



**PvuI (7)**  
**SgfI (6)**  
1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA  
101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGCTGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCC

**HindIII (245)**  
**Psp1406I (203)** **PvuII (239)** **Bsu36I (291)**  
201 GTGAACGTTCTTTTTTCGCAACGGGTTTGGCCGACAGTGAAGCTTCAGAGGGCTCGCATCTCTCTTACAGCGCCCGCCGCCCTACCTGAGGCC  
301 GCCATCCACGCGGTTGAGTGCAGTTCGCCGCTCCCGCCTGTGGTGCCTCTGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

**NgoMIV (441)**  
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCGGCTCTCCACGCTTTGCTGACCCTGTTGCTCAACTCTACGCTTTTGTTCGTTT

**KasI (535)** **AgeI (552)** **SphI (560)** **SmaI (574)** **KasI (582)**  
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCCTACCTGAGATCACCGGTCAGCATGCACACTCCCGGGACCCCGCGCCGGCCACCCGGA  
601 CCCGCCGCACTGTTGCTGCTCACGCTGTTCTGCTGCTGGCCGCTTCGGGACGCGCAGTTCCTTGTGCTTCTGTGGTTTGCCTAAACCTACAAATATC  
13▶ P P P L L L L T L L L L L A A S G R A V P C V F C G L P K P T N I  
701 ACCTTCTTATCCATCAACATGAAGAATGCTCTGCATTGGAATCCACCAGAGAGTCTACACGGAGTTGAAGTCACATACACTGTGCAATATTTTCATATATG  
47▶ T F L S I N M K N V L H W N P P E S L H G V E V T Y T V Q Y F I Y  
801 GGCAGAAGAAATGGCTGAATGCCTCTAAATGCGGGAGTATCAACAGGACCTACTGTGACCTTTCTGTTGAGACCTCAGACTATGAACACCAGTTCATGC  
80▶ G Q K K W L N A S K C G S I N R T Y C D L S V E T S D Y E H Q F Y A  
901 CAAAGTGAAGGCCATTTGGGAAGCCAGGTGCTCCGAATGGGCCGAGACGGAACGTTCTATCCTTTCTTGAAACTCAAGTCAGCCACCAGAGATTGCC  
113▶ K V K A I W E A R C S E W A E T E R F Y P F L E T Q V S P P E I A

**BstXI (1042)**  
1001 CTGACAACTGGCGAGAAGTCCATCTCTATTGCCCTGACAGCACCAGAGAAGTGGAAAAGAAATCCACAAGACCACACTGTTTCTATGCAACAGATATACC  
147▶ L T T G E K S I S I A L T A P E K W K R N P Q D H T V S M Q Q I Y

**XcmI (1166)** **PvuII (1185)**  
1101 CCAATTTGAAGTACAATGTGTCTGTGTATAACACTAAGTCGAGAAGAAGTGGTCCCAGTGTGTACCAACAGCACACTGGTCCCTCAGCTGGCTGGAGCC  
180▶ P N L K Y N V S V Y N T K S R R T W S Q C V T N S T L V L S W L E P

**BbrPI (1219)** **Bsp120I (1240)** **ScaI (1282)**  
1201 CAACACTGTATTGTGTCCACGTGGAGTCCCTTGTCCAGGGCCCCCTCGCCTCCCGATGCCTTCTCAGAAGCAGTGCATCACTTTTGAAGTTCAA  
213▶ N T L Y C V H V E S L V P G P P R L P M P S Q K Q C I S T L E V Q  
1301 ACATCAGCATGGAAGGCTAAAGTCATCTTCTGGTATGTCTTCCACATCTGTATCGTGTCTTTCTCCGCAATTGGCTACTTGGTTTACCGTTACA  
247▶ T S A W K A K V I F W Y V F L T S V I V F L F S A I G Y L V Y R Y  
1401 TCCATGTTGGCAAGGAAAAACACCCAGCAAATTTGGTACTGATTTATAGAAATGAAATGGCAAGAGTCTTTGAACCTACTGAAACACTCACTTAA  
280▶ I H V G K E K H P A N L V L I Y R N E I G T R V F E P T E T I T L N  
1501 TTTTATCACCTTCAGTATGTTGGATGATACTAAAATTTCTCAAAGGATATGAATTTACTGGACAAAAGCAGTGTGACATCAGTGTAAATGACCTGAG  
313▶ F I T F S M L D D T K I S P K D M N L L D K S S D D I S V N D P E

**StuI (1607)** **SapI (1655)** **Tth111I (1672)**  
1601 CACAATGAGGCTGGGAGCCGCACTGGGAGGAGGTGGAGGGGCAACATTTAGGATGCTCTTCGATTTGATGGAGCCTGTCTGTGGTGTGAGCAAAGAG  
347▶ H N E A W E P H W E E V E G Q H L G C S S H L M D A V C G A E Q R  
1701 ACGGAGACACCTCCCTAACCCAGCATGGGTGGCTTAACAGCACCATCCCCACAGGAGAGACAGACACTGAGCCTCAATACAAAGTCCCTAAGTGACTTCTA  
380▶ D G D T S L T Q H G W L N S T I P T G E T D T E P Q Y K V L S D F Y  
1801 CGGGGAGGGTGAATCCAAGTGTCTGTGAGCCGGAAGAGGGCGCCAGAACAGAGAAAATATCTGAGCCACTGGTGACTTCAGCAAACCTGGACCCACAG  
413▶ G E G E I Q L S C E P E E A A R T E K I S E P L V T S A N L D P Q

**SmaI (1985)**  
1901 CTTGAAGACCTACATCACCTGGGTGAGGAGCATACTGTCTCCGAGGATGGGCCAGAGGAAGAGACATCTATAACAGTAGTGGATTGGGACCTCAAACCTG  
447▶ L E D L H H L G Q E H T V S E D G P E E E T S I T V V D W D P Q T

**XbaI (2095)**  
2001 GCAGGCTGTGTATCCCTTCTTACCTATCTTTGGCCGTGATCCTGAGAATATGGTCATTATGAGAGAGACCAGCTCTTAGAGGGTGGCCTTTTGTCTAG  
480▶ G R L C I P S L P I F G R D P E N Y G H Y E R D Q L L E G G L L S R

**BsrGI (2184)** **BspLU11I (2181)**  
2101 ACTCTATGAGAACCAGGCACCTGACAAGCCAGAGAAAAGAAAATGAAAACCTGTCTCACAGGTTTATGGAGGAATGGGGTTACATGTACAAAATGGAAAGC  
513▶ L Y E N Q A P D K P E K E N E N C L T R F M E E W G L H V Q M E S

**MscI (2221)** **NheI (2215)**  
2201 TAGTGCCAGGCTTTCGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAATAAATGCTTTATTTGTG  
547▶ •

**HpaI (2353)**  
2301 AAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAACAATTGCATTCATTTTATGTTTCAGGTTTCAGGGGA

**EcoRI (2449)**  
2401 GGTGTGGGAGTTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATCTAAAATACAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTA  
2501 CTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTTAA

**SapI (2631)** **SspI (2688)**  
2601 GATATAGTGATTTTTCCCAAGGTTTGAAGTGTCTTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTTAGTAAAATATTCAGAAA

Swal (2702)

2701 TAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGAC

2801 TTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGGATGAGTTCCTCAATGGT  
 141 • N R T Y K L P I L E E I T

2901 GGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCCTG  
 127 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

3001 ATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCCGTTGCTCACAGCAGACCCAATGGCAATGGCTT  
 93 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 E

3101 CAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCTGTATGGCCGCCCGACATGGTGCTTGT  
 60 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 N

3201 GTCCTCATAGAGCATGGTGTCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCTGTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCTATAGTGA  
 27 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

3301 GTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGCAAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTG  
 AseI (3335) SacI (3392)

3401 CTTATATAGACCTCCCACGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCCTTGATTTACTAGTCAAA  
 SpeI (3490)

3501 ACAAACCTCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTAAGTCCAAAACCGCATCATCAT

3601 GGTAATAGCGATGACTAATACGTAGATGACTGCCAAGTAGGAAAGTCCATAAGTTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTG  
 SnaBI (3618)

3701 ACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGTACTGTACTGCCAAGTGGCAGTTCACCGTAAATACTCCACCATTGACGTCAATGGAAAGTCC  
 NdeI (3723)

3801 CTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGTCTGTTGGCGGTGTCAGCCAGGCGGGCCATTTACCGTAAAGTTATGTAAC

3901 GCCTGCAGGTTAATAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCC  
 PacI (3909) PstI (3902) SdaI (3901) BspLU11I (3919)

4001 CTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCTGGAAGCTCCCTGTGGC

4101 CTCTCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCCTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAGCTCACGCTGTAGGTATCTCAGT

4201 TCGGTGTAGGTCGTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACC  
 ApaLI (4233)

4301 CGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGCTACAGAGTCTTGAAGTGGTGGCC

4401 TAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAA

4501 ACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTG

4601 ACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCGCAATAAAATATCTTTATTTTCATTA  
 PacI (4649) Swal (4658) EagI (4669) NotI (4668)

4701 CATCTGTGTGTTGGTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCCAGTG

4801 CAAGTGCAGGTGCCAGAACATTTCTCTATCGAA