



PvuI (7)
SgfI (6) 1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
MfeI (82)
101 GAGAAGGTGGCGCGGGTAAACTGGAAAAGTATGTCGTGACTGGCTCCGCTTTTTCCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203) 201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCCTTACCGCGCCCGCCCTACCTGAGGCC
HindIII (245)
Bsu36I (291)
301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCTCCTGAACTGCGTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTCCTGACCCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

BstEII (555)
AgeI (552) **NcoI (560)** **MscI (568)** 501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTCCCATGGCATGGCCACCTCCCTACTGGCTGTGCATGTGGG
SphI (590)
1▶ M A W P P P Y W L C M L G
601 CACCTTGGTAGGACTCTCAGCTACCCTAGCCCCAAACAGCTGTCCAGACAACTACTGGACTGGGGGAGGACTCTGCTGCCGGATGTGTGAGCCAGGT
13▶ T L V G L S A T L A P N S C P D K H Y W T G G G L C C R M C E P G

Bst1107I (755)
701 ACATTCTTTGTGAAGGACTGTGAACAAGACAGAACAGCTGCTCAGTGTGATCCTGTATACCAGGCACCTCCTTCTCTCCAGACTACCACACCCGGCCCC
47▶ T F F V K D C E Q D R T A A Q C D P C I P G T S F S P D Y H T R P

PstI (810)
801 ACTGCGAGAGCTGCAGGCATTGTAACCTGTTTTCTTATCCGCAACTGCACAGTCACTGCCAATGCTGAGTGCAGCTGTTCCAAGAAGTGGCAGTGCAG
80▶ H C E S C R H C N S G F L I R N C T V T A N A E C S C S K N W Q C R

BsrGI (910)
901 GGACCAGGAATGTACAGAGTGTGACCCTCCTCTAAACCTGCACTGACCAGACAGCCATCTGAGACCCGAGCCACAGCCACCACCCACCCACTTACCT
113▶ D Q E C T E C D P P L N P A L T R Q P S E T P S P Q P P P T H L P
1001 CATGGCACAGAAAGCCATCCTGGCCCTACACAGGCAGCTTCCAACTCGACTGTCTATAGCCAGCGGTATCCCATAGACCCTGTGCAGCTCGGACT
147▶ H G T E K P S W P L H R Q L P N S T V Y S Q R S S H R P L C S S D

BspEI (1103) 1101 GCATCCGGATCTTTGTGACCTTCTCCAGCATGTTTCTTATCTTCGCTCGGGTGAATCTTGTCTTCCATCAAAGAAGAAACACGGGCCAAATGAAGA
180▶ C I R I F V T F S S M F L I F V L G A I L F F H Q R R N H G P N E D
BbsI (1195)

BstAPI (1203) **SapI (1216)**
1201 CCGGCAGGCAGTGCCTGAAGAGCCTTGTCTTACAGCTGCCCCAGGGAAGAGGAGGGCAGTGTCTATCCCTATCCAGGAGGACTACCGGAAACCCGAGCCT
213▶ R Q A V P E E P C P Y S C P R E E E G S A I P I Q E D Y R K P E P

MscI (1345)
Bsp120I (1328) **NheI (1339)**
1301 GCTTTCTACCCTTGACCGGTGCTGGTGGGCCCTTTCTGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCAACTAGAATGC
247▶ A F Y P •

HpaI (1477) **MfeI (1488)**
1401 AGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAATTGCATTCA

EcoRI (1573)
1501 TTTTATGTTTCAGGTTACAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAATGTGGTATGGAATTCTAAAATACAGCATAGCAAAC
1601 TTTAACTCCAAATCAAGCCTCTACTTGAATCCTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTGCCAATGTGCATTAGCTGTTTGCAGC

SapI (1755)
1701 CTCACCTCTTTTCATGGAGTTTAAAGATATAGTATTTTTCCCAAGGTTTGAAGTCTTTCATTCTTTATGTTTTAAATGCACTGACCTCCACATTC

SspI (1812) **SwaI (1826)**
1801 CCTTTTTAGTAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAA
1901 TATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTCGGTGTACTT
141▶ • N R T Y K

SacI (2087)
2001 GAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCAC
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 (2116)
2101 ATGCCACAGGGGTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCA
101▶ 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 V

StuI (2251)
2201 CAGCAGCCCAATGGCAATGGCTTCAGCACAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCGAGTCTTGGTCTGAT
68▶ 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

2301 GGCCGCCCGACATGGTGTCTTGTCTCATAGAGCATGGTATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTC
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

AseI (2459)

2401 TTCATGGTGGCCCTCTATAGTGAGTGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACGCGTGGATGGCGTCTCCAGCTTATC
1 K M

SacI (2516)

2501 TGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCACCCTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAA

SpeI (2614)

2601 AGTCCCGTTGATTTACTAGTCAAAACAAACTCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGAT

SnaBI (2742)

2701 GTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCACTGACTGGGCATAATGC

NdeI (2847)

2801 CAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGTACTGCCAAGTGGGCAGTTTACCGTAAATACTCCA

2901 CCCATTGACGTCAATGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTCAGCCAGGCGG

PacI (3033)

PstI (3026)

SdaI (3025)

BspLU11I (3043)

3001 GCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAATAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGCCGCGTTGCTGG

3101 CGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAATAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATAACAGGCGTT

3201 TCCCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCAT

ApaLI (3357)

3301 AGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTTCGCTCAAGCTGGGCTGTGTGCACGAACCCCCGTTCCAGCCGACCGTGCCTTATCCG

3401 GTAACATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGCGGTTGC

3501 TACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGTGAAGCCAGTTACCTTCGAAAAAGAGTT

3601 GGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGTTTTTTTGTGTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATC

EagI (3793)

PacI (3773) SwaI (3782) NotI (3792)

3701 CTTTGATCTTTTCTACGGGCTGACGCTCAGTGGAAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGC

3801 AATAAAATATCTTTATTTTTCATTACATCTGTGTGTTGTTTTTTGTGTTGAATCGTAACATAACGCTCTCCATCAAACAAAACGAAACAAAACAAC

3901 TAGCAAAATAGGCTGTCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA