



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

101 GAGAAAGTGGCGCGGGTAAACTGGGAAAGTATGTCGTGTACTGGCTCCGCTTTTTCCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCC

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

301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

**NgoMIV (441)**  
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGCTCAACTCTACGCTTTTGTTCGTTTT

**AgeI (552)** **SmaI (567)**  
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTCAACATGTGGGACCCGTGCCAAGCAGGGCCAGGTTTACAC  
1 M S G P V P S R A R V Y T

**XhoI (620)** **BstBI (686)**  
601 AGATGTTAATACACACAGACCTCGAGAATACTGGGATTACGAGTCACATGTGGTGAATGGGAAATCAAGATGACTACCAGCTGGTTCGAAAATTAGGC  
13 D V N T H R P R E Y W D Y E S H V V E W G N Q D D Y Q L V R K L G  
701 CGAGGTAATACAGTGAAGTATTTGAAGCCATCAACATCACAATAATGAAAAAGTTGTTGTTAAAATTCTCAAGCCAGTAAAAAAGAAGAAAATTAAGC  
47 R G K Y S E V F E A I N I T N N E K V V V K I L K P V K K K K I K  
801 GTGAAATAAAGATTTTGGAGAATTTGAGAGGAGGTCCCAACATCATCACACTGGCAGACATTTGAAAAGACCTGTGTACGAACCCCGCCTTGGTTTT  
80 R E I K I L E N L R G G P N I I T L A D I V K D P V S R T P A L V F

**HpaI (942)**  
901 TGAACACGTAAACAACACAGACTTCAAGCAATTGTACCAGACGTTAACAGACTATGATATTCGATTTTACATGTATGAGATTCTGAAGGCCCTGGATTAT  
113 E H V N N T D F K Q L Y Q T L T D Y D I R F Y M Y E I L K A L D Y

**BspHI [m] (1054)**  
**BspHI (1046)**  
1001 TGTACACAGCATGGGAATTATGCACAGAGATGTCAAGCCCCATAATGTCATGATTGATCATGAGCACAGAAAGCTACGACTAATAGACTGGGGTTTGGCTG  
147 C H S M G I M H R D V K P H N V M I D H E H R K L R L I D W G L A

**MscI (1113)**  
1101 AGTTTTATCATCTGGCCAAGAATAATGTCCGAGTTGCTTCCGATACTTCAAAGTCTGAGCTACTTGTAGACTATCAGATGTACGATTATAGTTT  
180 E F Y H P G Q E Y N V R V A S R Y F K G P E L L V D Y Q M Y D Y S L

**NcoI (1260)** **BstXI (1298)**  
1201 GGATATGTGGAGTTTGGGTTGTATGCTGGCAAGTATGATCTTTCGGAAGGAGCCATTTTCCATGGACATGACAATTATGATCAGTTGGTGGGATAGCC  
213 D M W S L G C M L A S M I F R K E P F F H G H D N Y D Q L V R I A

**EcoRV (1372)**  
1301 AAGGTTCTGGGGACAGAAGATTTATATGACTATATTGACAAATACAACATTGAATTAGATCCACGTTTCAATGATATCTTGGGCAGACACTCTCGAAAGC  
247 K V L G T E D L Y D Y I D K Y N I E L D P R F N D I L G R H S R K

**StuI (1448)**  
**Bsu36I (1444)**  
1401 GATGGAAACGCTTTGTCCACAGTAAAAATCAGCACCTTGTGAGCCCTGAGGCCTTGGATTTCCTGGACAAACTGCTGCGATATGACCACAGTCACGGCT  
280 R W E R F V H S E N Q H L V S P E A L D F L D K L L R Y D H Q S R L

**XmnI (1559)** **SphI (1574)**  
1501 TACTGCAAGAGAGCAATGGAGCACCCCTATTTCTACACTGTTGTGAAGGACCAGGCTCGAATGGGTTTCATCTAGCATGCCAGGGGCGAGTACGCCCGTC  
313 T A R E A M E H P Y F Y T V V K D Q A R M G S S S M P G G S T P V  
1601 AGCAGCGCAATATGATGTCAGGGATTTCTTCACTGCAACCCCTTACCCCTTGGACCTCTGGCAGGCTCACCAGTATTGCTGCTGCAACCCCTTG  
347 S S A N M M S G I S S V P T P S P L G P L A G S P V I A A A N P L

**MscI (1774)**  
**NheI (1768)**  
1701 GGATGCCTGTTCCAGCTGCCGCTGGCGCTCAGCAGTAACGGCCCTATCTGTCTCTGATGCCTGAGCAGCTAGCTGGCCAGACATGATAAGATACATTGA  
380 G M P V P A A A G A Q Q •

1801 TGAGTTTGGACAAACCACAACACTAGAATGCAGTAAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAAT

**HpaI (1906)**  
1901 AAACAAGTTAAACAACAACAAATTGCATTCAATTTATGTTTCAGTTTCAGGGGAGGTGTGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTA

**EcoRI (2002)**  
2001 TGGAAATCTAAAATACAGCATAGCAAACTTTAACCTCCAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCT

**SapI (2184)**  
2101 GTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTTCATGAGTAAAGATATAGTGTATTTCCCAAGGTTTGAAGTATAGCTCTTCAATTTCTTA

**SspI (2241)** **SwaI (2255)**  
2201 TGTTTTAAATGCACTGACCTCCACATTCCCTTTTGTAGTAAAAATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGC

2301 AGAATCCAGATGCTCAAGGCCCTTATAATATCCCCAGTTTGTAGTTGGACTTAGGGAACAAGGAACCTTTAATAGAAATTTGGACAGCAAGAAAGCG

2401 AGCTTCTAGCTTTAGTTCCTGGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAAGCAGTCAG  
141 N 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  
SacI (2516) BstXI (2545)

2501 GAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAAT  
111 A Y D S I 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  
StuI (2680)

2601 GGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTACGACAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCA  
78 T D F D K 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

2701 GAGATGATCTCCCAAGTCTTGGTCTGATGGCCGCCCGACATGGTGTGTTGTCTCATAGAGCATGGTGTCTTCTCAGTGGCGACCTCCACCAGCT  
44 S I I E G T 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  
BbsI (2826)

2801 CCAGATCCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAA  
11 L D Q Q S I N F T K M  
XmnI (2822) AseI (2888)

2901 AACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTGCGTCAA  
SacI (2945)

3001 TGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCCACTGACGTCAATGGGGTGGAGACTTGGAAATCCCCGT  
SpeI (3043)

3101 GAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGT  
SnaBI (3171)

3201 CCCATAAGGTCATGTACTGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGATGTACTGC  
NdeI (3276)

3301 CAAGTGGGAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGTCAATGGG

PacI (3462)

3401 CGGGGGTCTGTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAATAAGAACATGTGAGCAAAAGGCCAGCAAAAGGC  
PstI (3455) SdaI (3454)

3501 CAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAAC

3601 CCGACAGGACTATAAAGATACCAGGCGTTTTCCCGTGGAAAGTCCCTCGTGCCTCTCTGTTCCGACCTGCCGCTTACCGGATACCTGTCCGCTTTTC

3701 TCCCTTCGGGAAGCGTGGCGTTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTGTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCC  
ApaLI (3786)

3801 CGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCGGTAAGACAGACTTATGCCACTGGCAGCAGCCACTGGTAACAGG

3901 ATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGC

4001 TGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAACACCGCTGGTAGCGGTGTTTTTTGTTTGAAGCAGCAGATTAC

4101 GCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTACGGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCT

EagI (4222)

4201 AGTTAATTAACATTTAAATCAGCGGCCGCAATAAAATATCTTTATTTTATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCT  
PacI (4202) SmaI (4211) NotI (4221)

4301 CCATCAAAAACAAAACGAAAACAAAACAACTAGCAAAATAGGCTGTCCCAGTGAAGTGCAGGTGCCAGAACATTTCTCTATCGAA