



PvuI (7)
SgfI (6)
1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCC

Psp1406I (203) **HindIII (245)**
201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGTGAAGCTTCGAGGGCTCGCATCTCTCTTACGCGCCCGCCCTACCTGAGGCC
301 GCCATCCACGCGGGTTGAGTCGCGTTTCTGCCGCCTCCCGCTGTGGTGCCTCTGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCTGCTTGTCAACTCTACGCTTTTGTTCGTTT

NcoI (560)
BstEII (555)
KasI (535) **AgeI (552)** **AvrII (585)**
501 TCTGTTCTGCGCCGTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTACCATTGGGAGACCACCTGGACCTTCTCTAGGAGTGGTGTCT
601 CATGGCCGGTCTGTGTTTGAATTCTTCTGCTCTTTGATGGCCGAATAGCCTTTATCGTTTCTGCAACCTCACCCAGGTCCCCAGGTCTCAAC
130 M A G P V F G I P S C S F D G R I A F Y R F C N L T Q V P Q V L N
701 ACCATGAGAGGCTCTGCTGAGCTTCACTATATCAGGACAGTCACTGCTTATCCTTCCCTTTCTGGAACAGCTGCAGCTGTGGAGCTCGGGAGCC
47 T T E R L L L S F N Y I R T V T A S S F P F L E Q L Q L L E L G S
Bst1107I (801)
801 AGTATACCCCTTGACTATTGACAAGGAGGCTTCCAGAAACCTGCCAACCTTAGAATCTTGGACCTGGGAAGTAGTAAGATATACTTCTGCATCCAGA
80 Q Y T P L T I D K E A F R N L P N L R I L D L G S S K I Y F L H P D
901 TGCTTTTACAGGACTGTTCCATCTGTTTGAAGTACTGATTTCTGTGGTCTCTGATGCTGATTGAAAGATGGTTATTTTCAAAAATTTAAAGGCT
113 A F Q G L F H L F E L R L Y F C G L S D A V L K D G Y F R N L K A
1001 TTAAGTCCATCAGCAAAAAGCCAGGCTTCTCTTTGATTCTTCCACACCATGATGGGTGCCGGTTTGGCTTCCATAACATCAAAGATCCTGACCCAGA
147 L T R L D L S K N Q I R S L Y L H P S F G K L N S L K S I D F S S
SspI (1104) **XhoI (1129)**
1101 ACCAAATATTCTTGTATGTGAACATGAGCTCGAGCCCTACAAGGAAAACGCTCTCTTTTTAGCCTCGCAGCTAATAGCTTGTATAGCAGAGTCTC
180 N Q I F L V C E H E L E P L Q G K T L S F F S L A A N S L Y S R V S
1201 AGTGGACTGGGAAAAATGTATGAACCCATTGAGAAACATGGTGTGGAGATACTAGATGTTTCTGAAATGGCTGGACAGTGGACATCACAGGAACTTT
213 V D W G K C K M N P F R N M V L E I L D V S G N G W T V D I T G N F
1301 AGCAATGCCATCAGCAAAAAGCCAGGCTTCTCTTTGATTCTTCCACACCATGATGGGTGCCGGTTTGGCTTCCATAACATCAAAGATCCTGACCCAGA
247 S N A I S K S Q A F S L I L A H H I M G A G F G F H N I K D P D Q
MscI (1415) **BbsI (1459)**
1401 ACACATTTGTGGCCTGGCAGAAAGTTCAGTGAGACACCTGGATCTTTCACATGGGTTTGTCTTCCCTGAACTCACGAGTCTTTGAGACACTCAAGGA
280 N T F A G L A R S S V R H L D L S H G F V F S L N S R V F E T L K D
1501 TTTGAAGTTCTGAACTTGCCTACAACAAAGATAAATAAGATTGCAGATGAAGCATTTTACGGACTTGACAACCTCAAAGTTCTCAATTTGTCATATAAC
313 L K V L N L A Y N K I N K I A D E A F Y G L D N L Q V L N L S Y N
BstBI (1620)
1601 CTTCTGGGGAACTTTACAGTTCGAATTTCTATGGACTACCTAAGGTAGCCTACATTGATTTGCAAAAGAATCACATTGCAATAATTCAAGACCAAACAT
347 L L G E L Y S S N F Y G L P K V A Y I D L Q K N H I A I I Q D Q T
EcoRV (1780)
1701 TCAAATCTGGAAAAATTACAGACCTTGATCTCCGAGACAATGCTCTTACAACATTATTTTATTCCAAGCATACCCGATATCTTCTGAGTGGCAA
380 F K F L E K L Q T L D L R D N A L T T I H F I P S I P D I F L S G N
SpeI (1803) **XbaI (1872)** **Acc65I**
1801 TAAACTAGTGACTTTGCCAAAGATCAACCTTACAGCGAACCTCATCCACTTATCAGAAAAAGCTAGAAAATCTAGATATTCTCTACTTTCTCTACGG
413 K L V T L P K I N L T A N L I H L S E N R L E N L D I L Y F L L R
1901 GTACCTCATCTCCAGATTCTCATTTAAATCAAATCGCTTCTCTCTCTGATGGAGATCAAACCCCTCAGAGAATCCAGCTTAGAACAGCTTTTCC
447 V P H L Q I L I L N Q N R F S S C S G D Q T P S E N P S L E Q L F
2001 TTGGAGAAATATGTTGCAACTTGCCTGGGAAACTGAGCTGTGGGATGTTTTGAGGACTTTCTCATCTCAAGTCTGTATTTGAATCATACTA
480 L G E N M L Q L A W E T E L C W D V F E G L S H L Q V L L N H N Y
2101 TCTTAATTCCTTCCACCAGGAGATTTAGCCATCTGACTGCATTAAGGGACTAAGCCTCAACTCCAACAGGCTGACAGTCTTTTCTACAATGATTTA
513 L N S L P P G V F S H L T A L R G L S L N S N R L T V L S H N D L
DraIII (2270)
2201 CCTGCTAATTTAGAGATCCTGGACATATCCAGGAACAGCTCCTAGCTCCTAATCCTGATGATTTGTATCATTAGTGTCTTGGATATAACTCATAACA
547 P A N L E I L D I S R N Q L L A P N P D V F V S L S V L D I T H N
2301 AGTTCAATTTGTAATGTGAACCTTAGCACTTTTATCAATTTGGCTTAATCACACCAATGCTACTATAGCTGGGCTCCTGCAGACATATATTGTGTATACC
580 K F I C E C E L S T F I N W L N H T N V T I A G P P A D I Y C V Y P
2401 TGACTCGTTCTCTGGGTTTCCCTCTTCTCTTTCCACGGAAGGTTGTGATGAAGAGGAAGTCTTAAAGTCCCTAAAGTCTCCCTTTTCTTGTATGC
613 D S F S G V S L F S L S T E G C D E E E V L K S L K F S L F I V C
BspHI (2522)
2501 ACTGTCACCTGACTCTGTTCTCATGACCATCCTCACAGTCACAAAGTTCGGGGCTTCTGTTTTATCTGTTATAAGACAGCCAGAGACTGGTGTTC
647 T V T L T L F L M T I L T V T K F R G F C F I C Y K T A Q R L V F
BsrGI (2630)
2601 AGGACCATCCCCAGGGCACAGAACCTGATATGACAAAATATGATGCCTATTTGTGCTTCCAGCAGCAAAGACTTACATGGGTGCAGAATGCTTTGCTCAA
680 K D H P Q G T E P D M Y K Y D A Y L C F S S K D F T W V Q N A L L K
Tth111I (2758)
2701 ACACCTGGACACTCAATACAGTGACAAAACAGATTCAACCTGTGCTTTGAAGAAAGAGACTTTGCCCAGGAGAAAACCGATTGCCAATATCCAGGAT
713 H L D T Q Y S D Q N R F N L C F E E R D F V P G E N R I A N I Q D
2801 GCCATCTGGAACAGTAGAAAAGATCGTTTGTCTTGTGAGCAGACACTTCTTAGAGATGGCTGGTGCCTTGAAGCCTTCAAGTATGCCAGGGCAGGTGCT
747 A I W N S R K I V C L V S R H F L R D G W C L E A F S Y A O G R C

BsrGI (2988)

2901 TATCTGACCTAACAGTGCTCTCATCATGGTGGTGGTGGTCCCTTGTCCCAGTACCAGTTGATGAAACATCAATCCATCAGAGGCTTTGTACAGAAACA
780▶ L S D L N S A L I M V V V G S L S Q Y Q L M K H Q S I R G F V Q K Q

BstXI (3027)

3001 GCAGTATTTGAGGTGGCCTGAGGATCTCCAGGATGTTGGCTGGTTTCTCATAAACTCTCTCAACAGATACTAAAGAAAGAAAAAGAAAGAAAGAC
813▶ Q Y L R W P E D L Q D V G W F L H K L S Q Q I L K K E K E K K K D

MscI (3146)

3101 AATAACATTCCGTTGCAAACTGTAGCAACCATCTCCTAAAAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACAGATAAG
847▶ N N I P L Q T V A T I S •

HpaI (3278)

3201 CAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAGTTAACAAACAACATTGCATTC
3301 ATTTTATGTTTCAGGTTCCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAAA
3401 CTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAG
3501 CCTCACCTTCTTTTCATGGAGTTTAAAGATATAGTGATTTTTCCCAAGGTTTGAAGTACTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATT

SspI (3613) SwaI (3627)

3601 CCCTTTTTAGTAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAAATAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATA
3701 ATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACT
141◀ • N R T Y K

3801 TGAGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTCCATTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCA
135◀ L P 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

BstXI (3917)

3901 CATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTC
102◀ M G C 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

4001 ACAGCAGACCCAATGGCAATGGCTTCCAGCACAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCAGTCTTGGTCTGTA
68◀ V A S 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

BbsI (4198)

4101 TGGCCGCCCCGACATGGTGTGTTGTCTCATAGAGCATGGTATCTTCTCAGTGGCGACTCCACCAGCTCCAGATCTGTGAGAGATGTTGAAGGT
35◀ A A 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

BspHI (4202) AseI (4260)

4201 TTTCATGATGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTA
2◀ K M

4300 TCTGACGGTTCATAAACGAGCTCTGCTTATATAGACCTCCACCCTACACGCTACCGCCATTTCGCTCAATGGGGCGGAGTTGTTACGACATTTTGG

SpeI (4415)

4400 AAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCATTGACGTCAATGGGGTGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATT

SnaBI (4543)

4499 GATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGACTGCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAA

NdeI (4648)

4599 TGCCAGGCGGGCATTACCCTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCAAGTGGGCAGTTTACCGTAAATACT
4699 CCACCCATTGACGTCAATGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGTGCTTGGGCGGTGAGCCAGG

SdaI (4826) PacI (4834) BspLU11I (4844)

4799 CGGGCCATTTACCCTAAGTTATGTAACGCCCTG C A G G T T A A T T A A G A A C A T G T G A G C A A A A G G C C A G A A A A G G C C A G A A C C G T A A A A G G C C G C T T
4897 GCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCAGAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATACCA
4997 CGGTTTTCCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGAAGCGTGGCGCTTT

ApaLI (5158)

5097 CTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCAAGCTGGGCTGTGTGCACGAACCCCGTTCCAGCCGACCCTGCGCCTT
5197 ATCCGGTAACTATCGTCTTGTAGTCAACCCGGTAAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGC
5297 GGTGCTACAGAGTCTTGAAGTGGTGGCCTAACCTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGA AAAA
5397 GAGTTGGTAGCTCTTGTATCCGGCAAACAAACCCTGGTGGTGGTGGTTTTTTTGGTTCGAAAGCAGAGATTACGCGCAGAAAAAAGGATCTCAAGA

EagI (5594)
NotI (5593)

5497 AGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAACTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCG
PacI (5574) SwaI (5583)

5597 GCCGCAATAAAATATCTTTATTTTACATCTGTGTGGTTTTTTTGTGTGAATCGTAACATAACGCTCTCCATCAAAAACAAACGAAACAAAA
5697 CAAACTAGCAAAATAGGCTGTCCCCAGTCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA