



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

101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTATGTCGTGACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

**Psp1406I (203)** **HindIII (245)**  
201 GTGAACGTTCTTTTTTCGCAACGGGTTTCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCCTTCACGCGCCCGCCCTACCTGAGGCC

301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCAACTCTACGCTTTTGTTCGTTT

**AgeI (552)** **SphI (569)**  
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTAGGGAGGGCCAGCATGCCAGGTGTCTGTGATAGGGCCCTGA  
1▶ M P G V C D R A P D

**BbsI (616)**  
601 CTTCTCTCCCGTCTGAAGACCAGGTGCTGAGGCCTGCCTTGGGAGCTCAGTGGCTCTGAACTGCACGGCTTGGGTAGTCTCTGGGCCCACTGCTCC  
10▶ F L S P S E D Q V L R P A L G S S V A L N C T A W V V S G P H C S

**ScaI (767)**  
701 CTGCCTTCAGTCCAGTGGCTGAAAGACGGGCTTCCATTGGGAATTGGGGCCACTACAGCCTCCACGAGTACTCTGGGTCAAGGCCAACCTGTCAGAGG  
44▶ L P S V Q W L K D G L P L G I G G H Y S L H E Y S W V K A N L S E

**BstXI (809)**  
801 TGCTTGTGTCAGTGTCTGGGGTCAACGTGACCAGCACTGAAGTCTATGGGCCTTCCACTGCTCCATCCAGAACATCAGTTCTCTCTCTCACTCT  
77▶ V L V S S V L G V N V T S T E V Y G A F T C S I Q N I S F S S F T L

**BbrPI (922)**  
901 TCAGAGAGCTGGCCCTACAAGCCACGTGGCTGCGGTGCTGGCCTCCCTCCTGGTCTGCTGGCCCTGCTGCTGGCCGCTGCTCTATGTCAAGTGCCGT  
110▶ Q R A G P T S H V A A V L A S L L V L L A L L L A A L L Y V K C R

**MluI (1025)**  
**XcmI (1020)**  
**Acc65I (1016)**  
1001 CTAACGTGCTGCTCTGGTACCAGGACGCGTATGGGGAGTGGAGATAAACGACGGGAAGCTCTACGACGCTACGCTCCTACAGCGACTGCCCCGAGG  
144▶ L N V L L W Y Q D A Y G E V E I N D G K L Y D A Y V S Y S D C P E

**BsrBI (1138)** **SapI (1158)** **BssHII (1188)**  
1101 ACCGCAAGTTCGTAACCTCATCTAAAGCCGACGTGGAGCGGCTCGGGCTACAAGCTCTCTGGACGACCGGACCTCTGCCGCGCTGAGCC  
177▶ D R K F V N F I L K P Q L E R R R G Y K L F L D D R D L L P R A E P

1201 CTCGCGGACCTCTTGGTGAACCTGAGCCGCTGCCGACGCTCATCGTGGTGTTCGAGCGCTTCTGAGCCGGGCTGGTGCAGCCACAGCTTCCGG  
210▶ S A D L L V N L S R C R R L I V V L S D A F L S R A W C S H S F R

**NgoMIV (1310)**  
1301 GAGGGCTGTGCCGGCTGCTGGAGCTACCCGAGACCCATCTTCATCACCTTCGAGGGCCAGAGGCGGACCCCGCGACCCGGCGCTCCGCTGCTGC  
244▶ E G L C R L L E L T R R P I F I T F E G Q R R D P A H P A L R L L

**BstEII (1416)**  
**DraIII (1411)** **SacII (1492)**  
1401 GCCAGCACCGCCACCTGGTGACCTTGTGCTCTGGAGGCCGGCTCCGTGACTCCTTCTCCGATTTTGGAAAGAAGTGCAGCTGGCGTGGCGGGAA  
277▶ R Q H R H L V T L L L W R P G S V T P S S D F W K E V Q L A L P R K

**PstI (1540)**  
1501 GGTGCAGTACAGGCTGTGGAAGGAGACCCCCAGACGACGACAAGGACCCCATGCTGATTCTTCGAGGCCGAGTCCCTGAGGGCCGGGCC  
310▶ V Q Y R P V E G D P Q T Q L Q D D K D P M L I L R G R V P E G R A

1601 CTGGACTCAGAGTGGACCCGGACCCTGAGGGGACCTGAGGCTGCGGGGCTGTCTTTGGAGAGCCATCAGCTCCACCGCACACCAGTGGGGTCTCGC  
344▶ L D S E V D P D P E G D L G V R G P V F G E P S A P P H T S G V S

**NruI (1744)**  
1701 TGGGAGAGAGCCGAGCAGCGAAGTGGACGCTCTCGATCTCGGCTCGCGAAACTACAGTGCCCGCACAGACTTCTACTGCCTGGTGTCCAAGGATGATAT  
377▶ L G E S R S S E V D V S D L G S R N Y S A R T D F Y C L V S K D D M

**MscI (1812)**  
**NheI (1806)**  
1801 GTAGCTGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAAGTGAAGTGCAGTGAATAAATGCTTTATTTGTGAAATTTGTG  
410▶ •

**HpaI (1944)** **MfeI (1955)**  
1901 ATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAAGTTAAACAACAATTGCATTCATTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGA

**EcoRI (2040)**  
2001 GGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACTTTAACCTCCAATCAAGCCTCTACTGAAATCC

2101 TTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGACGCTCACCTTCTTCATGGAGTTAAGATATAGTG

**SapI (2222)** **SspI (2279)** **Swal (2293)**  
2201 TATTTTCCAAGTGTGAAGTGTCTCTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTGTAGTAAAATTCAGAAAATATTTAAA

2301 TACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAAC

2401 AAAGGAACCTTTAATAGAAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTGAC  
 141 • N R T Y K L P I L E E I T T K V

2501 CAGCTTGCCATTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTG  
 124 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 R

2601 TCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCAGCACAGA  
 90 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 V

2701 CAGTGACCTGCCAATGTAGGCCTAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCTGATGGCCGCCCGACATGGTGCTTGTTCCTCATA  
 57 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 Y

BbsI (2864)

XmnI (2860)

2801 GAGCATGGTGATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGTCTTTCATGGTGGCCCTCTATAGTGAGTCGTATTA  
 24 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 (2926)

2901 TACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCATAAACGAGCTCTGCTTATATAG

SpeI (3081)

3001 ACCTCCCACCGTACACGCTACCGCCATTTGCGTCAATGGGCGGAGTTGTTACGACATTTTGAAAGTCCCCTGATTTACTAGTCAAAACAAACTCC

3101 CATTGACGTCAATGGGGTGGAGACTTGAAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGC

SnaBI (3209)

3201 GATGACTAATACGTAGATGACTGCCAAGTAGGAAAGTCCATAAGGTGATGACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATA

NdeI (3314)

3301 GGGGGCGTACTTGGCATATGATACACTTGTACTGCAAGTGGGCGAGTTTACCCTAAATACTCCACCCATTGACGTCAATGAAAGTCCCTATTGGCG

PstI (3493)  
SdaI (3492)

3401 TTAATATGGAACATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGTCCAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGG

PacI (3500) BspLU11I (3510)

3501 TTAATTAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCGTTTTTCCATAGGCTCCGCCCTGACGAGC

3601 ATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCCTGGAAGCTCCCTCGTGCGCTCTCTGT

3701 TCCGACCCTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAAGCGTGGCGTTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAG

ApaLI (3824)

3801 GTCGTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTAGCCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGAAGTCCAACCCGGTAAGAC

3901 ACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGG

4001 CTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAGAGTTGGTAGCTCTTGTATCCGGCAACAAACCACCGCT

4101 GGTAGCGGTGGTTTTTTTGTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGT

EagI (4260)  
PacI (4240) SwaI (4249) NotI (4259)

4201 GGAACGAAAACCTCACGTTAAGGGATTTTGGTATGGCTAGTTAATTAACATTTAAATCAGCGGCCCAATAAAATATCTTTATTTTCATTACATCTGTGT

4301 GTTGTTTTTTTGTGTAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCCAGTGCAAGTGCAG

4401 GTGCCAGAACATTTCTCTATCGAA