



**PvuI (7)**  
**SgfI (6)** 1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACCGGTGCCTA MfeI (82) AgeI (89)

101 GAGAAAGTGGCGGGGTAACCTGGAAAGTGATGTCGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGC

**Psp1406I (203)** **HindIII (245)** **Bsu36I (291)**  
201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCCTTACGCGCCCGCCCTACCTGAGGCC

301 GCCATCCACGCGGTTGAGTCGCGTTTCTGCCGCCCTCCCGCTGTGGTGCCTCCTGAAGTGCCTCCGCGCTCTAGGTAAGTTAAAGCTCAGGTGCAGACC

**NgoMIV (441)**  
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTCTCAACTCTACGTCTTTGTTTCGTTT

**KasI (535)** **AgeI (552)** **SphI (568)**  
501 TCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGGGCGCTACCTGAGATCACCGGTAGGAGGGCCAGCATGACGGCCCTGGTACTCTCTGCATT BamHI (698)  
1 M Q A L V L L L C I

601 GGAGCCCTCTCGGGCACAGCAGCTGCCAGAACCCTGCCAGCCCCCGGAGGAGGGCTCCCCAGACCCCGACAGCACAGGGGCGCTGGTGGAGGAGGAGG  
11 G A L L G H S S C Q N P A S P P E E G S P D P D S T G A L V E E E  
701 ATCCTTTCTTCAAAGTCCCCGTGAACAAGCTGGCAGCGGCTGTCTCAACTTCGGCTATGACCTGTACCGGTGCGATCCAGCACGAGCCCCACGACCAA  
44 D P F F K V P V N K L A A A V S N F G Y D L Y R V R S S T S P T T N

**MscI (823)** **SfiI (830)** **BsrBI (853)**  
801 CGTGCTCCTGTCTCCTCTCAGTGTGGCCACGGCCCTCTCGGCCCTCTCGTGGGAGCGGAG CAGCGAACAGAATCCATCATTACCGGGCTCTACTAT  
77 V L L S P L S V A T A L S A L S L G A E Q R T E S I I H R A L Y Y

**Acc65I (927)** **BstEII (953)**  
901 GACTTGATCAGCAGCCAGACATCCATGGTACCTATAAGGAGCTCCTTGACACGGTCAACGCCCCAGAGAAGCTCAAGAGTGCCTCCCGGATCGTCT  
111 D L I S S P D I H G T Y K E L L D T V T A P Q K N L K S A S R I V

**FspI (1012)** **BstXI (1024)** **NdeI (1051)**  
1001 TTGAGAAGAAGCTGCGCATAAAAATCCAGCTTTGTGGCACCTCTGAAAAGTCAATGGGACAGCCAGAGTCTGACGGGCAACCCTCGTTGGACCT  
144 F E K K L R I K S S F V A P L E K S Y G T R P R V L T G N P R L D L  
1101 GCAAGAGATCAACAACTGGGTGCAAGCGCAGATGAAAGGGAAGCTCGCCAGGTCCACAAGGAAATCCCGATGAGATCAGCATTCTCCTTCTCGGTGTG  
177 Q E I N N W V Q A Q M K G K L A R S T K E I P D E I S I L L G V

**XmnI (1240)** **XhoI (1251)** **SandI (1288)**  
1201 GCGCACTTCAAGGGCAGTGGGTAACAAAGTTTACTCCAGAAAAGACTTCCCTCGAGGATTTCTACTTGGATGAAGAGAGGACCGTGAGGGTCCCCATGA  
211 A H F K G Q W V T K F D S R K T S L E D F Y L D E E R T V R V P M

**BglII (1340)**  
1301 TGTCGGACCCCTAAGGCTGTTTTACGCTATGGCTTGATTGATTGATCTCAGCTGCAAGATTGCCAGCTGCCCTTACCGGAAGCATGAGTATCATCTTCTT  
244 M S D P K A V L R Y G L D S D L S C K I A Q L P L T G S M S I I F F

**BspHI (1463)** **BbsI (1484)**  
1401 CCTGCCCTGAAAGTGACCCAGAATTTGACCTTGATAGAGGAGAGCCTCACCTCCGAGTTTCATTGACATAGACCGAGAAGTGAAGACCGTGCAGGCG  
277 L P L K V T Q N L T L I E E S L T S E F I H D I D R E L K T V Q A

**SdaI (1553)**  
1501 GTCCTCACTGTCCCAAGCTGAAGCTGAGTTATGAAGGGGAAGTCAACCAAGTCCCTGCAGGAGATGAAGCTGCAATCCTTGTGTTGATTACCAGACTTTA  
311 V L T V P K L K L S Y E G E V T K S L Q E M K L Q S L F D S P D F  
1601 GCAAGATCAGCGCAAACCCATCAAGCTGACTCAGGTGGAACACCCGGCTGGCTTTGAGTGGAAACGAGGATGGGGCGGGAACCCCGCCAGCCAGGCT  
344 S K I T G K P I K L T Q V E H R A G C F E W N E D G A G T T P S G G L  
1701 GCAGCCTGCCACCTCACCTTCCGCTGGACTATCACCTTAACAGCCTTTTATCTTCTGACTGAGGGACACAGACACAGGGGCCCTTCTTTCATTGGC  
377 Q P A H L T F P L D Y H L N Q P F I F V L R D T D T G A L L F I G

**SspI (1838)** **NheI (1852)** **MscI (1858)**  
1801 AAGATTCTGGACCCAGGGGCCCTAATATCCAGTTTAAATATCCAATACCGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACC  
411 K I L D P R G P •

**HpaI (1990)**  
1901 ACAACTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACA

**MfeI (2001)** **EcoRI (2086)**  
2001 ACAATTGCATTCATTTTATGTTTCAGGTTACGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAATGTGGTATGGAATTCTAAAATAC  
2101 AGCATAGCAAACTTTAACCTCCAATCAAGCCTTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTGCCAATGTGCATT

**SapI (2268)**  
2201 AGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGTATTTTCCCAAGTTTTGAACTAGCTCTTCATTCTTTATGTTTTAAATGCACTG

**SspI (2325)** **SwaI (2339)**  
2301 ACCTCCACATTCCTTTTTAGTAAAATATTCAGAAAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCA  
2401 AGGCCCTTCAATAATCCCCAGTTTAGTGTGGACTTAGGGAACAAAGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGACTTCTAGCTTTAGT  
141 • N  
2501 TCCTGGTGTACTTGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGAT  
139 R 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

BstXI (2629)

2601 GAGCTCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCCTTC  
 106 L E 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

StuI (2764)

2701 TGCCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTGACCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCAG  
 72 Q G 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

2801 TCTTGGTCTGATGGCCGCCGACATGGTGCTTGTCTCATAGAGCATGGTGATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGA  
 39 K 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

BspHI (2914)  
 BbsI (2910)  
 XmnI (2906)

2901 GATGTTGAAGGTCCTCATGATGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACAGCGTGGATGGCG  
 6 I N F T K M

AseI (2972)

3001 TCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTT

SpeI (3127)

3100 ACGACATTTTGAAAGTCCC GTT GATTACTAGTCAAAAACAACTCCCATTGACGTCAATGGGGTGGAGACTTGAAATCCC GTGAGTCAAACCGCTA

SnaBI (3255)

3199 TCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCCATAAGGTCATG

NdeI (3360)

3299 TACTGGGCATAATGCCAGGGCGGCCATTTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTT

3399 ACCGTAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGGCGGGGTGTTGGG

SdaI (3538) PacI (3546) BspLU11I (3556)

3499 CGGTCAGCCAGGGCGGCCATTTACCGTAAGTTATGTAACGCCTGCAGTTAA TTAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAA  
 3597 AAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTA  
 3697 TAAAGATACCAGGCGTTTCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGAA

ApaLI (3870)

3797 GCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCAAGCTGGGCTGTGTGCACGAACCCCGTTCCAGCCGA  
 3897 CCGCTGCGCTTATCCGTAACATATCGTCTTGTAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCG  
 3997 AGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTA  
 4097 CCTTCGAAAAAGAGTTGGTAGCTCTTGTATCCGCAAACAAACCACCGCTGGTAGCGGTGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAA

EagI (4306)  
 NotI (4305)

4297 TTTAAATCAGCGCCGCAATAAAATATCTTTATTTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAA  
 4397 AACGAAACAAAACAACTAGCAAATAGGCTGTCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA

PacI (4286) SwaI (4295)

4197 AGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGGAAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACA