



**PvuI (7)**  
**SgfI (6)** 1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA  
**MfeI (82)**  
101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

**HindIII (245)**  
**Psp1406I (203)** 201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACACGCCGCCGCCCTACCTGAGGCC  
**PvuII (239)**  
**Bsu36I (291)**  
301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCTCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC  
401 GGGCCTTTGTCCGGGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCTGCTTCTCAACTCTACGCTTTTGTTCGTTT

**SphI (560)**  
**AgeI (552)** 501 TCTGTTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCGCCTACCTGAGATCACCGGTACAGCATGCTGGCCCGAGGAAGCCGGTGTGCCGGCGCTCAC  
1 M L A R R K P V L P A L T

**Bsp120I (621)** 601 CATCAACCCTACCATCGCCGAGGCGCCATCCCTACCAGCGAGGGCGCTCCGAGGCAAACCTGGTGGACCTGCAGAAGAAGCTGGAGGAGCTGGAACCT  
13 I N P T I A E G P S P T S E G A S E A N L V D L Q K K L E E L E L  
**XmnI (724)**  
**BstBI (775)** 701 GACGAGCAGCAGAAGAAGCGGCTGGAAGCCTTTCTACCCAGAAAGCCAAGGTCGGCAACTCAAAGACGATGACTTCGAAAGGATCTCAGAGCTGGCGG  
47 D E Q Q K K R L E A F L T Q K A K V G E L K D D D F E R I S E L G

**BstEII (816)** 801 CGGCAACGGCGGGTGGTCACCAAAGTCCAGCACAGACCCTCGGCTCATCATGGCCAGGAAGCTGATCCACCTTGAGATCAAGCCGCCATCCGGAA  
**BspEI (893)**  
80 A G N G G V V T K V Q H R P S G L I M A R K L I H L E I K P A I R N  
901 CCAGATCATCCGGAGCTGCAGGCTCTGCACGAATGCAACTCGCCGTACATCGTGGGCTTCTACGGGCTTCTACAGTGACGGGGAGATCAGCATTTGC  
113 Q I I R E L Q V L H E C N S P Y I V G F Y G A F Y S D G E I S I C  
1001 ATGGAACACATGGATGGCGGCTCCCTGGACCAGGTGCTGAAAGAGGCCAAGAGGATCCCGAGGAGATCTGGGAAAGTCAAGTCCGCGTTCTCCGGG  
147 M E H M D G G S L D Q V L K E A K R I P E E I L G K V S I A V L R

**XbaI (1171)** 1101 GCTTGGCGTACCTCCGAGAGAAGCACCAGATCATGCACCGAGATGTGAAGCCCTCAACATCCTCGTGAACCTTAGAGGGGAGATCAAGCTGTGTGACTT  
180 G L A Y L R E K H Q I M H R D V K P S N I L V N S R G E I K L C D F

**XcmI (1232)** 1201 CGGGGTGAGCGGCCAGCTCATCGACTCCATGGCAAACCTCTCGTGGGCACGGCTCCTACATGGCTCCGGAGCGGTTGCAGGGCACACATTACTCGGTG  
**Neol (1226)** 213 G V S G Q L I D S M A N S F V G T R S Y M A P E R L Q G T H Y S V  
**BspEI (1266)**

**Acc65I (1352)** 1301 CAGTCGGACATCTGGAGCATGGGCTGTCCCTGGTGGAGCTGGCCGTGGAAAGTACCCCATCCCCCGCCGACGCCAAAGAGCTGGAGGCCATCTTTG  
**BstXI (1376)**  
247 Q S D I W S M G L S L V E L A V G R Y P I P P P D A K E L E A I F

**SalI (1411)** 1401 GCCGCGCCGTGGTGCAGCGGGGAAGAAGGAGAGCCTCACAGCATCTCGCTCGGCCGAGGCCCGCCCGGGCGCCCGTACGCGGTACGGGATGGATAGCCG  
**EagI (1450)** 280 G R P V V D G E E G E P H S I S P R P R P P G R P V S G H G M D S R  
**XmaI (1462)**

**Neol (1505)** 1501 GCCTGCCATGGCCATCTTTGAACCTCTGGACTATATTGTGAACGAGCCACCTCCTAAGCTGCCAACGGTGTGTTACCCCGACTTCCAGGAGTTTGTG  
313 P A M A I F E L L D Y I V N E P P P K L P N G V F T P D F Q E F V

**RsrII (1672)** 1601 AATAAATGCCTCATCAAGAACCCAGCGAGCGGGCGGACCTGAAGATGCTCACAAACACACCTTTCATCAAGCGGTCGAGGTGGAAGAAGTGGATTTTG  
347 N K C L I K N P A E R A D L K M L T N H T F I K R S E V E E V D F

**NheI (1779)** 1701 CCGGCTGTTGTGTAACCCCTGCGGCTGAACAGCCCGGCACACCCACGCGCACCCGCGTGTGACAGTGGCCGGGCTCGTAGCTGGCCAGACATGATA  
380 A G W L C K T L R L N Q P G T P T R T A V •

1801 AGATACATTGATGAGTTTGGACAAACCACAAGTGAAGTGCAGTGAATAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACATTA

**HpaI (1917)** 1901 TAAGCTGCAATAAACAAGTTAAACAACAATTGCATTCAATTTATGTTTCAGGTTACAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTA  
**MfeI (1928)**

**EcoRI (2013)** 2001 CAAATGTGGTATGGAATCTAAAATACAGCATAGCAAACTTTAACCTCAAATCAAGCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGG  
2101 CATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGTATTTTCCCAAGGTTTGAAGTACTCT

**SspI (2252)** 2201 TCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTTAGTAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTT  
**SwaI (2266)**

2301 TTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTCATAATATCCCCAGTTTAGTAGTTGACTTAGGGAACAAAGAACCTTAAATAGAAATGGACA  
2401 GCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTACTTGGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTTCATCTCAATGAGCAC  
141 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

**SacI (2527)** 2501 AAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGCACATGCCACAGGGGCTGACCACCTGTAGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTG  
115 F C 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

2601 ACAGCCACAATGGTGTCAAAGTCTTCTGCCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTACCCTGCCAATGTAGGCCTCAA  
81 V A V 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  
2701 TGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCTGATGGCCGCCGACATGGTGTCTTGTTCCTCATAGAGCATGGTATCTTCTCAGTGGCGAC  
48 H V 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

BspHI (2841)  
BbsI (2837)  
XmnI (2833)

2801 CTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCATGATGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGA  
15 E V L E L D Q Q S I N F T K M

AseI (2899)

2901 TTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCCACCGTACACGCCTACCGCC

SacI (2956)

3000 CATTTCGCTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCCTTGATTTACTAGTCAAAACAAACTCCCATTGACGTCAATGGGGTGGAGACT

SpeI (3054)

3099 TGGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGC

SnaBI (3182)

3199 CAAGTAGGAAAGTCCATAAGGTCACTGTACTGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACA

NdeI (3287)

3299 CTTGATGTACTGCCAAGTGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTAT

3399 TGACGTCAATGGCGGGGGTCTGTTGGCGGTGAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCC T G C A G G T T A A T T A A G A A C A T G T G A C A A A  
3497 AGGCCAGCAAAGGCCAGGAACCGTAAAAAGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCAAAAATCGACGCTCAAGT  
3597 CAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCTGGAAGTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGAT  
3697 ACCTGTCCGCTTCTCCCTTCGGGAAGCGTGGCGTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTGCTTCGCTCCAAGCTGGGCTG

SdaI (3465) PacI (3473) BspLU11I (3483)

3797 TGTGCAGAACCCCCGTTCCAGCCGACCCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAAACCGGTAAGACACGACTTATCGCCACTGGCAGCA

ApaLI (3797)

3897 GCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTG

3997 GTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTGTTG

4097 CAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGG

EagI (4233)  
PacI (4213) SwaI (4222) NotI (4232)

4197 ATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCGCAATAAAATATCTTTATTTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTA

4297 ACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCAGTGAAGTGCAGGTGCCAGAACATTTCTCTATCGA  
4397 A