



PvuI (7) SgfI (6) MfeI (82)  
1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTCCGCAATTGAACGGGTGCCTA  
101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTATGTCGTGTACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203) HindIII (245) Bsu36I (291)  
201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCCTTCACGCGCCCGCCCTACCTGAGGCC  
301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)  
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTTT

SphI (566) NcoI (580)  
501 TCTGTTCTGCCCGTTACAGATCCAAGCTGTGACCGGCGCTACCTGAGATCACCGGCTCCGAGACAGCATGCGGTACCTACCATTGGCTGTTGCTGTGGGC  
601 ATTCTACAGGTCTGGGACAATCTGAAGCCCAGAAAAGAATTACACCTTCCGCTGCCTGCAGATGTCTTCTTTGCAAACAGAAGCTGGTCCCGCACA  
11▶ F L Q V W G Q S E A Q Q K N Y T F R C L Q M S S F A N R S W S R T  
1▶ M R Y L P W L L L W A

NcoI (775)  
701 GACAGCGTGGTCTGGCTGGGGATCTGCAGACTCACCGTTGGAGTAATGACTCAGCCACCATCAGCTTACGAAGCCATGGTCCCAGGGCAAGTTGAGTA  
45▶ D S V V W L G D L Q T H R W S N D S A T I S F T K P W S Q G K L S

NdeI (823)  
801 ACCAGCAGTGGGAGAAGTTGCAGCATATGTTTCAAGTCTATCGAGTCACTTTACCAGGGACATACAGGAATTAGTCAAAATGATGTCACCTAAAAGAAGA  
78▶ N Q Q W E K L Q H M F Q V Y R V S F T R D I Q E L V K M M S P K E D

HindIII (960)  
901 CTATCCCATTGAGATCCAGCTGTCTGCCGGCTGTGAAATGTACCCTGGGAATGCTTCGGAAAGCTTTTACACGTAGCATTTCAGGAAAATATGTCGTG  
111▶ Y P I E I Q L S A G C E M Y P G N A S E S F L H V A F Q G K Y V V

Bsp120I (1034)  
1001 AGATTCTGGGAACTCCTGGCAGACAGTCCCAGGGCCCATCTTGGTTAGACTTGGCCATCAAAGTCTCAACGCTGATCAAGGGACAAGTGAACCG  
145▶ R F W G T S W Q T V P G A P S W L D L P I K V L N A D Q G T S A T

BstXI (1186)  
1101 TGCAAGTCTCCTGAATGACACCTGCCCCCTATTTGTCGCTGGTCTCCTAGAGGCAGGGAAGTCAAGCAAGGCAAGGCAAGCCAGTGGCCTGGTT  
178▶ V Q M L L N D T C P L F V R G L L E A G K S D L E K Q E K P V A W L

MscI (1224) XcmI (1264) BstEII (1294)  
1201 GTCCAGTGTCCCAGCTCTGCA\_CATGGCCATAGGCAGCTGGTGTGTATGCTCTGGCTTCTACCCAAAACCTGTGTGGTGATGTGGATGCGGGGTGAC  
211▶ S S V P S S A H G H R Q L V C H V S G F Y P K P V W V M W M R G D

SdaI (1406) AvrII (1428) EcoRV (1441) ScaI (1497)  
1301 CAGGAGCAACAGGGTACTCACAGAGGTGATTTCTGCCAAATGCTGATGAGACATGGTATCTTCAAGCAACCTGGATGTGGAGGCTGGAGAGGAAGCTG  
245▶ Q E Q Q G T H R G D F L P N A D E T W Y L Q A T L D V E A G E E A

1401 GCCTGGCTGCAGGGTGAAGCACAGCAGCCTAGGAGGACAGGATATCATCCTCTACTGGGATGCCAGGCAAGCACCCGTGGGCTGATCGTCTTCATAGT  
278▶ G L A C R V K H S S L G G Q D I I L Y W D A R Q A P V G L I V F I V

Eco47III (1555)  
1501 ACTGATCATGCTAGTGGTGGTGGTGTGTAGTCTACTATATCTGGAGAAGGAGAAGCGCTTATCAAGACATCCGGTACTTCTTACACCTGCCTCT  
311▶ L I M L V V V G A V V Y Y I W R R R S A Y Q D I R •

MscI (1611) NheI (1605)  
1601 CCTGAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGA

HpaI (1743) MfeI (1754)  
1701 TGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAACATTGCATTATTTATGTTTCAGGTTCCAGGGGAGGTGTGGGAG

EcoRI (1839)  
1801 GTTTTTTAAAGCAAGTAAACCTCTACAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACCTTAACTCCAATCAAGCCTCTACTTGAATCCT  
1901 TTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTTGGCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGT

SapI (2021) SspI (2078) SwaI (2092)  
2001 ATTTTCCAAGGTTTGAAGTCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTTAGTAAAATATTCAGAAAATAATTTAAAT  
2101 ACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACA  
2201 AAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTACTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTGACC  
141▶ • N R T Y K L P I L E E I T T K V

SacI (2353) BstXI (2382)  
2301 AGCTTGCCATTCTCAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGT  
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

2401 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 (2517)**

2501 AGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCGAGTCTTGGTCTGATGGCCGCCCGACATGGTGTCTTGTGCTCCTCATAG  
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

**XmnI (2659)**

2601 AGCATGGTATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCTGCTGAGAGATGTTGAAGGTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTAT  
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 (2725)** **SacI (2782)**

2701 ACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCACATAAACGAGCTCTGCTTATATAGA

**SpeI (2880)**

2801 CCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCGTTGATTTACTAGTCAAAACAACTCCC  
2901 ATTGACGTC AATGGGGTGGAGACTTGGAAATCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCG

**SnaBI (3008)**

3001 ATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAG

**NdeI (3113)**

3101 GGGGCGTACTTGGCATATGATACTTGTACTGCTCAAGTGGGCGAGTTTACCGTAAATACTCCACCATTGACGTCAATGGAAAGTCCCTATTGGCGT

**SdaI (3291)PacI (3299)**

3201 TACTATGGGAACATACGTCAATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAAGTTATGTAACCGCTGCAGGT

**BspLU11I (3309)**

3301 TAAATAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGTGCGGTTTTTCCATAGGCTCCGCCCCCTGACGAGCA  
3401 TCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTT

3501 CCGACCCTGCCGTTACCGGATACCTGTCCGCCTTCTCCCTTCGGAAGCGTGGCGCTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGGTGATGG

**ApaLI (3623)**

3601 TCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTGACGCCGACCGTGGCGCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGTAAGACA  
3701 CGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGC

3801 TACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTG  
3901 GTAGCGGTGGTTTTTTTGTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTG

**EagI (4059)** **PacI (4039) SwaI (4048) NotI (4058)**

4001 GAACGAAACTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAATATCTTTATTTTATTACATCTGTGTG  
4101 TTGGTTTTTTGTGTAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCGAGTGCAAGTGCAGG  
4201 TGCCAGAACATTTCTCTATCGAA