



**PvuI (7)**  
**SgfI (6)** 1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA MfeI (82) EcoNI (96)

101 GAGAAGTGGCGGGGTAACGGAAAGTGTGCTGTACTGGTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

**HindIII (245)** 201 **Psp1406I (203)** GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCAGAGGGCTCGCATCTCTCTTACAGCGCCCGCCCTACCTGAGGCC EcoNI (287) Bsu36I (291) PvuII (239)

301 GCCATCCACGCGGTTGAGTTCGCGTTCTGCCGCTCCCGCCTGTGGTGCCTCCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

401 GGGCCTTTGTCCGGCCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCTGCTTCTCAACTCTACGCTTTTGTTCGTTT

**NcoI (560)** 501 **BstEII (555)** TCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTACCATTGACCCATCTGTGACGCTGTGGCAGTTTCTGCTGCA PvuII (598) **AgeI (552)** 1 M D P S V T L W Q F L L Q **KasI (535)**

601 GCTGCTGAGAGAGCAAGCAATGGCCACATCTCCTGGACTTCACGGGATGGTGGTGAATTCAGAGTGGTGGATGCAGAGGAGGTGGCCCGCTGTGG MscI (621) EcoRI (658) 13 L L R E Q G N G H I I S W T S R D G G E F K L V D A E E V A R L W

701 GGGCTACGCAAGAACAAGACCAACATGAATTACGACAAGCTCAGCCGGCCTTGCGGTACTACTATGACAAGAACATCATCCGCAAGGTGAGCGGCCAGA BsrBI (789) 47 G L R K N K T N M N Y D K L S R A L R Y Y Y D K N I I R K V S G Q

801 AGTTCGTCTACAAGTTTGTGTCCTACCTGAGGTGCGAGGGTGTCCACTGAGGACTGCCCGCCAGCCAGAGGTGTCTGTTACCTCCACCATGCCAAA XcmI (890) 80 K F V Y K F V S Y P E V A G C S T E D C P P Q P E V S V T S T M P N

901 TGTGGCCCTGCTGCTATACATGCGCCCGAGGGGACACTGTCTGGAAAGCCAGGCACACCAGGGTGCAGGAATGGCAGGCCAGCGGTTTGGCA Tth111I (934) 113 V A P A A I H A A P G D T V S G K P G T P K G A G M A G P G G L A

1001 CGCAGCAGCCGGAACGAGTACATGCGCTCGGGCCTCTATTCCACCTTACCATCCAGTCTCTGCAGCCGAGCCACCCCTCATCTCGGCTGCTGTGG 147 R S S R N E Y M R S G L Y S T F T I Q S L Q P Q P P H P R P A V

1101 TGCTCCCAAGTGCAGCTCTGCGAGGGGAGCAGCGCCCTCGGGGAGCAGGAGCACCAGTCCAAGCCCTTGGAGGCTGTCTGGAGGCTGAAGAGGC SdaI (1117) StuI (1175) 180 V L P S A A P A G A A A P P S G S R S T S P S P L E A C L E A E E A

1201 CGGCTTGCCTCTGAGGTCATCTGACCCCGCCGAGGCCAAACCTGAAATCGAAAGAGCTTAATGTGGAGCCGGGTTTGGCCGGGCTTTGCCCCCA XcmI (1319) 213 G L P L Q V I L T P P E A P N L K S E E L N V E P G L G R A L P P

1301 GAAGTAAAAGTAGAAGGGCCCAAGGAAGAGTTGGAAGTTCGGGGGAGAGAGGGTTTGTGCCAGAAACCACCAAGGCCAGCCAGAAGTCCCTCCACAGG Bsp120I (1315) 247 E V K V E G P K E E L E V A G E R G F V P E T T K A E P E V P P Q

1401 AGGGCGTGCCAGCCCGGCTGCCCCGCGTTGTTATGACACCGCAGGGCAGGCGGGCGCCATGCGGCTTCCAGCCCTGAGATCTCCAGCCGAGAAAGGG BglIII (1478) 280 E G V P A R L P A V V M D T A G Q A G G H A A S S P E I S Q P Q K G

1501 CCGGAAGCCCGGACCTAGAGCTTCCACTCAGCCCGAGCCTGCTAGGTGGGCGGGACCCGAAACGCCAGCCAGGATCGGGAAGTGGCTCCGGCCTCCAG XmaI (1508) SandI (1554) 313 R K P R D L E L P L S P S L L G G P G P E R T P G S G S G S G L Q

1601 GCTCCGGGCGCGCTGACCCATCCCTGCTTCTACGCATACATTGACCCCGGTGCTGCTGACACCCAGCTCGCTGCTCCTAGCATTCACTTCTGGA 347 A P G P A L T P S L L P T H T L T P V L L T P S S L P P S I H F W

1701 GCACCTGAGTCCATTGCGCCCGTAGCCCGCAAGCTCTCCTTCCAGTTTCCATCCAGTGGCAGCGCCAGGTGCACATCCCTTCTATCAGCGTGG AapaLI (1774) 380 S T L S P I A P R S P A K L S F Q F P S S G S A Q V H I P S I S V D

1801 TGGCCTCTCGACCCCGTGGTGTCTCCCCAGGCCCCAGAAGCCATGACTACTACCACCACCACCACCACCAGCTAGCTGGCCAGACATGATAAGATACA MscI (1878) NheI (1872) 413 G L S T P V V L S P G P Q K P •

1901 TTGATGAGTTTGACAAACCACAAGTGAATGCAGTGAATAAATGCTTTATTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTG

**HpaI (2010)** 2001 MfeI (2021) CAATAAACAAGTTAAACAACAATTGCATTATTTTATGTTTCAGGTTACAGGGGAGGTGTGGGAGTTTTTTAAAGCAAGTAAAACCTCTACAAATGT

2101 **EcoRI (2106)** GGTATGGAATTCTAAAATACAGCATAGCAAACTTAACTCCAAATCAAGCCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGG

2201 GGCTGTTGCCAATGTGCATTAGCTGTTTGACGCTCACCTTTTCATGGAGTTAAGATATAGTGATTTTTCCCAAGTTTGAAGTACTAGCTTTCATTTT

2301 TTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTTAGTAAAATATTGAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATT SspI (2345) SwaI (2359)

2401 AGGCAGAATCCAGATGCTCAAGCCCTTATAATATCCCCAGTTTAGTAGTTGACTTAGGGAACAAGGAACCTTTAATAGAATTGGACAGCAAGAA

2501 AGCGAGCTTCTAGCTTTAGTTTCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAAGCAG 1414 • 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

2601 TCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGTGCCTGACAGCCA  
 112 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 V  
 SacI (2620) BstXI (2649) StuI (2784)

2701 CAATGGTGTCAAAGTCCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGAC  
 79 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

2801 AGCAGAGATGATCTCCCCAGTCTTGGTCTGATGGCCGCCGACATGGTGCTTGTTCCTCATAGAGCATGGTGATCTTCTCAGTGGCGACCTCCACC  
 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  
 BspHI (2934) BbsI (2930) XmnI (2926) AseI (2992)

2901 AGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGATGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTG  
 12 L E L D Q Q S I N F T K M

3001 TCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTGCGG  
 SacI (3049)

3101 TCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCGTTGATTTACTAGTCAAACAACTCCCATTGACGTCAATGGGGTGGAGACTTGGAAATC  
 SpeI (3147)

3200 CCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGG  
 SnaBI (3275)

3300 AAAGTCCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGATGT  
 NdeI (3380)

3400 ACTGCCAAGTGGGAGTTTACCGTAAATACTCCACCCATTGACGTCAATGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCATTATTGACGTCA

3500 ATGGGCGGGGTCGTTGGGCGGTACGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAA TTAAGAACATGTGAGCAAAAGGCCAGC  
 SdaI (3558) PacI (3566) BspLU11I (3576)

3598 AAAAGGCCAGGAACCGTAAAAAGCCGCGTTGCTGGCGTTTTTTCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTG

3698 GCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCGACCCCTGCCGCTTACCGGATACCTGTCC

3798 GCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCCGGTGTAGGTGCTTCGCTCCAAGCTGGGCTGTGTGCACG  
 ApaLI (3890)

3898 AACCCCCGTTACGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGTAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGG

3998 TAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAAGCAGTATTTGGTATCTGC

4098 GCTCTGCTGAAGCGATTACCTTCGAAAAAGAGTTGGTAGCTCTTGTATCGGCAACAAACCACCGTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGC

4198 AGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGCTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGT

4298 CATGGCTAGTTAATTAACATTTAAATC AGCGGCCGCAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACAT  
 PacI (4306) SmaI (4315) EagI (4326) NotI (4325)

4398 ACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCGAGTGAAGTGCAGGTGCCAGAACATTTCTCTATCGAA