



PvuI (7)
SgfI (6) 1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
MfeI (82)
101 GAGAAAGTGGCGCGGGTAAACTGGAAAAGTGTGCTGTACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)
Psp1406I (203) 201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACCGCGCCGCCCTACCTGAGGCC
PvuII (239)
Bsu36I (291)
301 GCCATCCACGCCGGTTGAGTCGCGTTTCTGCCGCTCCCGCTGTGGTGCCTCTGAAGTGCCTCCCGCTCTAGGTAAGTTAAAGCTCAGGTCGAGACC
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCTGCTTGTCAACTCTACGCTTTTGTTCGTTT

AgeI (552) **BspHI (560)**
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTATCATGAGTTCTTCGCCTGTAAATGTCAAGAAGCTGAAGGT
601 GTCGGAGCTGAAGGAGGAGCTCAAGAAGCGGCGCTCTCCGACAAGGCGCTCAAGGCCGATCTCATGGATCGACTCCAGGCCGCTGGACAACGAGCA
13▶ S E L K E E L K K R R L S D K G L K A D L M D R L Q A A L D N E A

NcoI (713) **XmaI (721)** **AvrII (741)** **EagI (755)**
701 GGAGGCCGCCCGCCATGGAGCCCGGAACGGCAGTCTCGACTAGGTGGCGATGCGGCCGGGCGCTCGGAGCGGGCTAGAGCAGGAGGCCGCGGCTG
47▶ G G R P A M E P G N G S L D L G G D A A G R S G A G L E Q E A A A

SgrAI (894)
801 GCGCCGAAGACGACGAGGAGGAGGGCATCGCCGCTCTGGACGGCAGCAGATGGAGCTGGGCGAGGAGAACGGGGCGGGGGCGGCTGACCGCGG
80▶ G A E D D E E E E G I A A L D G D Q M E L G E E N G A A G A A D A G
901 CGCGATGGAGGAAGAGGAGGAGCGCTCGGAAGACGAGAACGGCAGCAGCAGGCTTCCAGGAGGGGAAGACGAGCTCGGCGACGAGGAGGAGGGCGCG
113▶ A M E E E E A A S E D E N G D D Q G F Q E G E D E L G D E E E G A

BstXI (1068)
1001 GCGCAGGAGAACGGTACCGGGAGCAGCAGTCCAACCGCCGCGAGCGGCGCGCAGCAGCAGCTTCCAGCAGCGTGGTCCGGCAAGGAGGCCGCGG
147▶ G D E N G H G E Q Q G S Q P P A A A A Q Q Q P S Q Q R G A G K E A A
1101 GCAAGACGACGGCCCCACCTCGCTTCCGGTGACGGTGGCGCCAGGGCGAGGAGGCAACAGCAGGCGGGAGGAGCGGCAAAACAGAACA
180▶ G K S S G P T S L F A V T V A P P G A R Q G Q Q Q A G D G K T E Q
1201 GAAAGGTGGAGATAAAAAAGAGGGCTTAAAGACCGCAGAAAGATCATGGCCGAGGGTATTTTGTGATACATCGAAGAAAACAAGTACAGCAGAGCCAAG
213▶ K G G D K K R G V K R P R E D H G R G Y F E Y I E E N K Y S R A K

XhoI (1392)
1301 TCTCCTCAGCCACCTGTTGAAGAAGAAGACGAACACTTCGATGACACAGTGGTTTGTCTTGATACTTATAATTGTGATCTGCATTTTAAAATCTCGAGAG
247▶ S P Q P P V E E E D E H F D D T V V C L D T Y N C D L H F K I S R

BstAPI (1484)
1401 ACCGTCGAGTGCTTCTCCCTTACTATGGAGAGTTTTGCTTCTGTGGGCTGGAGGAAGAGCTTCTACGGTGTGTCAAAGGCAAAAGTCTGCTTTGA
280▶ D R L S A S S L T M E S F A F L W A G G R A S Y G V S K G K V C F E
1501 GATGAAGTAACAGAGAAGATCCAGTAAGACACTTATATACAAAAGATATTGATATACATGAAGTTCGGATTGGCTGGTCACTAACCACAAGTGAATG
313▶ M K V T E K I P V R H L Y T K D I D I H E V R I G W S L T T S G M
1601 TTGCTTGGTGAAGAAGAAATTTTCTTACGGGATTTCTCTGAAAGGAATAAAAACATGCAACTGTGAGACAGAAGATTATGGGGAGAAGTTTGTGAAAATG
347▶ L L G E E E F S Y G Y S L K G I K T C N C E T E D Y G E K F D E N

BglII (1767)
1701 ATGTGATTACATGCTTTGCTAACTTTGAAACTGATGAAGTTGAACTCTTATGCGAAGAATGGACAAGATCTGGTGTTCCTTTAAGATCAGTAAGGA
380▶ D V I T C F A N F E T D E V E L S Y A K N G Q D L G V A F K I S K E

BspLU11I (1827)
1801 AGTTCTTGTGACCGGCCACTATTTCCACATGTTCTCTGCCATAACTGTGAGTTGAATTTAATTTCCGGTCAAAGGAAAAGCCATACTTTCCAATACCT
413▶ V L A D R P L F P H V L C H N C A V E F N F G Q K E K P Y F P I P
1901 GAAGACTGTACTTTTATCCAAAATGTCCCCTTAGAGGACCGAGTTAGAGGACCAAAAGGACCTGAAGAGAAGAAGGATTGTGAGGTTGTAATGATGATTG
447▶ E D C T F I Q N V P L E D R V R G P K G P E E K K D C E V V M M I

PvuII (2042)
2001 GCTTGCCAGGAGCTGGAAAACTACCTGGGTTACTAAACATGCAGCTGAAAACCTGGGAAATACAACATTCTTGAACAAATACGATTATGGACAAGAT
480▶ G L P G A G K T T W V T K H A A E N P G K Y N I L G T N T I M D K M
2101 GATGGTGGCAGGTTTTAAGAAGCAAATGGCAGATACTGGAAAACCTGAACACACTGTTGCGAGAGAGCCCAACAGTGTCTTGGCAAGTTTATTGAAATTGCT
513▶ M V A G F K K Q M A D T G K L N T L L Q R A P Q C L G K F I E I A
2201 GCCCGTAAGAAGCGAAATTTTATTCTGGATCAGACAAATGTGTCTGCTGCTGCCAGAGAAGAAAATGTGCTGTTTCCAGGCTTCCAGCGGAAAGCTG
547▶ A R K K R N F I L D Q T N V S A A Q R R K M C L F A G F Q R K A
2301 TTGTAGTGTGCCAAAAGATGAAGACTATAAGCAGAGGACACAGAAGAAGGCAGAAGTAGAGGGGAAGGACCTACCAGAACATGCTGTCTCAAGATGAA
580▶ V V V C P K D E D Y K Q R T Q K K A E V E G K D L P E H A V L K M K

HindIII (2479)
2401 AGGAAACTTCACCTTCCAGAGTTGCAGAATGCTTTGATGAAATAACCTATGTTGAACTTCAGAAAGAGGAAGCCAAAAGCTTTTGGAGCAATATAAA
613▶ G N F T L P E V A E C F D E I T Y V E L Q K E E A Q K L L E Q Y K
2501 GAAGAAAGCAAAAAGGCACTGCCACCAGAAAAGCAAAAACACTGGCTCAAAGAAAAGCAATAAGAATAAGAGTGGCAAGAACCAGTTCAACAGAGGTG
647▶ E E S K K A L P P E K K Q N T G S K K S N K N K S G K N Q F N R G

XcmI (2604)
SfiI (2602)
MscI (2601)
2601 GTGGCCATAGAGGCCGTGGAGGATTCAATATGCGAGGTGGCAATTTTCAGAGGAGGAGCTCCTGGGAATCGTGGTGGATATAATAGGAGAGGCAACATGCC
680▶ G G H R G R G G F N M R G G N F R G G A P G N R G G Y N R R G N M P

BbrPI (2747)
2701 ACAGAGAGGTGGTGGCGTGGAAAGTGGTGAATTGGCTATCCATACCCACGTGGCCCTGTTTTCTGGCCGAGGTGGTACTCAAACAGAGGGAATTAC
713▶ Q R G G G G S G G I G Y P Y P R G P V F P G R G G Y S N R G N Y
2801 AACAGAGGTGGAATGCCCAACAGAGGAACTATAACCAAGAAGTTCAGAGGACGAGGAAATAATCGTGGCTACAAAAATCAATCTCAGGGCTACAATCAGT
747▶ N R G G M P N R G N Y N Q N F R G R G N N R G Y K N Q S Q G Y N Q

NcoI (2929)
NheI (2987)
MscI (2993)
2901 GGCAGCAGGGTCAATTCTGGGGTCAAGCCATGGAGTCAGCATTATACCAAGGATATTATTGAATACCCAAATAAAACGAAGTCTAGCTAGCTGGCCAG
780▶ W Q Q G Q F W G Q K P W S Q H Y H Q G Y Y •
3001 ACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTAAAAAATGCTTTATTGTGAAATTTGTGATGCTATTGCTTTATTTGT

HpaI (3125) **MfeI (3136)**
3101 AACCAATTATAAGCTGCAATAAAACAAGTTAAACAACAACCAATTGCATTCATTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAA

EcoRI (3221)
3201 AACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAAACCTTAACTCCAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAA
3301 GGCATAGGCATCAGGGGCTGTGCCAATGTGCATTAGCTGTTGCAGCCTCACCTTCTTCATGGAGTTTAAGATATAGTGATTTTCCCAAGGTTTGA

SspI (3460) **SwaI (3474)**
3401 CTAGCTCTTCATTTCTTTATGTTTTAAATGCACCTGCCACATTCCTTTTTAGTAAATATTAGAAATAATTTAAATACATCATTGCAATGAAAA
3501 TAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAA
3601 ATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCA
141◀ • N R T Y K L P I L E E I T T K V L K G N M E

BstXI (3764)
3701 ATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGG
117◀ I L V 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

StuI (3899)
3801 GGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTACCCTGCCAATGTA
84◀ H R 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
3901 GGCCTCAATGTGGACAGCAGAGATGATCTCCCAAGTCTTGGTCTGATGGCCGCCGACATGGTGTGCTTGTCTCATAGAGCATGGTATCTTCTCA
51◀ A E I 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
4001 GTGGGCACCTCCACCAGTCCAGATCCTGCTGAGAGATGTTGAAGGCTTTCATGGTGGCCCTCTATAGTGAGTCTGATTATACTATGCCGATATACTAT
17◀ T A V E V L E L D Q Q S I N F T K M

AseI (4107)
4101 GCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCCTAAACGAGCTCTGCTTATATAGACCTCCACCCTACACGCC

SpeI (4262)
4201 TACCGCCATTTGCGTCAATGGGCGGAGTTGTTACGACATTTTGAAAGTCCCGTTGATTTACTAGTCAAACAACCTCCATTGACGTCAATGGGGTG

SnaBI (4390)
4301 GAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTAAGTCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATG

NdeI (4495)
4401 TACTGCCAAGTAGGAAAGTCCCATAGGTCATGTAAGTGGGATAATGCCAGGCGGGCCATTTACCGTCAATGACGTCAATAGGGGGCTACTTGGCATAT
4501 GATACACTTGTACTGCAAGTGGGAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGT

PaeI (4681)
PstI (4674)
SdaI (4673) **BspLU11I (4691)**
4601 CATTATTGACGTCAATGGGCGGGGTGTTGGGCGTTCAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAAATAAGAACATGTGAG
4701 CAAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTC
4801 AAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATACCAGGCTTTCCCTGGAAGCTCCCTCGTGGCTCTCTGTTCCGACCCTGCCGCTTACC
4901 GGATACCTGTCCGCTTTCTCCCTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCAAGCTGG

ApaLI (5005)
5001 GCTGTGTGCACGAACCCCGTTCAGCCGACCGCTGCGCCTTATCCGGTAATATCGTCTTGTAGTCCAAACCGTAAGACACGACTTATCGCCACTGGC

5101 AGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTA

5201 TTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTG

5301 TTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACACAGTTA

EagI (5441)

PacI (5421) SmaI (5430) **NotI (5440)**

5401 AGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGGAAT

5501 CGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTA

5601 TCGAA