



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

**HindIII (245)**  
**Psp1406I (203)** 201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACACGGCCCGCCGCTACCTGAGGCC  
**PvuII (239)**  
301 GCCATCCACGCGGTTGAGTCGCGTTTCTGCCGCTCCCGCCTGTGGTGCCTCTGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

**NgoMIV (441)**  
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

**BspHI (560)**  
**AgeI (552)** 501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCCTACCTGAGATCACCGGTCATCATGAGCGACGTGGCTATTGTGAAGGAGGGTTGGCTGCA  
1 M S D V A I V K E G W L H

**NotI (681)**  
601 CAAACGAGGGAGTACATCAAGACCTGGCGGCCACGCTACTTCTCCTCAAGAATGATGGCACCTTCATTGGCTACAAGGAGCGGCCAGGATGTGGAC  
13 K R G E Y I K T W R P R Y F L L K N D G T F I G Y K E R P Q D V D

**PvuII (742)**  
701 CAACGTGAGGCTCCCTCAACAATTCTGTGGCGCAGTGCCAGCTGATGAAGACGGAGCGGCCCGCCCAACACCTTCATCATCCGCTGCCTGCAGT  
47 Q R E A P L N N F S V A Q C Q L M K T E R P R P N T F I I R C L Q

**PshAI (801)** 801 GGACCACTGTCATCGAACGCACCTTCCATGTGGAGACTCTGAGGAGCGGGAGGAGTGGACAACCGCCATCCAGACTGTGGCTGACGGCCTCAAGAAGCA  
80 W T T V I E R T F H V E T P E E R E E W T T A I Q T V A D G L K K Q

**XcmI (866)**  
901 GGAGGAGGAGGAGATGGACTTCCGGTCGGGCTCACCCAGTGACAACCTAGGGGCTGAAGAGATGGAGGTGTCCTGGCCAAGCCCAAGCACCGGTGACC  
113 E E E E M D F R S G S P S D N S G A E E M E V S L A K P K H R V T

**DraIII (988)**  
1001 ATGAACGAGTTTGTAGTACCTGAAGCTGTGGGCAAGGGCACTTTCGGCAAGGTGATCCTGGTGAAGGAGAAGGCCACAGCGCGTACTACGCCATGAAGA  
147 M N E F E Y L K L L G K G T F G K V I L V K E K A T G R Y Y A M K

**XcmI (1124)**  
1101 TCCTCAAGAAGGAAGTATCGTGGCCAAAGGACGAGGTGGCCACACACTACCAGAGAACCAGCTCCTGCAGAACTCCAGGCACCCCTTCTCACAGCCCT  
180 I L K K E V I V A K D E V A H T L T E N R V L Q N S R H P F L T A L

**ScaI (1202)** 1201 GAAGTACTCTTCCAGACCCACGACCGCCTCTGCTTTGTGATGGAGTACGCCAACGGGGGCGAGCTGTTCTTCCACCTGTCCCGGGAACGTGTGTTCTCC  
213 K Y S F Q T H D R L C F V M E Y A N G G E L F F H L S R E R V F S

**XmaI (1280)**  
1301 GAGGACCGGGCCCGCTTCTATGGCGCTGAGATTGTGTCAGCCCTGGACTACCTGCACTCGGAGAAGAAGCTGGTGTACCGGGACCTCAAGCTGGAGAACC  
247 E D R A R F Y G A E I V S A L D Y L H S E K N V V Y R D L K L E N

**Bsp120I (1307)** 1401 TCATGTGACAAAGGACGGGACATTAAGATCAGAGCTTCGGGCTGTGCAAGGAGGGGATCAAGGACGGTGCACCATTGAAGACCTTTTGGGCGACACC  
280 L M L D K D G H I K I T D F G L C K E G I K D G A T M K T F C G T P

1501 TGAGTACCTGGCCCCGAGGTGCTGGAGGACAATGACTACGGCCGTGCACTGGTGGGCTGGGCGTGGTGTGACGAGATGATGTGCGGTGCG  
313 E Y L A P E V L E D N D Y G R A V D W W G L G V V M Y E M M C G R

**HindIII (1627)**  
1601 CTGCCCTTCTACAACCAGGACCATGAGAAGCTTTTTGAGTCTATCCTCATGGAGGAGATCCGCTTCCCGCGCACGTTGGTCCCAGGGCCAAGTCTTTCG  
347 L P F Y N Q D H E K L F E L I L M E E I R F P R T L G P E A K S L

1701 TTTGAGGCTGCTCAAGAAGGACCCCAAGCAGAGGCTTGGCGGGGCTCCGAGGACGCCAAGGAGATCATGCAGCATCGCTTCTTTGCCGGTATCGTGTG  
380 L S G L L K K D P K Q R L G G G S E D A K E I M Q H R F F A G I V W

**BbrPI (1804)** 1801 GCAGCAGTGTACGAGAAGAAGCTCAGCCACCCTTCAAGCCCCAGGTACGTCGGAGACTGACACCAGGTATTTTGTGAGGAGTTCACGGCCAGATG  
413 Q H V Y E K K L S P P F K P Q V T S E T D T R Y F D E E F T A Q M

**BsaBI** 1901 ATCACCATCACACCACCTGACCAAGATGACAGCATGGAGTGTGGACAGCGAGCGCAGGCCCACTTCCCCAGTTCCTACTCGGCCAGCGGCACGG  
447 I T I T P P D Q D D S M E C V D S E R R P H F P Q F S Y S A S G T

**NheI (2032)** 2001 CCTGAGGCGCGGTGGACTGCGCTGGACGATAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGACAAACCACAACCTAGAATGCAGTGAAA  
480 A •

**HpaI (2170)** **MfeI (2181)**  
2101 AAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAACATTGCATTCTTTTATG

**EcoRI (2266)**  
2201 TTTCAGGTTACAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACCTTTAACC  
2301 TCCAAATCAAGCCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCT

**SapI (2448)**  
2401 TCTTTCATGGAGTTAAGATATAGTATTTTCCCAAGTTTGAAGTCTTCTCATTCTTTATGTTTTAAATGCAGTACCTCCACATTCCTTTT

**SspI (2505)** **SwaI (2519)**  
2501 AGTAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCC  
2601 CAGTTTAGTAGTTGACTTAGGGAACAAAGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTCTGGTGTACTTGAGGGGG  
141 • N R T Y K L P

2701 ATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCAC  
132 I 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

**BstXI (2809)**

2801 AGGGGCTGACCACCTGATGGATCTGCCACCTCATCAGAGTAGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCCGTTGCTCACAGAGA  
99 P 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

**StuI (2944)**

2901 CCCAATGGCAATGGCTTCCAGCACAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCAGTCTTGGCTCTGATGGCCGCC  
66 G 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

**XmnI (3086)**

3001 CCGACATGGTGGTGTGCTCTCATAGAGCATGGTGTCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCTGCTGAGAGATGTTGAAGGTCTTCATGG  
32 G 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

**AseI (3152)**

3101 TGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGT  
3201 TCACTAAACGAGCTCTGCTTATATAGACCTCCACCCTACACGCCTACCGCCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCG

**SpeI (3307)**

3301 TTGATTTACTAGTCAAAAACAACTCCCATGACGTCAATGGGGTGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGC

**SnaBI (3435)**

3401 CAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGACTGCCAAGTAGGAAAGTCCATAAGGTATGTACTGGGCATAATGCCAGGCGG

**NdeI (3540)**

3501 GCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTG  
3601 ACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTGAGCCAGGCGGGCCATTT

**PacI (3726)**

**SdaI (3718)**      **BspLU11I (3736)**

3701 ACCGTAAGTTATGTAACGCCTGCAGGTTAATTAAGAACATGTGAGCAAAGGCCAGGAAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTT  
3801 CCATAGGCTCCGCCCCCTGACGAGCATCAAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCT  
3901 GGAAGCTCCCTCGTGCCTCTCCTGTTCCGACCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCAC

**ApaLI (4050)**

4001 GCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTGAGCCGACCGCTGCGCCTTATCCGGTAACCTA  
4101 TCGTCTTGAGTCCAAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAG  
4201 TTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGATTGGTAGCT  
4301 CTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGAT

**PacI (4466)**    **SwaI (4475)**    **NotI (4485)**

4401 CTTTTCTACGGGTCTGACGCTCAGTGGAACGAAAACCTCACGTTAAGGGATTTTGGTCAATGGCTAGTTAATTAACATTTAAATCAGCGCCGCAATAAAA  
4501 TATCTTTATTTTATTACATCTGTGTGTTGTTTTTGTGTGAATCGTAACTAACATACGCTCCTCATAAAACAAAACGAAACAAAACAACTAGCAAA  
4601 ATAGGCTGTCCCCAGTGCAAGTGACAGGTGCCAGAACATTTCTCTATCGAA