



**PvuI (7)**  
**SgfI (6)** MfeI (82) EcoNI (96)  
1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

101 GAGAAGTGGCGCGGGTAAACTGGAAAGTGTATGCTGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

**HindIII (245)** **Bsu36I (291)**  
**Psp1406I (203)** PvuII (239) EcoNI (287)  
201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACCGCGCCGCCCGCCCTACCTGAGGCC

301 GCCATCCACGCGGTTGAGTGCAGTCTGCCGCTCCCGCCTGTGGTGCCTCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

**NgoMIV (441)**  
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCGGCTCTCCACGCTTGGCTGACCCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

**NcoI (560)** **BstEII (555)** **EagI (587)**  
**AgeI (552)** SandI (659)  
501 TCTGTTTGCGCCGTTACAGATCCAAGCTGTGACCGGCCCTACCTGAGATCACCGGTCACCATGGAACAACGGGGACAGAAGCCCGCGCGCTTCGGG  
1 M E Q R G Q N A P A A S G

601 GGCCCGAAAAGGCACGGCCAGGACCCAGGGAGGCGCGGGGAGCCAGGCTGGGCCCGGGTCCCAAGACCCCTTGCTGCTGTTGTCGCGCGGTCCTG  
13 A R K R H G P G P R E A R G A R P G P R V P K T L V L V V A A V L

**PvuII (710)** **BsrBI (758)**  
701 CTGTTGGTCTCAGCTGAGTCTGCTGTGATCACCAACAAGACCTAGCTCCCCAGCAGAGAGCGGCCCAACAAAAGAGGTCCAGCCCTCAGAGGGAT  
47 L L V S A E S A L I T Q Q D L A P Q Q R A A P Q Q K R S S P S E G

**BbsI (826)** **BstAPI (842)**  
801 TGTGTCCACCTGGACACCATATCTCAGAAGACGGTAGAGTTGCATCTCTGCAAAATATGGACAGGACTATAGCACTCACTGGAATGACCTCCTTTTCTG  
80 L C P P G H H I S E D G R D C I S C K Y G Q D Y S T H W N D L L F C  
901 CTTGCGCTGCACAGGTGTGATTGAGTGAAGTGGAGCTAAGTCCCTGCACCACGACCAGAAACACAGTGTGTGAGTGCAGAAAGGCACCTTCCGGAA  
113 L R C T R C D S G E V E L S P C T T T R N T V C Q C E E G T F R E

**BstXI (1043)** **BsrGI (1069)**  
1001 GAAGATTCTCCTGAGATGTGCCGAAGTCCGCACAGGGTGTCCAGAGGGTGTCAAGGTCGGTGTGATGTACACCCCTGGAGTGACATCGAATGTGTCC  
147 E D S P E M C R K C R T G C P R G M V K V G D C T P W S D I E C V  
1101 ACAAAGAATCAGGCATCATCAGGAGTACAGTTGCAGCCGAGTCTTGTGTTGGCTGTGTTTGTGCAAGTCTTACTGTGGAAGAAAGTCTTCC  
180 H K E S G I I I G V T V A A V V L I V A V F V C K S L L W K K V L P

**SandI (1232)** **Tth111I (1279)**  
1201 TTACCTGAAAGGCATCTGCTCAGGTGGTGGTGGGACCTGAGCGTGTGGACAGAAGCTCACAACGACCTGGGCTGAGGACAATGTCCTCAATGAGATC  
213 Y L K G I C S G G G D P E R V D R S S Q R P G A E D N V L N E I  
XmaI (1387)

**BspLU11I (1376)**  
1301 GTGAGTATCTTGACGCCACCCAGTCCCTGAGCAGGAATGGAAGTCCAGGAGCCAGCAGGCAACAGGTGTCAACATGTTGTCGCCCGGGAGTCAG  
247 V S I L Q P T Q V P E Q E M E V Q E P A E P T G V N M L S P G E S  
1401 AGCATCTGCTGGAACCGGCAGAAGTCAAAGTCTCAGAGGAGGAGGCTGCTGGTCCAGCAAATGAAGTGTATCCACTGAGACTCTGAGACAGTGTCT  
280 E H L L E P A E A E R S Q R R R L L V P A N E G D P T E T L R Q C F

**BspHI (1544)** **BsrBI (1540)**  
1501 CGATGACTTTGCAGACTTGGTGCCTTTGACTCCTGGGAGCCGCTCATGAGGAAGTTGGGCTCATGGACAATGAGATAAAGTGGCTAAAGTGAAGCA  
313 D D F A D L V P F D S W E P L M R K L G L M D N E I K V A K A E A

**BsrGI (1619)**  
1601 GCGGGCCACAGGGACACCTGTACAGATGCTGATAAAGTGGTCAACAAAACCGGGCGAGATGCTCTGTCCACACCCCTGCTGGATGCCTTGGAGACGC  
347 A G H R D T L Y T M L I K W V N K T G R D A S V H T L L D A L E T

**XbaI (1764)** **BstAPI (1777)**  
1701 TGGGAGAGAGACTTGCCAAGCAGAAGATTGAGGACCACTTGTGAGCTCTGAAAAGTTCATGTATCTAGAAGTAAATGCAGACTCTGCCATGTCTAAGT  
380 L G E R L A K Q K I E D H L L S S G K F M Y L E G N A D S A M S •

**MscI (1815)** **NheI (1809)**  
1801 GTGATTCTCGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAAGTGAAGTGCAGTGAATAAATGCTTTATTTGTGAAATTT

**HpaI (1947)** MfeI (1958)  
1901 GTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAATTGCATTCAATTTATGTTTCAGGTTTCAGGGGAGGTGTG

**EcoRI (2043)**  
2001 GGAGGTTTTTAAAGCAAGTAAACCTCTACAATGTGGTATGGAATTTCAAAATACAGCATAGCAAACTTTAACTCCAAATCAAGCCTCTACTTGA  
2101 TCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTCATGGAGTTAAGATATA

**SapI (2225)** **SspI (2282)** **SwaI (2296)**  
2201 GTGTATTTTCCAAGTTTGAAGTACTGCTCTTCAATTTATGTTTAAATGCACTGACCTCCACATTCCTTTTGTAGTAAATATTCAGAAATAATTT  
2301 AAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGAGCAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGG  
2401 AACAAAGGAACCTTAAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTT  
141 • N R T Y K L P I L E E I T T K

BstXI (2586)

2501 GACCAGCTTGCCATTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGCACATGCCACAGGGGCTGACCACCTGATGGAT  
125 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 S  
2601 CTGTCCACCTCATCAGAGTAGGGTGCCTGACAGCCACAATGGTGTCAAAGTCCTTCTGCCCGTTGCTCAGAGCAGACCAATGGCAATGGCTTCAGCAC  
91 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 A C

StuI (2721)

2701 AGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCAGTCTTGGTCTGATGGCCGCCCCGACATGGTGCTTGTGTCCTC  
58 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 D E

BbsI (2867)

XmnI (2863)

2801 ATAGAGCATGGTGATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGTCTTTCATGGTGGCCCTCTATAAGTGAAGTCGTA  
25 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 (2929)

2901 TTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCACTAAACGAGCTCTGCTTATA

SpeI (3084)

3001 TAGACCTCCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAAACAAC

3101 TCCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCGTGAGTCAAACCGTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAAT

SnaBI (3212)

3201 AGCGATGACTAATACGTAGATGTAAGTCCCAAGTAGGAAAGTCCATAAGGTCATGTAAGTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCA

NdeI (3317)

3301 ATAGGGGGCGTACTTGGCATATGATACACTTGTACTGCAAGTGGGCAGTTTACCCTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTG

PstI (3496)

SdaI (3495)

3401 GCGTACTATGGGAACATACGTCAATTATTGACGTCAATGGGCGGGGGTCTGGGCGGTGAGCCAGGCGGGCCATTTACCCTAAGTTATGTAACGCTCG

PacI (3503) BspLU11I (3513)

3501 AGGTTAATTAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCGTTTTCCATAGGCTCCGCCCCCTGACG

3601 AGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCTGGAAAGCTCCCTCGTGGCTCTCC

3701 TGTTCGACCCTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGAAGCGTGGCGCTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTG

ApaLI (3827)

3801 TAGGTCGTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAA

3901 GACACGACTTATCGCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTA

4001 CGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACC

4101 GCTGGTAGCGGTGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTC

EagI (4263)

PacI (4243) SmaI (4252) NotI (4262)

4201 AGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCCAATAAAATATCTTTATTTTATTACATCTG

4301 TGTGTTGGTTTTTGTGTGAATCGTAACATAACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCAGTGCAAGTG

4401 CAGGTGCCAGAACATTTCTATCGAA