



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

101 GAGAAAGTGGCGGGGTAAGTGGAAAGTGATGCTGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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

301 GCCATCCACGCGGTTGAGTCGCGTTTCTGCCGCTCCCGCTGTGGTGCCTCTGAAGTGCCTCCGCGCTAGGTAAGTTAAAGCTCAGGTCGAGACC

**NgoMIV (441)**  
401 GGGCCTTTGTCCGGGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

**KasI (535)** **AgeI (552)** **BspLU11I (560)**  
501 TCTGTTTGTGCGCGTTACAGATCCAAGCTGTGACCGGGCCTACCTGAGATCACCGGTCAACATGTCGCTGCTGCTAAGCCTGGCCGCGTGTGCAG  
601 GAGCGCCGTACCCGAGAGCCGACGTTCAATGTGGCTCTGAACTGGGCCATCTCCAGAGTGGATGCTACAACATGATCTAATCCCGGAGACTTGAGG  
13> S A V P R E P T V Q C G S E T G P S P E W M L Q H D L I P G D L R  
1> M S L V L L S L A A L C R

**SpeI (724)**  
701 GACCTCCGAGTAGAACCTGTTACAACACTAGTGTGCAACAGGGACTATTCAATTTTGTGAATGTAAGCTGGTACTCCGGGAGATGCCAGCATCCGCT  
47> D L R V E P V T T S V A T G D Y S I L M N V S W V L R A D A S I R

**StuI (878)**  
801 TGTTGAAGCCACCAAGATTTGTGTGACGGGCAAAAGCAACTTCCAGTCTACAGCTGTGTGAGGTGCAATTACACAGAGGCTTCCAGACTCAGACCAG  
80> L L K A T K I C V T G K S N F Q S Y S C V R C N Y T E A F Q T Q T R

**SspI (979)** **Bsp120I (971)**  
901 ACCCTCTGGTGGTAAATGGACATTTTCTATATCGGCTTCCCTGTAGAGCTGAACACAGTCTATTTTCATTGGGGCCATAATATTCCTAATGCAAAATG  
113> P S G G K W T F S Y I G F P V E L N T V Y F I G A H N I P N A N M  
1001 AATGAAGATGGCCCTTCCATGTCTGTGAATTTACCTACCAGGCTGCCTAGACCACATAATGAAATATAAAAAAAGTGTGCAAGGCCGGAAGCCTGT  
147> N E D G P S M S V N F T S P G C L D H I M K Y K K K C V K A G S L

**BamHI (1101)**  
1101 GGGATCCGAACATCACTGCTTGTAAAGAAGATGAGGAGACAGTAGAAGTGAACCTTCAACCACTCCCTGGGAAACAGATACATGGCTCTTATCCAACA  
180> W D P N I T A C K K N E E T V E V N F T T T P L G N R Y M A L I Q H  
1201 CAGCACTATCATCGGTTTTCTCAGGTGTTGAGCCACACCAGAAGAAACAAACGCGAGCTTCACTGTTGATTCCAGTACTGGGATAGTGAAGGTGCT  
213> S T I I G F S Q V F E P H Q K K Q T R A S V V I P V T G D S E G A  
1301 ACGGTGCAGCTGACTCCATATTTTCTACTTGTGGCAGCGACTGCATCCGACATAAAGGAACAGTTGTGCTCTGCCACAAACAGGCGTCCCTTTCCCTC  
247> T V Q L T P Y F P T C G S D C I R H K G T V V L C P Q T G V P F P

**MscI (1460)**  
1401 TGGATAACAACAAAAGCAAGCCGGGAGGCTGGCTGCTCTCCTCTGCTGCTCTGCTGCTGGTGGCCACATGGGTGCTGGTGGCAGGGATCTATCTAATGTG  
280> L D N N K S K P G G W L P L L L L S L L V A T W V L V A G I Y L M W  
1501 GAGGCACGAAAGGATCAAGAAGACTTCTTTTCTACCACCACACTACTGCCCCCATTAAGGTTCTTGTGTTTACCCATCTGAAATATGTTTCCATCAC  
313> R H E R I K K T S F S T T T L L P P I K V L V V Y P S E I C F H H

**XmnI (1618)**  
1601 ACAATTTGTTACTTCACTGAATTTCTTCAAACCATTGCAGAAGTGAAGTGCATCCTTGAAGAGTGGCAGAAAAAGAAAATAGCAGAGATGGGTCCAGTGC  
347> T I C Y F T E F L Q N H C R S E V I L E K W Q K K K I A E M G P V

**Tth111I (1729)** **Acc65I (1777)**  
1701 AGTGGCTTGCACCTAAAAGAAGGCAGCAGACAAAGTGTCTTCTTCTTCAATGACGTCAACAGTGTGTGCGATGGTACCTGTGGCAAGAGCGAGGG  
380> Q W L A T Q K K A A D K V V F L L S N D V N S V C D G T C G K S E G

**PstI (1851)**  
1801 CAGTCCCAGTGAGAACTCTAAGACCTCTTCCCTTGCCTTTAACCTTTTCTGCACTGATCTAAGAAGCCAGATTCTCTGCACAAATACGTGGTGGTC  
413> S P S E N S Q D L F P L A F N L F C S D L R S Q I H L H K Y V V V

**BspHI (1964)**  
1901 TACTTTAGAGAGATTGATACAAAAGACGATTACAATGCTCTCAGTGTCTGCCCAAGTACCACCTCATGAAGGATGCCACTGCTTTCTGTGCAGAACTTC  
447> Y F R E I D T K D D Y N A L S V C P K Y H L M K D A T A F C A E L  
2001 TCCATGTCAAGCAGCAGGTGTGACGAGGAAAAAGATCAAAAGCTGCCACGATGGCTGCTGCTCTTGTAGCCACCCATGAGAAGCAAGAGACCTTAAA  
480> L H V K Q Q V S A G K R S Q A C H D G C C S L •

**MscI (2123)** **NheI (2117)**  
2101 GGCTTCTATCCCACAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAAATGCAGTGAAGAAAAATGCTTATTTG

**HpaI (2255)** **MfeI (2266)**  
2201 TGAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAATTGCATTATTTTATGTTTCAGGTTACAGGGG

**EcoRI (2351)**  
2301 GAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGGTATGGAATCTAAAATACAGCATAGCAAACTTTAACCTCAAATCAAGCCTC

2401 TACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTGCCAATGTCATTAGCTGTTGAGCCTCACCTCTTTTATGAGTGT

**SspI (2590)**  
2501 AAGATATAGTGTATTTTCCAAGGTTTGAAGTACTCTTCAATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTATGATAAATATTGAGA

SwaI (2604)  
 2601 AATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGG  
 2701 ACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTTCCTGGTGTACTTGAGGGGGATGAGTTCCTCAATG  
 141 • N R T Y K L P I L E E I  
 SacI (2865)  
 2801 GTGGTTTTGACCAGCTTGCCATTCACTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCC  
 127 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 R  
 2901 TGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCCTTCTGCCCGTTGCTCACAGCAGACCCAATGGCAATGGC  
 94 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 A  
 StuI (3029)  
 3001 TTCAGCACAGACAGTGCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCAGTCTTGGTCTGATGGCCGCCCCGACATGGTGCTTG  
 61 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  
 BspHI (3179)  
 XmnI (3171)  
 3101 TTGTCCTCATAGAGCATGGTGATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGATGGCCCTCTATAGT  
 27 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 (3237) SacI (3294)  
 3201 GAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTC  
 SpeI (3392)  
 3301 TGCTTATATAGACCTCCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCGTTGATTTACTAGTC  
 3400 AAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCAT  
 SnaBI (3520)  
 3500 CATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCCATAAGGTCATGTACTGGCATAATGCCAGGCGGGCCATTTACCGTCA  
 NdeI (3625)  
 3600 TTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCGAGTTTACCATAAATACTCCACCATTGACGTCAATGAAAG  
 3700 TCCCTATTGGCGTTACTATGGAAACATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTCAGCCAGGCGGGCCATTTACCGTAAGTTATGT  
 PstI (3804)  
 SdaI (3803) PacI (3811) BspLU11I (3821)  
 3800 AACGCCCTGCAGGTTAA TTAAGAACATGTGAGCAAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGCTTGGCTGGCGTTTTTCCATAGGCTCCG  
 3898 CCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCTGGAAGCTCCCTC  
 3998 GTGCGCTCTCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATC  
 ApaLI (4135)  
 4098 TCAGTTCGGTGTAGGTCGTTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTC  
 4198 CAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGG  
 4298 TGGCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCA  
 4398 AACAAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGG  
 EagI (4571)  
 PacI (4551) SwaI (4560) NotI (4570)  
 4498 GTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAATATCTTTATTTT  
 4598 CATTACATCTGTGTGTTGGTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCC  
 4698 CAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA