





**BbrPI (2700)**  
2701 CACGTGCAGCAAGAGCAGCTTCGACTACACGCACGACATGGAGGGCCACATGGCGGCCACCGCCATCCTCAACCTGTCCACGCGCTGCCGCGAGATG  
711▶ T C S K S S F D Y T H D M E A A H M A A T A I L N L S T R C R E M

**SmaI (2872)**  
2801 CCGCAGAACCTGAGCACCAAGCCGAGGACCTGTGCGCCACGCGGAACCTGACATGGAGGTGGATGAGAACGGGACCTGGACCTCAGCATGAACAAGC  
745▶ P Q N L S T K P Q D L C A T R N P D M E V D E N G T L D L S M N K

**SacII (2905)** **AgeI (2978)**  
2901 AGAGGCCGCGGGACAGCTGCCCCATCTGACCCCTCTGGAGCCATGTCCCCCAGCAGCAGGCAGTGATGAACAACCGGTGTTCCAGCTGGGCGA  
778▶ Q R P R D S C C P I L T P L E P M S P Q Q Q A V M N N R C F Q L G E

3001 GGGCGACTGCTGGGACTTGGCCGTAGACTACACAAAATGAAACCCCGAGGATAGACGAGGACGAGTCAAAGACATTACTCCAGAAGACTTGGACCCA  
811▶ G D C W D L P V D Y T K M K P R R I D E D E S K D I T P E D L D P

**XbaI (3111)** **BstEII (3138)**  
3101 TTCCAGGAGGCTTAGAAGAAAGACGGTATCCCGGGGAGGTGACCATCCCAAGTCCCAAAACCAAGTACCCTCAGTGCAGGAGACAAAAGGACTTAA  
845▶ F Q E A L E E R R Y P G E V T I P S P K P K Y P Q C K E S K K D L

**BstBI (3236)**  
3201 TAACTCTGTCTGGCTGCCCCCTGGCGGACAAAAGCATTGCAAGTATGTGGCCACCAGCTCCCAAGAACTCAAGTGCCCCACGCCTGGCTGTGATGGTTC  
878▶ I T L S G C P L A D K S I R S M L A T S S Q E L K C P T P G C D G S

3301 TGGACATATCACCGGCAATTATGCTTCTCATCGGAGCCTTTCAGGTTGCCCAAGAGCAAAGAAAAGTGGTATCAGGATAGCACAGAGCAAAGAAGATAAA  
911▶ G H I T G N Y A S H R S L S G C P R A K K S G I R I A Q S K E D K

**MluI (3467)**  
3401 GAAGATCAAGAACCATCAGGTGTCCGGTCCCGGGTGCACGGCCAGGGCCACATCACTGGGAAGTACGCGTCCCATCGCAGCGCCTCCGGGTGCCCT  
945▶ E D Q E P I R C P V P G C D G Q G H I T G K Y A S H R S A S G C P

**Acc65I (3524)**  
3501 TGGCGGCCAAGAGGCAGAAAGACGGGTACTGAAATGGCTCCAGTTCCTCTGGAAGTCGGTCAAGACGGAAGGCATGTCTGCCCCACGCCAGGATGCCA  
978▶ L A A K R Q K D G Y L N G S Q F S W K S V K T E G M S C P T P G C D

**HindIII (3685)**  
3601 CGGCTCAGGCCACGTGAGCGGCAGCTTCTCACACACCGCAGCTTGTGAGGATGCCCGAGAGCCAGTCAAGGATGAAGAAGGCAAAGCTTTCTGGAGAG  
1011▶ G S G H V S G S F L T H R S L S G C P R A T S A M K K A K L S G E

**XcmI (3794)**  
3701 CAGATGCTGACCATCAAACAGCGGGCCAGCAACGGTATAGAAAATGATGAAGAAATCAAACAGTTAGATGAAGAAATCAAGGAGCTAAATGAATCCAATT  
1045▶ Q M L T I K Q R A S N G I E N D E E I K Q L D E E I K E L N E S N

3801 CCCAGATGGAAGCCGATATGATTAACCTCAGAAGTACAGATTACACGATGGAGAGCAACCTGAAGACCATCGAAGAGGAGAACAAGTATTGAGCAGCA  
1078▶ S Q M E A D M I K L R T Q I T T M E S N L K T I E E E N K V I E Q Q

**BamHI (3981)**  
3901 GAACGAGTCTCTCCACGAGCTGGCGAACCTGAGCCAGTCTCTGATCCACAGCCTGGCTAACATCCAGCTGCCGCACATGGATCCAATCAATGAACAA  
1111▶ N E S L L H E L A N L S Q S L I H S L A N I Q L P H M D P I N E Q

**BsaBI (4048)**  
**Bst1107I (4035)**  
4001 AATTTTGTGCTTACGTGACTACTTTGACGGAAATGTATCAAAATCAAGATCGTTATCAGAGTCCAGAAAATAAGCCCTACTGGAAAATATAAAGCAGG  
1145▶ N F D A Y V T T L T E M Y T N Q D R Y Q S P E N K A L L E N I K Q

**EcoRI (4109)** **NheI (4129)**  
4101 CTGTGAGAGGAATTGAGTCTGAACAGCTGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTGGACAAACCACAACCTAGAATGCAGTAAAAAA  
1178▶ A V R G I Q V •

**HpaI (4267)** **MfeI (4278)**  
4201 ATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAACAACCAATTGCATTCAATTTATGTTT

**EcoRI (4363)**  
4301 CAGGTTCAGGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAATGTGGTATGGAAATCTAAAATACAGCATAGCAAACTTTAACCTCC

4401 AAATCAAGCCTCTACTTGAATCCTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCT

4501 TTCATGGAGTTTAAAGATATAGTGTATTTTCCCAAGTTTGAACAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATCCCTTTTTAGT

**SspI (4602)** **SwaI (4616)**  
4601 AAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAG

4701 TTTAGTAGTTGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGGATG

4801 AGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGACATGCCACAGG  
131▶ 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 C M G C P

4901 GGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCCGTTGCTCAGCAGACCC  
98▶ 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 S V A S G

**StuI (5041)**  
5001 AATGGCAATGGCTTACGACAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCTGATGGCCGCCCG  
65▶ 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 I A A G

**BspHI (5191)**  
5101 ACATGGTCTTGTTCCTCATAGAGCATGGTATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGCTTTCATGATGG  
31▶ 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 T K M

**XmnI (5183)**  
5201 CCTCCTATAGTGAGTCGATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTC

**AseI (5249)**  
5300 ACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGAGTTGTACGACATTTTGAAAAGTCCCCTT

5400 **SpeI (5404)**  
GATTTACTAGTCAAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTA CTGCC

5499 **SnaBI (5532)**  
AAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGG

5599 **NdeI (5637)**  
CCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCCTAAATACTCCACCCATTGA

5699  
CGTCAATGGAAAGTCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGTCAATGGGCGGGGTCGTTGGCGGTCAGCCAGGCGGGCCATTTA

5799 **PstI (5816)** **SdaI (5815)** **PacI (5823)** **BspLU11I (5833)**  
CCGTAAGTTATGTAACGCC TGCAG G TT AA TTAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCGTTTT

5897  
TCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCC

5997  
TGGAAGCTCCCTCGTGGCTCTCCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAGCTCA

6097 **ApaLI (6147)**  
CGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTACGCCGACCGCTGCGCCTTATCCGGTAACT

6197  
ATCGTCTTGAGTCCAACCCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGA

6297  
GTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGC

6397  
TCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGA

6497 **EagI (6583)** **PacI (6563)** **SwaI (6572)** **NotI (6582)**  
TCTTTTCTACGGGTCTGACGCTCAGTGAACGAAACTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCGCAATAAA

6597  
ATATCTTTATTTTATTACATCTGTGTGTTGGTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAACGAAACAAACAACTAGCAA

6697  
AATAGGCTGTCCCAGTGAAGTGCAGGTGCCAGAACATTTCTCTATCGAA