



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

HindIII (245)
Psp1406I (203) 201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTCACGCGCCGCCCTACCTGAGGGC
PvuII (239)
Bsu36I (291)
301 GCCATCCACGCCGGTTGAGTCGCGTTTCTGCCGCTCCCGCTGTGGTGCTCCTGAACTGCGTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCTGCTTCTCAACTCTACGCTTTTGTTCGTTT

BstEII (555)
AgeI (552) 501 TCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTACCATGGAATCTCAACCTTTCCTGAATATGAAATTTGAAAC
NcoI (560) 1 M E S Q P F L N M K F E T
601 GGATTATTTTCGTAAGGTTGTCCTTTTCTTCCATTAACAAACGAAAGCAATTACCACCTTTCTTCTTAGAACCCGAGCCTGTGACCTGTTGTTACAG
13 D Y F V K V V P F P S I K N E S N Y H P F F F R T R A C D L L L Q
701 CCGACAATCTAGCTTGTAAACCTTCTGGAAGCCTCGGAACCTGAACATCAGCCAGCATGGCTCGGACATGCAGGTGCTTTCGACCACGCACCCGACA
47 P D N L A C K P F W K P R N L N I S Q H G S D M Q V S F D H A P H

PvuII (897)
801 ACTTCGGCTTCCGTTTCTTCTATCTTCACTACAAGCTCAAGCAGCAAGGACCTTCAAGCGAAAGACCTGTAAGCAGGAGCAAACCTACAGAGATGACCAG
80 N F G F R F F Y L H Y K L K H E G P F K R K T C K Q E Q T T E M T S
NsiI (976) 901 CTGCCTCCTTCAAAATGTTTCTCCAGGGGATTATATAATTGAGCTGGTGGATGACACTAACACAACAAGAAAAGTGATGCATTATGCCTTAAAGCCAGTG
ApaI (997) 113 C L L Q N V S P G D Y I I E L V D D T N T T R K V M H Y A L K P V

XcmI (1019)
Bsp120I (1015) 1001 CACTCCCCGTGGGCGGGCCCATCAGAGCCGTGGCCATCACAGTGCCACTGGTAGTCATATCGGCATTGCGGACGCTCTTCACTGTGATGTGCCGAAGA
147 H S P W A G P I R A V A I T V P L V V I S A F A T L F T V M C R K
NruI (1067) 1101 AGCAACAAGAAAATATATATTACATTTAGATGAAGAGAGCTCTGAGTCTTCCACATACACTGCAGCACTCCAAGAGAGAGGCTCCGGCCGCGGCCGAA
180 K Q Q E N I Y S H L D E E S S E S S T Y T A A L P R E R L R P R P K
PstI (1160) 1201 GGTCTTCTCTGCTATTCAGTAAAGATGGCCAGAATCACATGAATGTCGTCAGTGTTCGCTACTTCTCCAGGACTTCTGTGGCTGTGAGGTGGCT
213 V F L C Y S S K D G Q N H M N V V Q C F A Y F L Q D F C G C E V A
1301 CTGGACCTGTGGGAAGACTTCAGCCTCTGTAGAGAAGGCGAGAGAGAAATGGGTGATCCAGAAGATCCACGAGTCCAGTTCATCATTGTGGTTTGTCCA
247 L D L W E D F S L C R E G Q R E W V I Q K I H E S Q F I I V V C S

ScaI (1409)
1401 AAGGTATGAAGTACTTTGTGACAAGAAGAACTACAACACAAAGGAGGTGGCCGAGGCTCGGGGAAAGGAGAGCTTCTCCTGGTGGCGGTGTGAGCCAT
280 K G M K Y F V D K K N Y K H K G G G R G S G K G E L F L V A V S A I
1501 TGCCGAAAAGCTCCGCCAGGCAAGCAGAGTTCGTCGCGGCGCTCAGCAAGTTTATCGCCGCTACTTTGATTATTCTGCGAGGGAGAGCTCCCGGT
313 A E K L R Q A K Q S S S A A L S K F I A V Y F D Y S C E G D V P G
1601 ATCCTAGACCTGAGTACCAAGTACAGACTCATGGACAATCTTCTCAGCTCTGTTCCACCTGCACTCCGAGACCACGGCCTCCAGGAGCCGGGGCAGC
347 I L D L S T K Y R L M D N L P Q L C S H L H S R D H G L Q E P G Q

BspEI (1730)
XmnI (1722) 1701 ACACGCGACAGGGCAGCAGAAGAACTACTTCCGGAGCAAGTCAAGCCGGTCCCTATACGTCGCCATTTGCAACATGCACCAGTTTATTGACGAGGAGCC
380 H T R Q G S R R N Y F R S K S G R S L Y V A I C N M H Q F I D E E P
BstBI (1807) 1801 CGACTGGTTCGAAAAGCAGTTTCCCTTCCATCCTCCTCCACTGCCTACCGGGAGCCAGTCTTGAGAAAATTTGATTCGGGCTTGGTTTTAAATGAT
413 D W F E K Q F V P F H P P P L R Y R E P V L E K F D S G L V L N D
1901 GTCATGTGCAACCCAGGCGCTGAGAGTACTTCTGCCTAAAGTAGAGCGGCTGTTCTTGGGCAACCGGACCGAGCTCCAGCAGGAGAGTCCAGC
447 V M C K P G P E S D F C L K V E A A V L G A T G P A D S Q H E S Q

BstAPI (2058) 2001 ATGGGGGCTGGACCAAGACGGGAGGCGCGCTGCCCTTGACGGTAGCGCCGCCCTGCAACCCCTGCTGCACACGGTGAAGCCGGCAGCCCTCGGA
480 H G G L D Q D G E A R P A L D G S A A L Q P L L H T V K A G S P S D
2101 CATGCCGCGGACTCAGGCATCTATGACTCGTCTGTGCCCTATCCGAGCTGTCTCTGCCACTGATGGAAGGACTCTCGACGGACCAGACAGAAACGCTC
513 M P R D S G I Y D S S V P S S E L S L P L M E G L S T D Q T E T S
StuI (2229) 2201 TCCCTGACGGAGAGCGTGTCTCCTCTTCAAGCCTGGGTGAGGAGAACTCCTGCCCTTCTTCCAAGTCTCTTCTGCGGTGATGCAAAAGCAGATC
547 S L T E S V S S S S G L G E E E P P A L P S K L L S S G S C K A D
2301 TTGGTTGCCGAGCTACTGATGAACTCCACGCGGTGCCCCCTTTGTAACAAAACGAAAGAGTCTAAGCATTGCCACTTTAGCTGCTGCCCTCCTCTGA
580 L G C R S Y T D E L H A V A P L •

NheI (2414)
2401 TTCCCCAGCTCATCGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAAAAAATGCTTTATTTGTGA

HpaI (2552) **MfeI (2563)**
2501 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAATTGCATTCATTTTATGTTTCAGGTTTCAGGGGGAG

EcoRI (2648)
2601 GTGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAATGTGGTATGGAATTCATAAATACAGCATAGCAAACTTTAACCTCCAAATCAAGCCTCTAC
2701 TTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTTAAAG

SspI (2887)
2801 ATATAGTGTATTTTCCCAAGTTTGAACCTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTGTAGTAAATATTCAGAAAT

SwaI (2901)
2901 AATTTAAATACATCATTGCAATGAAAAATAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACT

3001 TAGGGAACAAAGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGCTGTAAGTTGAGGGGATGAGTTCCTCAATGGTG
141 • N R T Y K L P I L E E I T

BstXI (3191)
3101 GTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGTCACATGCCACAGGGGCTGACCACCCTGA
126 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 R I
3201 TGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTC
93 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 A E

StuI (3326)
3301 AGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCAGTCTTGGTCTGATGGCCGCCGACATGGTCTTGTG
60 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 N

XmnI (3468)
3401 TCCTCATAGAGCATGGTATCTTCTCAGTGGCGACCTCCACCAGTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCCTATAGTGAG
26 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 (3534)
3501 TCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCACTAAACGAGCTCTGC

SpeI (3689)
3601 TTATATAGACCTCCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAA
3701 CAACTCCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATG

SnaBI (3817)
3801 GTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGTCAATGACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGA

NdeI (3922)
3901 CGTCAATAGGGGGCTACTTGGCATATGATACACTTGTACTGCAAGTGGGCGAGTTTACCGTAAATACTCCACCATTGACGTCAATGGAAAGTCCC
4001 TATTGGCGTACTATGGGAACATACGTCAATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACG

PacI (4108)
PstI (4101)
SdaI (4100) **BspLU11I (4118)**
4101 CCTGCAGGTTAAITAAGAACAATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCC
4201 TGACGAGCATCACAATAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATAACAGGCGTTTCCCCTGGAAGCTCCCTCGTGC
4301 TCTCCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGAAAGCGTGGCGCTTCTCATAGCTCAGCTGTAGGTATCTCAGTT

ApaLI (4432)
4401 CCGTGTAGGTCGTTTCGCTCAAGCTGGGCTGTGTGCACGAACCCCGTTTCAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCAACCC
4501 GGTAAGACACGACTTATCGCCTAGGCAAGCAGCAGCAGGTTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCT
4601 AACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAA
4701 CCACCGCTGGTAGCGGTGTTTTTTTTGTTTGAAGCAGCAGATTACCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGA

PacI (4848) **SwaI (4857)** **NotI (4867)**
4801 CGCTCAGTGAACGAAAACCTCACGTTAAGGATTTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAATATCTTTATTTTCATTAC
4901 ATCTGTGTGGTTTTTTTTGTGTGAATCGTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAAATAGGCTGTCCCCAGTGC
5001 AAGTGCAGGTGCCAGAACATTTCTCTATCGAA