



**PvuI (7)**  
**SgfI (6)** 1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

101 GAGAAGGTGGCGCGGGTAAACTGGAAAAGTATGTCGTGACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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

301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

**NgoMIV (441)**  
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

**AgeI (552)** **SphI (560)**  
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTGAGCATGCCCTCCATGTTGGAACGCATTAGCAAAAATTTGGT  
1▶ M P S M L E R I S K N L V

**PshAI (624)**  
601 CAAAGAGATTGGAAGCAAAGACCTGACACCTGTCAAATACCTATTGAGTGCCACCAAATTACGTCAGTTTGTATATTACGAAAGAAGAAGGATTCTCGT  
13▶ K E I G S K D L T P V K Y L L S A T K L R Q F V I L R K K K D S R

**EcoRI (736)**  
701 TCATCATTTTGGGAACAATCTGACTATGTTCCAGTTGAATTCCTCAATGACATCCTGGAGCCAAGTTCTCAGTCCTAGAAAAGTGTGTGACAGGAC  
47▶ S S F W E Q S D Y V P V E F S L N D I L E P S S S V L E T V V T G

**NcoI (897)**  
801 CGTTCACCTTCAGTGACATTATGATCCAGAAGCATAAGGCTGACATGGGTGTGAATGTTGGTATAGAAGTGAAGTGTGTGAGGGGAGGCTCTGTGGACCA  
80▶ P F H F S D I M I Q K H K A D M G V N V G I E V S V S G E A S V D H

**XhoI (910)** **BbsI (949)** **BamHI (975)**  
901 TGGATGCTCCCTCGAGTTCAAATTGTTACCATCCCATCACCAAACCTGGAAGACTTTCAAAAAGGAAAAGTGGATCCAGAGCCATCATTCTGAAG  
113▶ G C S L E F Q I V T I P S P N L E D F Q K R K L L D P E P S F L K

**SspI (1090)**  
1001 GAGTGCCGGAGGAGAGGGGACAACCTGTACGTGGTGACAGAGGCTGTTGAACTGATCAACAATACTGTGCTGTACGATAGCAGTAGTGTGAATATTTTAG  
147▶ E C R R R G D N L Y V V T E A V E L I N N T V L Y D S S S V N I L

1101 GAAAAATTGCTCTTTGGATTACCTATGGCAAGGGTCAAGGCCAAGGAGAGTCTCAGAGTGAAGAAGAAGGCGCTGACTCTCAGAAAAGGCATGGTGAT  
180▶ G K I A L W I T Y G K G Q G Q G E S L R V K K K A L T L Q K G M V M

1201 GGCTTATAAGAGAAAAGCAGCTGGTTATCAAGGAGAAAAGCCATTCTCATCTCAGATGATGATGAACAGAGAACCTTTCAAGATGAGTACGAAATTTCCGAA  
213▶ A Y K R K Q L V I K E K A I L I S D D D E Q R T F Q D E Y E I S E

1301 ATGGTAGGCTACTGTGCTGCGAGGAGTGAAGGGTGTACCACATTTCCATACCATCTCTCAACCCCTCTTCAATGCCTCATCCAATGATGAAGTTAA  
247▶ M V G Y C A A R S E G L L P S F H T I S P T L F N A S S N D M K L

**BsrBI (1431)**  
1401 AACAGAGCTATTTCTGACACAGCAATTTTTGAGCGGGCATTGCCAAAATACGAACAAGTTCACATCCTCCCAGTAGGAAGAATAGAGGAACCCCTTCTG  
280▶ K P E L F L T Q Q F L S G H L P K Y E Q V H I L P V G R I E E P F W

1501 GCAAAATTTCAAGCATCTACAAGAGGAGGTTTTCCAGAAAATAAAGACTGCTCAGCTCTCAAAGGATGTTCCAGGATGTCATGTTCTACAGTATCCTG  
313▶ Q N F K H L Q E E V F Q K I K T L A Q L S K D V Q D V M F Y S I L

1601 GCCATGCTCAGAGACAGGGGCTCTACAGGACCTGATGAACATGCTGGAATTGGACAGCTCAGGTCATTTGGATGGCCCTGGTGGTCCATCCTAAAGA  
347▶ A M L R D R G A L Q D L M N M L E L D S S G H L D G P G G A I L K

**NsiI (1721)**  
1701 AACTTCAACAGGATTCAAACCATGCATGGTTTAAACCCAAAGACCCCATCTTTATCTCCTTGAAGCCATAATGGTGTGAGTACTTCAACACGATTT  
380▶ K L Q Q D S N H A W F N P K D P I L Y L L E A I M V L S D F Q H D L

**NcoI (1811)** **BamHI (1823)**  
1801 GCTGGCCTGTTCCATGGAGAAGAGGATCCTGCTTCAGCAACAGGAGCTGGTAAAGGAGCATCCTGGAGCCAACTTCAGATACCCCTGGAGCATTCCCTTC  
413▶ L A C S M E K R I L L Q Q Q E L V R S I L E P N F R Y P W S I P F

**Bsu36I (1977)**  
1901 ACCCTCAAACCTGAGCTCCTCGCCCACTCCAGAGTGAAGGTTTGGCCATCACCTATGGCCTGCTGGAGGAGTGTGGCCTTAGGATGGAGCTGGATAACC  
447▶ T L K P E L L A P L Q S E G L A I T Y G L L E E C G L R M E L D N

**PstI (2065)**  
2001 CCAGGTCAACCTGGGATGTAGAAGCAAAGATGCCCTGTCTGCCCTCTATGGACTCTCTCGTTGCTGAGCAGCTGGCTGAGGCCTAAGCCCTCCCTGA  
480▶ P R S T W D V E A K M P L S A L Y G T L S L L Q Q L A E A •

**NheI (2120)**  
2101 TGGGCAGTCAGTCCAGAGATGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTGGACAAACCACAACCTAGAATGCAGTGAAAAAATGCTTTAT

**HpaI (2258)** **MfeI (2269)**  
2201 TTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAATTCGATTTCATTTTATGTTTCAGGTTACG

**EcoRI (2354)**  
2301 GGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACTTAACTCCAAATCAAGC

2401 CTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGCTGTTGCCAATGTGCATTAGCTGTTGCAGCCTCACCTCTTTTCATGGAG

2501 **SapI (2536)** TTTAAGATATAGTGTATTTTCCCAAGGTTTGAAGTACTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCCACATTCCCTTTTTAGTAAAATATTC **SspI (2593)**

2601 **SwaI (2607)** AGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGT

2701 TGGACTTAGGGAACAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTACTTGAGGGGGATGAGTTCCTCA  
141 • N R T Y K L P I L E E **BstXI (2897)**

2801 ATGGTGGTTTTGACCAGCTTGCCATTCACTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCA  
128 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 S V V

2901 CCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAAATGGCAAT  
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

3001 GGCTTCAGCACAGACAGTACCCTGCCAATGTAGGCCCTCAATGTGGACAGCAGAGATGATCTCCCAAGTCTTGGTCTGATGGCCGCCCGACATGGTGC  
62 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 **BbsI (3178)**

3101 TTGTTGCTCATAGAGCATGGTGTCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGGTGGCCCTCTAT  
28 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 **AseI (3240)**

3201 AGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCCTAAACGAG **SpeI (3395)**

3301 CTCTGCTTATATAGACCTCCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCGTTGATTTACTAG **SnaBI (3523)**

3401 ICAAAAACAACTCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCGTGAGTCAAACCGCTATCCACGCCATTGATGACTGCCAAAACCGCATC

3501 ATCATGGTAATAGCGGATGACTAATACGTAGATGACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGT **NdeI (3628)**

3601 CATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAA

3701 AGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGGGGGGTCTGTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAAGTTAT **PacI (3814)**

3801 **PstI (3807)** **SdaI (3806)** **BspLU11I (3824)** GTAACGCCTGCAGGTTAATAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCG

3901 CCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTC

4001 GTGCGCTCTCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATC **ApaLI (4138)**

4101 TCAGTTCGGTGTAGGTGCTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTACGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTC

4201 CAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAAGTGG

4301 TGGCCTAACTACGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCA

4401 AACAAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTCTACGGG **EagI (4574)**

4501 **PacI (4554)** **SwaI (4563)** **NotI (4573)** GTCTGACGCTCAGTGGAAACGAAAACCTACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAATATCTTTATTTT

4601 CATTACATCTGTGTGTTGGTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAAATAGGCTGTCCC

4701 CAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA