



**PvuI (7)**  
**SgfI (6)**  
1 GGATCTGCATCGCTCCGGTGCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGTGCTGTACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

**HindIII (245)**  
**Psp1406I (203)** **PvuII (239)** **Bsu36I (291)**  
201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTCACGCGCCGCCCTACCTGAGGCC

301 GCCATCCACGCCGGTTGAGTCGCGTTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

**NgoMIV (441)**  
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTGCCTGACCTGCTTGTCTCAACTCTACGCTTTGTTTCGTTT

**BstEII (555)** **AgeI (552)** **NcoI (560)** **Bsp120I (587)**  
501 TCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTACCATGGTTGCTGGGAGCGACGCGGGGCGGCCCTGGGGGT

1 M V A G S D A G R A L G V

**PvuII (639)** **XcmI (651)**  
601 CCTCAGCGTGGTCTGCCTGCTGCACTGCTTTGGTTTTCATCAGCTGTTTTCCCAACAAATATATGGTGTGTATGGGAATGTAACCTTCCATGTACCA

13 L S V V C L L H C F G F I S C F S Q Q I Y G V V Y G N V T F H V P

**EcoRI (769)**  
701 AGCAATGTGCTTTAAAAAGAGTCTATGAAAAAACAAAAGGATAAAGTTGCAGAAGTGGAAAATCTGAATTCAGAGCTTCTCATCTTTAAAAATA

47 S N V P L K E V L W K K Q K D K V A E L E N S E F R A F S S F K N

**SspI (886)**  
801 GGGTTTATTTAGACACTGTGTCAGGTAGCCTACTATCTACAACCTAACATCATCAGATGAAGATGAGTATGAAATGGAATCGCCAAATATTACTGATAC

80 R V Y L D T V S G S L T I Y N L T S S D E D E Y E M E S P N I T D T

**NsiI (984)**  
901 CATGAAGTCTTTCTTTATGTGCTTGTGCTCTTCCATCTCCACACTAATTGTGCATTGACTAATGGAAGCATTGAAGTCCAATGCATGATACCAGAG

113 M K F F L Y V L E S L P S P T L T C A L T N G S I E V Q C M I P E

1001 CATTACAACAGCCATCGAGGACTTATAATGTACTCATGGGATTGCTCTATGGAGCAATGTAACGTAACCTCAACCAGTATATTTTTAAGATGAAAAATG

147 H Y N S H R G L I M Y S W D C P M E Q C K R N S T S I Y F K M E N

1101 ATCTTCCAAAAAATACAGTGTACTCTTAGCAATCCATTATTTAATACAACATCATCAATCATTTTGAACCTGTATCCCAAGCAGCGGTCATTCAAG

180 D L P Q K I Q C T L S N P L F N T T S S I I L T T C I P S S G H S R

**BspLU11I (1243)**  
1201 ACACAGATATGCACCTTATACCCATACCATTAGCAGTAATTACAACATGTATTGTGCTGTATATGAATGGTATTCTGAAATGTGACAGAAAACAGACAGA

213 H R Y A L I P I P L A V I T T C I V L Y M N G I L K C D R K P D R

**MscI (1349)**  
**BstXI (1307)** **BbsI (1330)** **NheI (1343)**  
1301 ACCAACTCCAATTGATTGGTAACAGAAGATGAAGACAACAGCAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGA

247 T N S N •

**HpaI (1481)**  
1401 ATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAAACAATTGCA

**EcoRI (1577)**  
1501 TTCATTTTATGTTTCAGTTTCAGGGGAGGTGTGGGAGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTATGGAATTCATAAAATACAGCATAGCA

1601 AAACTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTG

**SapI (1759)**  
1701 CAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGTATTTCCCAAGTTTGAAGTACTGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCCAC

**SspI (1816)** **SwaI (1830)**  
1801 ATTCCCTTTTATGTAATAATTCAGAAATAATTTAAATACATCATTGCAATGAAAAATAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTC

1901 ATAATATCCCCAGTTTAGTAGTTGACTTAGGGAACAAAGAACCTTAAATAGAAATTTGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGT

141 N R T Y

**SacI (2091)**  
2001 ACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTCTCAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCT

136 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 L E R

**BstXI (2120)**  
2101 GCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGTGCCTGACAGCCACAATGGTGTCAAAGCTTCTGCCCGTTG

103 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 Q G N

**StuI (2255)**  
2201 CTCACAGCAGACCAATGGCAATGGCTTCAGCAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCAGTCTTGGTCC

69 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 K T R

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 K T R

XmnI (2397)

2301 TGATGGCCGCCCCGACATGGTGTCTGTTGTCCTCATAGAGCATGGTGTATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAA  
36 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 I N F

BbsI (2401)

AseI (2463)

2401 GGTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCT  
3 T K M

SacI (2520)

2501 IATCTGACGGTTCATAAACGAGCTCTGCTTATATAGACCTCCACCCTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTT

SpeI (2618)

2601 GGAAAGTCCCCTGATTACTAGTCAAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCCGTGAGTCAAACCGCTATCCAGCCCAT

SnaBI (2746)

2701 TGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCCATAGGTCATGTACTGGGCATA

NdeI (2851)

2801 ATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCGAGTTTACCGTAAATAC

2901 TCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCAATTATTGACGTCAATGGGCGGGGGTCTTGGGCGGTGAGCCAG

PacI (3037)

PstI (3030)

SdaI (3029)

BspLU11I (3047)

3001 GCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAAITAAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGCCGCGTTG

3101 CTGGCGTTTTTTCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGG

3201 CGTTTCCCCTGGAAGCTCCCTCGTGGCTCTCCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTCTCCCTTCGGGAAGCGTGGCGCTTTC

ApaLI (3361)

3301 TCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTGTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTCCAGCCGACCGCTGCGCCTTA

3401 TCCGGTAACTATCGTCTTGAGTCCAACCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGCGG

3501 GTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAG

3601 AGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAA

EagI (3797)

PacI (3777) SmaI (3786) NotI (3796)

3701 GATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGG

3801 CCGCAATAAAATATCTTTATTTTATTACATCTGTGTGTTGGTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAAC

3901 AAAC TAGCAAATAGGCTGTCCCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA