



PvuI (7)
SgfI (6) MfeI (82) EcoNI (96)
1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203) Bsu36I (291)
EcoNI (287)
201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACACGCCGCCGCCCTACCTGAGGGCC
301 GCCATCCACGCCGGTTGAGTGCAGTTCGCCGCTCCCGCCTGTGGTGCCCTCTGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTAACTCTACGTCTTTGTTTCGTTT

BstEII (555)
AgeI (552) **NcoI (560)**
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCCTACCTGAGATCACCGGTACCATTGGAGGTGGCTGTGGAGAAGCGCGCGGGCAGCGGGC
1 M E V A V E K A A A A A A

Bsp120I (660)
NgoMIV (653)
601 TCCGGCCGGAGGCCCGCAGCGGGCGCGGAGCGGGGAGAATGAGGCCGAGAGCCGGCAGGGCCGGACTCGGAGAGCGGGCGGAGGGCTCCCGGCTC
13 P A G G P A A A A P S G E N E A E S R Q G P D S E S G G E A S R L

Eco47III (785)
701 AACCTGTTGGACACTTGGCCGTGTGCCACCAGAACATCCAGAGCCGGGTGCCAAGCTGCTGCCTGCCTGCACTCGTTCTGCCAGCGCTGTTTGGCCG
47 N L L D T C A V C H Q N I Q S R V P K L L P C L H S F C Q R C L P

Eco47III (806) **XmaI (882)**
801 CGCCGACGCTATCTCATGCTGACGGCGCCCGCTGGGCTCGCAGAGACCCCTCCACCCGCTCCCGCCCCGCCCGGGCTCCCGGGCCGG
80 A P Q R Y L M L T A P A L G S A E T P P A P A P A P A P A P G S P A G
901 TGGTCTTCGCCATTCGCCACCAAGTTGGAGTATTGATGCCAGTTTGCAGTCAAGAGTGTGTGAGAGACACATCATAGACAACTTTTTGTGAAG
113 G P S P F A T Q V G V I R C P V C S Q E C A E R H I I D N F F V K
1001 GACACCACTGAAGTTCCTAGTAGTACAGTAGAAAAGTCTAATCAGGTATGTACAAGCTGTGAAGACAATGCAGAAGCTAATGGGTTTTGTGTAGAGTGTG
147 D T T E V P S S T V E K S N Q V C T S C E D N A E A N G F C V E C
1101 TTGAATGGCTCTGAAGACATGTATTAGAGTCCACAGAGGGTGAAGTTCACAAAAGACCACACAGTCCAGGCAGAAAGAAGTATCTCCAGAGGCAGT
180 V E W L C K T C I R A H Q R V K F T K D H T V R Q K E E V S P E A V

BstEII (1203)
1201 TGGGTGACCACTGACGACAGTGTGTTTGTCCCTTCCATAAAAAGGAGCAGTTGAACTTTACTGTGAAACATGTGATAAACTGACCTGTCGAGACTGC
213 G V T S Q R P V F C P F H K K E Q L K L Y C E T C D K L T C R D C
1301 CAGCTGCTAGAACAAGAACAACAGGTATCAATTTATAGAAGAAGCTTTTTCAGAAATCAAAAAGTGTATCATAGATACTAATCACAAAAGTGTGAAA
247 Q L L E H K E H R Y Q F I E E A F Q N Q K V I I D T L I T K L M E

Bst1107I (1416)
1401 AAACAATAATATAAAGTATACAGGAAATCAGATCCAAAATAGGATAATTGAAATAAATCAAAAACAAAAGCAGGTGGAACAGGATATTAAGTTGCCAT
280 K T K Y I K Y T G N Q I Q N R I I E I N Q N Q K Q V E Q D I K V A I
1501 CTTACATTGATGGTGGAGATAAAACAAAAGGAAAGCTCTGCTGCACCAGCTTGAGAGTCTTGCAAAGGACCATCGAATGAAACTCATGCAACAACAG
313 F T L M V E I N K K G K A L H Q L E S L A K D H R M K L M Q Q Q

NsiI (1639)
BstAPI (1632)
1601 CAGGAAGTGGCTGGGCTTTCTAAGCAGTTAGACGTCATGCAATTTTCTAATGGGCTGTTTCCAGTGGCAGCAGCACAGCCTTGTGTACAGCAAGC
347 Q E V A G L S K Q L E H V M H F S K W A V S S G S S T A L L Y S K
1701 GGCTGATTACATACAGGTTACGGCACCTTCTCGTGAAGGTGTGATGCTTCTCTGTGACCAACACCACCATCCAGTTTCACTGTGATCCTAGTTTCTG
380 R L I T Y R L R H L L R A R C D A S P V T N T T I Q F H C D P S F W

Spl (1807)
1801 GGCTCAAAATATTATCAACTTGGGTTCTTTAGTAATCGAGGATAAAGAGACCCAGCCACAAATGCCTAAGCAGAATCCTGTCGTGGAGCAGAGTTCACAG
413 A Q N I I N L G S L V I E D K E S Q P Q M P K Q N P V V E Q S S Q

DraIII (1901)
1901 CCACCAGGTGGTTTACCTTCCAACAGTTATCCAAGTCCCAACACAGATCAGCCTAGCTCAGTTACGACTCCAGCATATTCAGCAACAGGTAATGGCTC
447 P P G G L P S N Q L S K F P T Q I S L A A Q L R L Q H I Q Q Q V M A

BstAPI (2004) **Bsp120I (2059)**
2001 AGAGGCAACAGGTGCAACGGAGGCCAGCACCTGTGGGTTTACCAAACCTAGAATGCAGGGGCCATCCAGCAGCCTTCCATCTCTCATCAGCATCCGCC
480 Q R Q Q V Q R R P A P V G L P N P R M Q G P I Q Q P S I S H Q H P P
2101 ACCACGCTTAATAAACTTTCAGAAATCACAGCCCTAAGCCCAATGGACCAGTCTTCTCTTATCCTCAGCAGCTGAGATATTCACCAAGCCAGAATGTA
513 P R L I N F Q N H S P K P N G P V L P P Y P Q Q L R Y S P S Q N V
2201 CCTCGCAGACAACAATAAAGCCCAACCCCTTGAATGGCTTTTGGCTCAACAGGCCATAAAACAGTGGCAGATCAGCAGTGTACAGGCTCCGCCCA
547 P R Q T T I K P N P L Q M A F L A Q Q A I K Q W Q I S S V Q A P P

ApaLI (2399)
2301 CAACTGCCAGCAGCTCCTCCTCCACGCCGTCCAGCCCCACAATCACAAGTGCAGCTGGGTACGATGGAAAAGCTTTTAGTTACCCCATGATTGATCTGAG
580 T T A S S S S T P S S P T I T S A A G Y D G K A F S S P M I D L S

AgeI (2403) **SgrAI (2402)** **ScaI (2455)**
2401 TGCACCGTGGGAGGGTCTTACAATCTTCTTCCAGATATTGATTGTTCAAGTACTATAATGTTGGACAACATTGCAAGGAAAGACACAGGTGTA
613 A P V G G S Y N L P S L P D I D C S S T I M L D N I A R K D T G V

PshAI (2592)
2501 GATCAGCCAGCCGAGGCTCCGTCAAACAGAACGGTGCAGTACCAAAATTCATCAGTCCATCTCCAGGCCTTGACGGCCTGTTACTATGACTAGCG
647 D H A Q P R P P S N R T V Q S P N S S V P S P G L A G P V T M T S

2601 TCCATCCCCAATACGTTTACCTAGTGCCTCCAGTGTGGAAAGTCGAGGAAGCTCTGGCTCTTCCAGCAAACAGCAGGAGCTGATTCTACTACAAGGT
 680▶ V H P P I R S P S A S S V G S R G S S G S S S K P A G A D S T H K V
 DraIII (2618) SapI (2657)
 BstBI (2723)
 Bsp119I (2723)
 2701 CCCAGTAGTCATGCTGGAGCCAATTGCAATAAAACAGGAAAACAGTGGACCACCTGAAAATTATGATTTTCTGTTGTTATAGTAAAACAAGAATCAGAT
 713▶ P V V M L E P I R I K Q E N S G P P E N Y D F P V V I V K Q E S D
 XbaI (2806)
 2801 GAAGAATCTAGACCTCAAATACTAATACTCAAGAAGCATACTTACCTCCCTCTTAAACAGCAGTCAGAGCTCTGCTTCTGAGGAAAACCGTGTAC
 747▶ E E S R P Q N T N Y P R S I L T S L L L N S S Q S S A S E E T V L
 2901 GATCTGATGCCCCGATAGTACAGGAGATCAGCCTGGACTCCATCAAGAAAATTCCTCAAATGGAAAGTCTGAGTGGTGGATGCCTCCAGAAAGTCCCC
 780▶ R S D A P D S T G D Q P G L H Q E N S S N G K S E W S D A S Q K S P
 3001 TGTGCATGTCGGAGAGACGAGGAAGGAGGATGACCCCAATGAAGACTGGTGTGCTGTTTGTCAAATGGTGGGAACTCTATGCTGTGAGAAAATGTCCT
 813▶ V H V G E T R K E D D P N E D W C A V C Q N G G E L L C C E K C P
 XcmI (3145)
 3101 AAAGTATTCATCTTACTTGTGATGTGCCACCTTGACAAATTTTCCAAGTGGAGAATGGATCTGTACTTTCTGCCGAGACTTATCTAAGCCAGAGGTTG
 847▶ K V F H L T C H V P T L T N F P S G E W I C T F C R D L S K P E V
 HpaI (3261)
 3201 ACTATGATTGTGATGTTCCAGTCACCAGTACAGAGAAACGGAAAAGTGAAGGCCCTTACTAAGTAAACGCAATAGACAAAAGGAAATGTGAACGCCTACT
 880▶ D Y D C D V P S H H S E K R K S E G L T K L T P I D K R K C E R L L
 3301 TCTGTTTCTTACTGCCATGAAATGAGCCTGGCTTCCAAGACCTGTTCTCTAAGTGTGCCTGATTATTATAAAAATAATAAAAACCAATGGACTTG
 913▶ L F L Y C H E M S L A F Q D P V P L T V P D Y Y K I I K N P M D L
 BstI107I (3438)
 3401 TCAACCATCAAGAAAAGACTTCAGGAGGATTATTGCATGTATACAAAGCCTGAAGACTTTGTAGCTGATTTTAGATTGATCTTTCAAACCTGTGCTGAAT
 947▶ S T I K K R L Q E D Y C M Y T K P E D F V A D F R L I F Q N C A E
 Bsu36I (3595)
 3501 TCAATGAGCCTGATTCTGAAGTAGCCAATGCTGGTATAAACTTGAAAGCTATTTTGAAGAACTTCTAAAGAATCTTTATCCAGAAAAAGGTTTCTCAA
 980▶ F N E P D S E V A N A G I K L E S Y F E E L L K N L Y P E K R F P K
 3601 GGTAGAATTCAGGCATGAAGCAGAAAGACTGTAAGTTCAAGTGCAGACTCAGACGATGACTTTGTACAGCCCCGGAAGAAGCGTCTCAAGAGCACCGAGGAT
 1013▶ V E F R H E A E D C K F S D D S D D D F V Q P R K K R L K S T E D
 MscI (3725)
 NheI (3719)
 3701 CGCCAGCTGCTTAAGTAACGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTGGACAACCCACAACCTAGAATGCAGTAAAAAATGCTTTATT
 1047▶ R Q L L K •
 HpaI (3857) MfeI (3868)
 3801 TGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAACAAGTAAACAACAATTGCATTCATTTATGTTTCAGGTTTCAGG
 3901 GGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACTTTAACCTCAAATCAAGCC
 4001 TCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGT
 SapI (4135) SspI (4192)
 4101 TTAAGATATAGTGTATTTTCCCAAGTTTGAACCTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTATGATAAATATTCA
 SwaI (4206)
 4201 GAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTT
 4301 GGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGGATGAGTTCCTCAA
 4401 TGGTGGTTTTGACCAGCTTGCATTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGACATGCCACAGGGGCTGACCC
 128▶ 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
 4501 CCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCAATGGCAATG
 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
 4601 GCTTCAGCACAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCTGATGGCCGCCCGACATGGTGT
 61▶ 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 K
 4701 TGTGTCTCATAGAGCATGGTGTCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCTGCTGAGAGATGTTGAAGTCTTTCATGGTGGCCCTCTATA
 28▶ 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 (4839)
 4801 GTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCACTAAACGAGC
 SpeI (4994)
 4901 TCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCCTTACTAGT
 5001 CAAAAAACTCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCA
 SnaBI (5122)
 5101 TCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCCATAAAGTCAATGACTGGGCATAATGCCAGGCGGGCCATTTACCGTC
 NdeI (5227)
 5201 ATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGTACTGCCAAGTGGGCAGTTTACCCTAAATACTCCACCCATTGACGTCAATGGAAA
 5301 GTCCTATTGGCGTTACTATGGGAACATACGTCAATATTGACGTCAATGGGGGGGGTCTTGGGCGTCCAGGCGGGCCATTTACCGTAAGTTATG

PacI (5413)

PstI (5406)

SdaI (5405)

5401 TAACGCCTGCAGGTTAA**TTAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGC**
5501 **CCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCG**
5601 **TGGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGAAGCGTGGCGCTTCTCATAGCTCACGCTGTAGGTATCT**

ApaLI (5737)

5701 **CAGTTCGGTGTAGGTCGTTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCC**
5801 **AACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGT**
5901 **GGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAA**
6001 **ACAAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGG**

PacI (6153) SwaI (6162) **NotI (6172)**

6101 **TCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCCAATAAAATATCTTTATTTTC**
6201 **ATTACATCTGTGTGTTGGTTTTTTGTTGTAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAAATAGGCTGTCCCC**
6301 **AGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA**