



100

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

101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGCTCCGCCTTTTCCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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

301 GCCATCCACGCGGTTGAGTCGCGTTTCTGCCGCCCTCCCGCTGTGGTGCCTCCTGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGTCAAGTGCAGGCC

**NgoMIV (441)**  
**NaeI (441)**  
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCAACTCTACGTCTTTGTTTCGTTT

**NcoI (560)**  
**BstEII (555)** **MluI (591)**  
501 TCTGTTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCGCTACCTGAGATCACCGGTACCATGGCCTTGGCTCCTGAGAGGGCAGCCCCACGCGTGTCT

601 GTTCCGAGAGTGGCTCCTTGGAGAGATCAGCAGCGGCTGATGAGGGGCTGCAGTGGCTGGACGAGGCCGACCTGTTCCGCGTGCCTGGAAAGCAC  
13> F G E W L L G E I S S G C Y E G L Q W L D E A R T C F R V P W K H

**StuI (743)**  
701 TTCGCGCGCAAGGACCTGAGCGAGGCCGACGCGCATCTTCAAGGCTGGGCTGTGGCCCGGCGAGGTGGCCGCTAGCAGCAGGGGAGGTGGCCCGC  
47> F A R K D L S E A D A R I F K A W A V A R G R W P P S S R G G G P

**NgoMIV (826)** **NaeI (826)** **FspI (850)** **FspI (857)** **MluI (865)** **SmaI (899)**  
801 CCCCCGAGGCTGAGACTGCGGAGCGCGCGGCTGGAAAACCACTTCCGCTGCGCACTGCGCAGCAGCGTTCGCTTCTGATGCTGCGAGATAACTCGGG  
80> P P E A E T A E R A G W K T N F R C A L R S T R R F V M L R D N S G

**EagI (905)** **DraIII (916)**  
901 GGACCCGGCCGACCCGCAAGGTGTACGCGCTCAGCCGGGAGCTGTGCTGGGAGAAAGGCCAGGCAGGACAGACTGAGGAGAGGCCCGCCGAGCT  
113> D P A D P H K V Y A L S R E L C W R E G P G T D Q T E A E A P A A

**DraIII (1010)** **SfiI (1019)**  
1001 GTCCACCACAGGGTGGGCCCCAGGGCCATTCTGGCACACACATGCTGGACTCCAAGCCCCAGGCCCCCTCCCTGCCCGAGCTGGTGACAAGG  
147> V P P P Q G G P P G P F L A H T H A G L Q A P G P L P A P A G D K

**Tth111I (1152)**  
1101 GGGACCTCCTGCTCCAGGCAAGTGAACAGAGCTGCCTGGCAGACCATCTGCTGACAGCGTCATGGGGGAGAGTCCAGTCCCAACCAAGGCTCCTGGAGA  
180> G D L L L Q A V Q Q S C L A D H L L T A S W G A D P V P T K A P G E

**XmaI (1297)**  
1201 GGGACAAGAAGGGCTTCCCTGACTGGGGCCTGTGCTGGAGGCCAGGGCTCCTGCTGGGGAGCTGTACGGTGGGAGTACGAGACACCCAGCCCC  
213> G Q E G L P L T G A C A G G P G L P A G E L Y G W A V E T T P S P

1301 GGGCCCCAGCCCGGCACTAACGACAGGCGAGGCCGCGGCCAGAGTCCCCGACAGGACAGGCGGTACCTGTCACCCTCCCAAGCGCTGCACCG  
247> G P Q P A A L T T G E A A A P E S P H Q A E P Y L S P S P S A C T

**BsrGI (1442)**  
1401 CGGTGCAAGAGCCAGCCAGGGGGCTGGACGTGACCATCATGTACAAGGGCCGACGGTGTGCTGAGAAGGTGGTGGGACCCGAGCTGCACGTTCT  
280> A V Q E P S P G A L D V T I M Y K G R T V L Q K V V G H P S C T F L

1501 ATACGGCCCCAGACCCAGCTGTCGGGCCACAGACCCAGCAGGTAGCATTCCCCAGCCCTGCCGAGCTCCCGAGCAGAAAGCAGCTGCGCTACACG  
313> Y G P P D P A V R A T D P Q Q V A F P S P A E L P D Q K Q L R Y T

**BbrPI (1615)**  
1601 GAGGAAGTGTGCGGCACGTGGCCCTGGGTTGACCTGGAGCTTCCGGGGCCACAGCTGTGGCCCGGCGCATGGGCAAGTGAAGGTGACTGGGAGG  
347> E E L L R H V A P G L H L E L R G P Q L W A R R M G K C K V Y W E

1701 TGGGCGGACCCAGGCTCCGCCAGCCCTCCACCCAGCCTGCCTGCTGCTGGAAGTGTGACACCCCATCTTCGACTTCAGAGTCTTCTTCAAGA  
380> V G P P G P G S A S P S T P A C L L P R N C D T P I F D F R V F F Q E

**EcoRI (1807)**  
1801 GCTGGTGAATTCCGGGCAGGCGAGCGCGTGGCTCCACAGCTATACATCTACCTGGGCTTCCGGCAGGACCTGTCAGCTGGGAGGCCAAGGAGAAG  
413> L V E F R A R Q R R G S P R Y T I Y L G F G Q D L S A G R P K E K

**ApaLI (1939)**  
1901 AGCCTGGTCTGTTGAAGCTGGAACCTGGCTGTGCCGAGTGCACCTAGAGGGCAGCAGCGTGGGGTGTGCTTCCCTGGATAGCAGCAGCCTCAGCC  
447> S L V L V K L E P W L C R V H L E G T Q R E G V S S L D S S S L S

**MscI (2079)** **NheI (2073)**  
2001 TCTGCTGTCCAGCGCAACAGCCTCTATGACGACATCGAGTCTTCTTATGGAGCTGGAGCAGCCCGCTAGCTAGCTGGCCAGACATGATAAGATAC  
480> L C L S S A N S L Y D D I E C F L M E L E Q P A •

2101 ATTGATGAGTTTGGACAAACCAACTAGAATGCAAGTGAAGGAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT

**HpaI (2211)** **MfeI (2222)**  
2201 GCAATAAACAAAGTTAAACAACAACAAATTGCAATTTTATGTTTCAGGTTTCAGGGGAGGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATG

**EcoRI (2307)**  
2301 TGGTATGGAATTTAAAATACAGCATAGCAAACTTTAACCTCCAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAG  
2401 GGGCTGTTGCCAATGTGCATTAGCTGTTTGAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGTATTTTCCAAGGTTTGAAGTCTCTTCAATTT

2501 **SspI (2546)** **SwaI (2560)**  
 CTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTAGTAAAAATTTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTAT  
 2601 TAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTTGGACAGCAAGA  
 2701 AAGCGAGCTTCTAGCTTTAGTTCCTGGTACTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAAGCA  
 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  
 2801 GTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCC  
 113 D P 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  
 2901 **StuI (2985)**  
 ACAATGGTGTCAAAGTCTTCTGCCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGA  
 79 V I 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  
 3001 CAGCAGAGATGATCTCCCAGTCTTGGTCTGATGGCGCCGACATGGTGTCTGTGTCTCATAGAGCATGGTGTCTTCTCAGTGGCGACCTCCAC  
 46 A 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  
 3101 **BspHI (3135)** **AseI (3193)**  
 CAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCCTCATGATGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATT  
 13 L E L D Q Q S I N F T K M  
 3201 **GTCAAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCACATAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTCG**  
 3301 **SpeI (3348)**  
 GTC AATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCGTTGATTTACTAGTCAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGAAAT  
 3400 **SnaBI (3476)**  
 CCCC GTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAG  
 3500 **NdeI (3581)**  
 GAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCATTACCCTGATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGATG  
 3600 TACTGCCAAGTGGGCAGTTTACCCTAAATACTCCACCCATTGACGTCAATGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGTC  
 3700 **SdaI (3759)** **PacI (3767)** **BspLU11I (3777)**  
 AATGGGCGGGGTCGTTGGGCGGTGAGCCAGGCGGCCATTTACCGTAAGTTATGTAACGCCCTGCAGGTTAA TTAAGAACATGTGAGCAAAAGGCCAG  
 3798 CAAAAGGCCAGGAACCGTAAAAAGCCGCGTTGCTGGCGTTTTCCATAGGCTCCGCCCCCTGACGAGCATCAAAAATCGACGCTCAAGTCAGAGGT  
 3898 GGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCTGGAAGCTCCCTCGTGGCTCTCCTGTTCCGACCCTGCCGTTACCGGATACCTGTC  
 3998 **ApaLI (4091)**  
 CGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTGTGTGCAC  
 4098 GAACCCCCGTTAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCAAACCGGTAAGACACGACTTATGCCACTGGCAGCAGCCACTG  
 4198 GTAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTG  
 4298 CGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGTTTTTTGTTTGAAGCAG  
 4398 CAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGGAACGAAAACCTCACGTTAAGGGATTTTGG  
 4498 **EagI (4527)** **PacI (4507)** **SwaI (4516)** **NotI (4526)**  
 TCATGGCTAGTTAATTAACATTTAAATC AGCGGCCGCAATAAAATATCTTTATTTTTCATTACATCTGTGTGTTGTTTTTTGTGTGAATCGTAACATAACA  
 4598 TACGCTCTCCATCAAACAAAACGAAACAAAACAAACTAGCAAATAGGCTGTCCCAGTGCAAGTGCAAGTGCCAGAGTCCAGAACATTTCTCTATCGAA