



**PvuI (7)**  
**SgfI (6)** 1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGCAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA MfeI (82)

101 GAGAAGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

**HindIII (245)**  
**Psp1406I (203)** 201 GTGAACGTTCTTTTTTCGCAACGGGTTTGGCCGACAGACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACCGCGCCCGCCGCTACCTGAGGCC PvuII (239) Bsp36I (291)

301 GCCATCCACGCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCTCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCGGCTCTCCACGCTTGGCTGACCCTGTTGCTCAACTCTACGTCTTTGTTTCGTTT

**NgoMIV (441)**  
**BspHI (560)**  
**AgeI (552)** 501 TCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGCGCGCTACCTGAGATCACCGGTCATCATGAACCTTCTGCTCTTTGGGTGCACTGGACCCTGGC ApaLI (583)

601 TTTACTGCTGTACTCCACCATGCCAAGTGGTCCAGGCTGCACCCACGACAGAAGGAGAGCAGAAGTCCCATGAAGTATCAAGTTCATGGATGTCTAC 1► M N F L L S W V H W T L A

13► L L L Y L H H A K W S Q A A P T T E G E Q K S H E V I K F M D V Y

701 CAGCGAAGCTACTGCCGTCGATTGAGACCCTGGTGGACATCTTCCAGGAGTACCCCGACGAGATAGGTACATCTTCAAGCCGCTCTGTGTCGCGCTGA 47► Q R S Y C R P I E T L V D I F Q E Y P D E I E Y I F K P S C V P L

**BstAPI (870)**  
 801 TGCCTGTGACGAGCTGCTGTAACGATGAAGCCCTGGAGTGGCTGCCACGTCAGAGAGCAACATCACCATGCAGATCATGCGGATCAAACCTCACAAAG 80► M R C A G C C N D E A L E C V P T S E S N I T M Q I M R I K P H Q S

901 CCAGCACATAGGAGAGATGAGCTTCTACAGCACAGCAGATGTGAATGCAGACCAAAGAAAGCAGAACAAGCCAGAAAATCACTGTGAGCCTTGTTC A 113► Q H I G E M S F L Q H S R C E C R P K K D R T K P E N H C E P C S

**BsrBI (1000)**  
 1001 GAGCGGAGAAAGCATTTGTTTGTCCAAGATCCGACAGCTGTAATGTTCTGCAAAAACACAGACTCGCGTTGCAAGGCGAGGCAGCTTGAGTTAAACG 147► E R R K H L F V Q D P Q T C K C S C K N T D S R C K A R Q L E L N

**PstI (1141)** 1101 AACGTAAGTGCAGATGTGACAAGCAAGCGGTGAGCCAGGCTGCAGGAAGGAGCTCCCTCAGGTTTTCGGGAACACAGACTCTCACCGAAAGACCGA MscI (1225)

180► E R T C R C D K P R R •

**NheI (1219)**  
 1201 TTAACCATGTCACCACCATGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGACAACCACTAGAATGCAGTAAAAAATGCTTTATT

**HpaI (1357)** 1301 TGTGAAATTTGTGATGCTATTGCTTTATTGTAACATTATAAGCTGCAATAACAAGTTAACAACAACCAATTGCATTCTTTATGTTTCAGGTTTCAGG MfeI (1368)

**EcoRI (1453)**  
 1401 GGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAATGTGGTATGGAATTTCAAAATACAGCATAGCAAACTTTAACCTCAAATCAAGCC

1501 TCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGT

**SapI (1635)** 1601 TTAAGATATAGTGTATTTTCCCAAGTTTGAAC TAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTGTAGTAAATATTCA SspI (1692)

**Swal (1706)** 1701 GAAATAATTTAAATACATCATTGCAATGAAATAAATGTTTTTTATTAGGCAGAAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTT

**EcoO109I (1767)**  
 1801 GGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTACTTGAGGGGATGAGTTCCTCAA 141► • N R T Y K L P I L E E I

**SacI (1967)** 1901 TGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGACATGCCACAGGGGCTGACCAC BstXI (1996)

128► 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 C M G C P S V V

2001 CCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTCTGCCCCTGCTCACAGCAGCAATGGCAATG 95► 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 S V A S G I A I

**StuI (2131)**  
 2101 GCTTCAGCACAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCGAGTCTTGGTCTGATGGCCGCCCGACATGGTGCT 61► 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 I A A G V H H K

**BbsI (2277)**  
**XmnI (2273)**  
 2201 TGTGTCTCATAGAGCATGGTATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGGTGGCCCTCCTATA 28► 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 T K M

**AseI (2339)** 2301 GTGAGTCGTATTATACTATGCGGATATACTATGCGGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCACTAAACGAGC SacI (2396)

**SpeI (2494)**  
 2401 TCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGT

2501 CAAAACAACTCCATTGACGTCAATGGGTGGAGACTTGAATCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTAAGTCCAAAACCGCATCA

2601 **SnaBI (2622)**  
TCATGGTAATAGCGATGACTAATACGTAGATGACTGCCAAGTAGGAAAGTCCCATAAAGGTCATGTA  
2701 **NdeI (2727)**  
ATTGACGTCAATAGGGGGCTACTTGCCATATGATACACTTGATGTA  
2801 **NdeI (2727)**  
GTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTCAGCCAGGCGGGCCATTTACCGTAAGTTATG

PacI (2913)  
PstI (2906)  
2901 **SdaI (2905)** **BspLU11I (2923)**  
TAACGCTGCAGGTTAATTAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGC  
3001 CCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATACCAGGCGTTTTCCCCTGGAAAGCTCCCTCG  
3101 TGGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAGCTCACGCTGTAGGTATCT

ApaLI (3237)  
3201 CAGTTCGGTGTAGGTCGTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCC  
3301 AACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGT  
3401 GGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAA  
3501 ACAAAACCACCGCTGGTAGCGGTGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGG

PacI (3653) SwaI (3662) **EagI (3673)**  
3601 **NotI (3672)**  
TCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCCAATAAAATATCTTTATTTTC  
3701 ATTACATCTGTGTGGTTTTTTTTGTGTGAATCGTAACATAACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAAATAGGCTGTCCCC  
3801 AGTGCAAGTGCAGGTGCCAGAACATTTCTATCGAA