



PvuI (7) SgfI (6) MfeI (82)  
1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA  
101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGTGCTGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)  
201 Psp1406I (203) PvuII (239) Bsu36I (291)  
GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACGCGCCGCCCTACCTGAGGCC  
301 GCCATCCACGCCGGTTGAGTCGGCTTCTGCCGCTCCCGCTGTGGTGCCTCTGAAGTGCCTCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)  
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTGGCTGACCTGCTTGTCTCAACTCTACGCTTTGTTTCGTTT

AgeI (552) BspLU11I (560)  
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCTACCTGAGATCACCGGTCAACATGTTTGCCAAAGCAACTCGAAATTTTCTTAAAGAAGT  
1 M F A K A T R N F L K E V  
BstEII (669)  
601 TGATGCTGGAGGAGACCTGATTTCACTCTCACACTTGAACGACTCTGACAAGTGCACACTTCTAAGTCTGGTGACCAAAAAGAAGAGATACTGGTGCTGG  
13 D A G G D L I S V S H L N D S D K L Q L L S L V T K K K R Y W C W  
701 CAGAGACCAAGTACCAGATTTATCTGCCACCTGGAAGATGTACTCACAGAAGGGCACTGTCTCAGTCCAGTGGTGTGGAGTCAGACTTCGTGAAT  
47 Q R P K Y Q I L S A T L E D V L T E G H C L S P V V V E S D F V K  
BsrBI (825) Psp1406I (865)  
801 ACGAGAGCAAGTGTGAGAACCATAAGAGCGGGCTATTGGACAGTCTGGGGAAGTCAAGCTGAACGTTGGTGGCAAAGCGTGGTGGAGAGTCACTC  
80 Y E S K C E N H K S G A I G T V V G K V K L N V G G K G V V E S H S  
Bsu36I (912)  
901 TTCGTTTGAACCTGAGGAAGCAGGAGGTGGACGTGCAGCAGCTCATCCAGGATGCCGTCAGAGAACAGTTAATATGGACAACCTGGTACTTCAGCAG  
113 S F G T L R K Q E V D V Q Q L I Q D A V K R T V N M D N L V L Q Q  
BspHI [m] (1044)  
1001 GTGCTAGAGAGCAGGAACGAGGTCTGTGTGCTGACGCAGAAGATCATGACCACGCAGAAGTGCCTGATTTCTGAGCATGTGCAGTCGGAGGAGACGT  
147 V L E S R N E V L C V L T Q K I M T T Q K C V I S E H V Q S E E T  
BamHI (1115)  
1101 GCGGAGGCATGGTGGGGATCCAGACCAAGACTATACAGGTGTGAGCAACGGAGGATGGGACIGTCACCACAGACCAATGTAGTGTGGAGATCCCTGC  
180 C G G M V G I Q T K T I Q V S A T E D G T V T T D T N V V L E I P A  
MscI (1248) EcoRI (1258)  
1201 TGCCACCACCATTGCCTATGGCATCATGGAGCTGTTTGTGAAACAAGATGGCCAGTTTGAATTCGCCTCCTCCAAGGAAACATGGTGGCTTCGAGCAT  
213 A T T I A Y G I M E L F V K Q D G Q F E F C L L Q G K H G G F E H  
Tth111I (1312)  
1301 GAGAGAACTAGACTCTGTCTACTTGGACCCCTGGCCTACAGAGAGTTCGCCTTTCTGGACATGCTGGATGGGGTCAAGGGATCTCTTCGAGGAGC  
247 E R K L D S V Y L D P L A Y R E F A F L D M L D G G Q G I S S Q D  
1401 GGCCCTACGAGTTGTAACAAGCAACCTGCACCTAGAGAGGATTTCCATCCCTTTGGCGTGTACCTGCCAGCAGCAGAGGGCGCTGTTCTGTGT  
280 G P L R V V K Q A T L H L E R S F H P F A V L P A Q Q Q R A L F C V  
PstI (1501) XmnI (1525)  
1501 CCTGCAGAAAATCCTGTTTGTGAAAGAATCCTTCGGGCCCTGGAGCAAGTGTGTGATGATGGCTGGTGGCTCTGGTCTCACAGGCTGTATTGGCA  
313 L Q K I L F D E E L L R A L E Q V C D D V A G G L W S S Q A V L A  
PvuII (1648)  
1601 ATGGAGGAGTGACCGACAGTCAGCAGCAGGACCTCACAGCCTTTCTGAGCTGGTGGGATACAGGATACAAGGAGAGCATCTGGCCACAGGATGAGG  
347 M E E L T D S Q Q Q D L T A F L Q L V G Y R I Q G E H P G P Q D E  
1701 TCAGCAACCAGAAGCTCTTTCGCAACAGCCTACTTCTGGTGCAGCGCATAGCAGAAATGCCTGATAATGCCACAGTTTCTGGGACTTGTGCAAACT  
380 V S N Q K L F A T A Y F L V S A L A E M P D N A T V F L G T C C K L  
1801 CCATGTTATTTCTTCGCTGTGCTGCTTCTCCATGCTGTCTGATGACAGCGTGTGTGATTTTCAACCCACCTTGGCTCCTCTGAGAGACACAGAG  
413 H V I S S L C C L L H A L S D D S V C D F H N P T L A P L R D T E  
1901 AGTGGTTCATGTCAGCGATTGTTTGCCTCTGCTGACATTGCCCTGGAGAGGATGCAGTTTCTGCGAAAGCCACCATCCTGAAGGACTCTTGATCT  
447 R F G I V Q R L F A S A D I A L E R M Q F S A K A T I L K D S C I  
SapI (2059)  
2001 TCCCCTAATTTCTCACATCACTAAGTGGGCTCAGCACTCTAAGCAAAGAGCATGAGGAAGAGCTTGTGAGTCCAGGACATGCTACAGGTCAAGACTA  
480 F P L I L H I T L S G L S T L S K E H E E E L C Q S G H A T G Q D •  
MscI (2120)  
NheI (2114)  
2101 GCTACTTTTCAGGAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAACCACAACCTAGAATGCAGTGAAAAAATGCTTTATTTGTGA  
513

HpaI (2252) MfeI (2263)  
2201 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAACAAATTGCATTCTTTATGTTTCAGGTTTCAGGGGGAG

EcoRI (2348)  
2301 GTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAATGTGGTATGGAATTCATAAATACAGCATAGCAAACTTTAACCTCCAATCAAGCCTCTAC

2401 TTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTCTTTCATGGAGTTTAAAG

SapI (2530) SspI (2587)

2501 ATATAGTGTATTTTCCCAAGGTTTGAAGTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTATGATAAATATTGAGAAAT

SwaI (2601)

2601 AATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACT

2701 TAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGTAGGGGGATGAGTTCCTCAATGGTG

141 • N R T Y K L P I L E E I T

SacI (2862) BstXI (2891)

2801 GTTTTGACCAGCTTGCCATTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGCACATGCCACAGGGGCTGACCACCTGA

126 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 V V R I

2901 TGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTC

93 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 A I A E

StuI (3026)

3001 AGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCAGTCTTGGTCTGATGGCCGCCCGACATGGTGTCTTGTG

60 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 H H K N

BbsI (3172)

XmnI (3168)

3101 TCCTCATAGAGCATGGTGTCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCTATAGTGAG

26 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 (3234) SacI (3291)

3201 TCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCATAAACGAGCTCTGC

SpeI (3389)

3301 TTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAA

3401 CAAACTCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCGTGAGTCAAACCGTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATG

SnaBI (3517)

3501 GTAATAGCGATGACTAATACGTAGTACTGCCAAGTAGGAAAGTCCATAAAGTCACTGACTGGGCATAATGCCAGGCGGGCCATTACCCTGATTGA

NdeI (3622)

3601 CGTCAATAGGGGCGTACTTGGCATATGATACACTTGTACTGCAAGTGGGCAGTTTACCCTAAATACTCCACCCATTGACGTCAATGGAAAGTCCC

3701 TATTGGCGTTACTATGGGAACATACGTATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTCAGCCAGGCGGGCCATTACCCTAAGTTATGTAACG

PacI (3808)

PstI (3801)

SdaI (3800) BspLU11I (3818)

3801 CCTGCAGGTTAAATAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCC

3901 TGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCTGGAAGCTCCCTCGTGCC

4001 TCTCTGTTCCGACCCTGCCGTTACCAGTACCTGTCCGCTTTCTCCCTTCGGAAAGCGTGGCGTTTTCTCATAGCTCAGCTGTAGGTATCTCAGTT

ApaLI (4132)

4101 CGGTGTAGGTCGTTTCGCTCAAGCTGGGCTGTGTGCACGAACCCCGTTCAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGTAGTCAACCC

4201 GGTAAGACACGACTTATGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCT

4301 AACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAA

4401 CCACCGCTGGTAGCGGTGTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGA

EagI (4568)

PacI (4548) SwaI (4557) NotI (4567)

4501 CGCTCAGTGAACGAAAACCTCACGTTAAGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAATATCTTTATTTTCATTAC

4601 ATCTGTGTGGTTTTTTGTGTGAATCGTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCCAGTGC

4701 AAGTGCAGGTGCCAGAACATTTCTCTATCGAA