTGAACCTCAGTGAATGTATGGACCCTAAAAGTTAGCTGAGTCATCAGTGGATCTAAATCTCAAACCTGATGTGTTGGAGATTGGTTCCT  
313> P R M V N L S E C M D P K R L A E S S V D L N L K L M C W R L V P

NgoMIV (1648)  
NaeI (1648)  
1601 ACTTTAGACTTGGACAAGTTGTGTCTGCAAAATGTCTGCTGCTTGGAGCCGGCACCTTGGGTTGCAATGTAGCTAGGACGTTGATGGGTTGGGGCGTGA  
347> T L D L D K V V S V K C L L L G A G T L G C N V A R T L M G W G V

AvrII (1779)  
1701 GACACATCACATTTGTGGACAATGCCAAGATCTCTACTCCAATCCTGTGAGGCAGCCTCTCTATGAGTTTGAAGATTGCCTAGGGGGTGGTAAGCCCAA  
380> R H I T F V D N A K I S Y S N P V R Q P L Y E F E D C L G G G K P K

SspI (1830)  
RsrII (1814) XmnI (1827)  
1801 GGCTCTGGCAGCAGCGGACCGGCTCCAGAAAATTTCCCGGTGTGAATGCCAGAGGATTCAACATGAGCATACTATGCCTGGGCATCCAGTGAACCTC  
413> A L A A A D R L Q K I F P G V N A R G F N M S I P M P G H P V N F

XcmI (1901)  
1901 TCCAGTGTCACTTGGAGCAAGCCCGCAGAGATGTGGAGCAACTGGAGCAGCTCATCGAAAGCCATGATGTCGTTCTTCTATTGATGGACACCAGGGAGA  
447> S S V T L E Q A R R D V E Q L E Q L I E S H D V V F L L M D T R E

Tth111I (2087)  
BspHI (2081)  
2001 GCCGGTGGCTTCTGCGTCAATTGCTGCAAGCAAGAGAAAGCTGGTCATCAATGCTGCTTTGGGATTTGACACATTTGTTGTCATGAGACATGGTCTGAA  
480> S R W L P A V I A A S K R K L V I N A A L G F D T F V V M R H G L K

PshAI (2125) DraIII (2140)  
2101 GAAACCAAAGCAGCAAGGAGCTGGGACTTGTGTCAAACCCCTGTGGCATCTGCTGACCTCCTGGGTCATCGCTTTTTGCCAATCCCTGGTTAC  
513> K P K Q Q G A G D L C P N H P V A S A D L L G S S L F A N I P G Y

ApaLI (2274)  
2201 AAGCTTGGCTGCTACTTCTGCAATGATGTGGTGGCCCCAGGAGATTCAACCAGAGACCGGACCTTGGACCAGCAGTGCAGTGTGAGTCCAGGACTGG  
547> K L G C Y F C N D V V A P G D S T R D R T L D Q Q C T V S R P G L

PvuI (2388)  
2301 CCGTATTGCAGGAGCCCTGGCCGTGGAATTGATGGTATCTGTTTTGCAGCATCCAGAAGGGGGCTATGCCATTGCCAGCAGCAGTGCAGTCCGATGAA  
580> A V I A G A L A V E L M V S V L Q H P E G G Y A I A S S S D D R M N

BsrGI (2497)  
2401 TGAGCTCAACCTCTTGGGCTTGTGCCTCACCAGATCCGGGATTTCTTTCACGGTTTGATAATGCTTCCCGTCAGCCTGGCATTGACAAATGT  
613> E P P T S L G L V P H Q I R G F L S R F D N V L P V S L A F D K C

2501 ACAGCTTGTTCCTCCAAAGTTCCTGATCAATATGAACGAGAAGGATTTAACTTCTAGCCAAGTGTTAATTCTTCACATTCCTTCTTAGAAGACTGA  
647▶ T A C S S K V L D Q Y E R E G F N F L A K V F N S S H S F L E D L  
2601 CTGGTCTTACATTGCTGCATCAAGAAACCAAGCTGCTGAGATCTGGGACATGAGCGATGATGAGACCATCTGAGATGGCCCCGTGTGGGGCTGACTTC  
680▶ T G L T L L H Q E T Q A A E I W D M S D D E T I •

**MscI (2711)**  
**NheI (2705)**

2701 TCCCCGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGACAAACCACAAC TAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGA

**HpaI (2843)**

2801 TGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAACAATTGCATTCATTTTATGTTTCAGGTTTCAGGGGAGGTGTGGAG

**EcoRI (2939)**

2901 GTTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACTTTAACCTCCAATCAAGCCTCTACTTGAATCCT  
3001 TTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTGCAGCCTCACCTTCTTTTATGAGTTTAAAGATATAGTGT

SspI (3178) SwaI (3192)

3101 ATTTTCCAAGGTTTGAAGTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTTAGTAAAAATTCAGAAATAATTTAAAT

**EcoO109I (3253)**

3201 ACATCATTGCAATGAAAAATAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACA  
3301 AAGGAACCTTAAATAGAAATGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTGACC  
141▶ N R T Y K L P I L E E I T T K V

**SacI (3453)**

3401 AGCTTGCCATTCTCAATGAGCACAAGCAGTCAAGGAGCATAGTCAGAGATGAGCTCTGTCACATGCCACAGGGGCTGACCACCCTGATGGATCTGT  
123▶ 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 D  
3501 CCACCTCATCAGAGTAGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGAC  
90▶ 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

**StuI (3617)**

3601 AGTGACCCTGCCAATGTAGGCCTCAATGGACAGCAGAGATGATCTCCCGAGTCTGGTCTGATGGCCGCCCGACATGGTGTGTTGTCTCATAG  
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

**BspHI (3767)**  
**XmnI (3759)**

3701 AGCATGGTATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGCTTTCATGATGGCCCTCTATAGTGAGTCGTATTAT  
23▶ 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 (3825)**  
**SacI (3882)**

3801 ACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTATCTGACGGTTCATAAACGAGCTCTGCTTATATAGA

**SpeI (3980)**

3901 CCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCC  
4000 CATTGACGTCAATGGGGTGGAGACTTGGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGC

**SnaBI (4108)**

4100 GATGACTAATACGTAGATGTAAGTACCAAGTAGGAAAGTCCATAAGGTCATGTAAGTGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATA

**NdeI (4213)**

4200 GGGGGCGTACTTGGCATATGATACACTTGTACTGCAAGTGGGCAGTTTACCCTAAATACTCCACCATTGACGTCAATGGAAAGTCCCTATTGGCG

**SdaI (4391)**

4300 TTAATATGGAACATACGTCAATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTGACGCGGGCCATTTACCGTAAGTTATGTAACGCCTG C A G

**PacI (4399)**  
**BspLU11I (4409)**

4399 G TT AA TTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGA  
4498 GCATCACA AAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCTGGAAGCTCCCTCGTGCGCTCTCT  
4598 GTTCCGACCTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCAGCTGAGGTATCTCAGTTCGGTGT

**ApaLI (4723)**

4698 AGGTCGTTCCGCTCAAGCTGGGCTGTGTGCACGAACCCCCGTTCCAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAG  
4798 ACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAAGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTAC  
4898 GGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAAACAAACCCG  
4998 CTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCA

**EagI (5159)**  
**PacI (5139)** **SwaI (5148)** **NotI (5158)**

5098 GTGGAACGAAAACCTCACGTTAAGGGATTTTGGTCAATGGCTGTAATTAACATTTAAATC AGCGGCCGCAATAAAATATCTTTATTTTTCATTACATCTGT  
5198 GTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAAATAGGCTGTCCCCAGTGCAAGTGC  
5298 AGGTGCCAGAACATTTCTATCGAA