



PvuI (7)
SgfI (6)
 1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTCGGCAATTGAACGGGTGCCTA

 101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203) **HindIII (245)** **Bsu36I (291)**
 201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCCTTACGCGCCCGCCCTACCTGAGGCC

 301 GCCATCCACGCCGGTTGAGTCGCGTTTCTGCCGCCTCCCGCCTGTGGTGCCTCCTGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
NaeI (441)
 401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCAACTCTACGCTTTTGTTCGTTT

KasI (535) **BspEI (558)** **Neol (566)**
 501 TCTGTTCTGGCGGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGCTCCGGACACCATGGCGGAGGAGCAGGGCCGGGAACGGGACTC
 1▶ M A E E Q G R E R D S

BsrBI (655) **PstI (685)**
 601 GGTTCCAAAGCCGTCGGTGTCTCCTCCACCCAGACCTGGGCGTGGGCGGCGCTGAGCGGCTGGTGTGGAGCGGGCGCTGGCGCTGCAGGCGCGGGG
 11▶ V P K P S V L F L H P D L G V G G A E R L V L D A A L A L Q A R G

BglII (710) **XmaI (732)** **AgeI (765)** **StuI (798)**
 701 TGTAGCGTGAAGATCTGGACAGCGCACTACGACCCGGGCCACTGTTTCGCCGAGAGCCGCGAGCTACCGGTGCCTGTGCCGGGACTGGCTGCCGCGAG
 45▶ C S V K I W T A H Y D P G H C F A E S R E L P V R C A G D W L P R

SacII (816)
EagI (813)
NotI (812) **KasI (820)** **FspI (842)**
 801 GCCTGGGCTGGGCGGCCGCGCCGCGCCGCTGCGCCTACGTGCGCATGGTTTTCTGGCGCTCTACGTGCTGTTCTCGCCGACGAGGAGTTCGACGT
 78▶ G L G W G G R G A A V C A Y V R M V F L A L Y V L F L A D E E F D V

BglIII (987)
 901 GGTAGTGTGCGACAGGTGTCTGCTGTATCCAGTGTTCAGGCTGGCTAGACGGCGGAAGAAGATCCTATTTTACTGTCACTTCCCAGATCTGCTTCTC
 111▶ V V C D Q V S A C I P V F R L A R R R K K I L F Y C H F P D L L L

Bsp120I (1034)
 1001 ACCAAGAGAGATTCTTTTCTTAAACGACTATACAGGGCCCAATTGACTGGATAGAGGAATACACCACAGGCATGGCAGACTGCATCTTAGTCAACAGCC
 145▶ T K R D S F L K R L Y R A P I D W I E E Y T T G M A D C I L V N S
 1101 AGTTCACAGCTGCTGTTTTTAAAGGAAACATTCAAGTCCCTGTCTCACATAGACCTGATGTCCCTATCCATCTTAAATGTCACCAGCTTTGACTCAGT
 178▶ Q F T A A V F K E T F K S L S H I D P D V L Y P S L N V T S F D S V

Tth11I (1219) **XmnI (1236)**
 1201 TGTTCTGAAAAGCTGGATGACCTAGTCCCAAGGGGAAAAAATTCTGCTGCTCCTCATCAACAGATACGAAAGGAAGAAAAATCTGACTTTGGCACTG
 211▶ V P E K L D D L V P K G K K F L L L S I N R Y E R K K N L T L A L

BsaBI (1325)
 1301 GAAGCCCTAGTACAGCTGCGTGGAAAGATTGACATCCCAAGATTGGGAGAGGGTTCATCTGATCGTGGCAGGTGGTTATGACGAGAGAGTCTGGAGAATG
 245▶ E A L V Q L R G R L T S Q D W E R V H L I V A G G Y D E R V L E N

MscI (1446)
 1401 TGGAACATTATCAGGAATTGAAGAAAATGGTCCACAGTCCGACCTTGGCCAGTATGTGACCTTCTTGAAGTCTTTCTCAGACAAACAGAAAATCTCCCT
 278▶ V E H Y Q E L K K M V Q Q S D L G Q Y V T F L R S F S D K Q K I S L

BbrPI (1512) **BsrGI (1571)**
 1501 CCTCCACAGCTGCACGTGTGTGCTTTACACACCAAGCAATGAGCACTTTGGCATTGTCCCTCTGGAAGCCATGTACATGCAGTCCCAGTTCATTGCTGTT
 311▶ L H S C T C V L Y T P S N E H F G I V P L E A M Y M Q C P V I A V

ApaLI (1666)
 1601 AATTCGGGTGGACCCTTGGAGTCCATTGACCACAGTGTACAGGGTTTCTGTGTGAGCCTGACCCGGTGCACCTCTCAGAAGCAATAGAAAAGTTCATCC
 345▶ N S G G P L E S I D H S V T G F L C E P D P V H F S E A I E K F I

Neol (1721)
XcmI (1718)
 1701 GTGAACCTTCTTAAAAGCCACCATGGGCTGGTGGAAAGAGCCAGAGTGAAGGAAAAATTTCCCTGAAGCATTTACAGAACAGCTCTACCGATATGT
 378▶ R E P S L K A T M G L A G R A R V K E K F S P E A F T E Q L Y R Y V

MscI (1833)
NheI (1827)
 1801 TACCAAAGTCTGGTATAATCAGATTGGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAAAAAAT
 411▶ T K L L V •

HpaI (1965)
 1901 GCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAGTTAAACAACAACATTGCATTCAATTTATGTTTCA

EcoRI (2061)
 2001 GGTTACAGGGGAGGTGTGGGAGTTTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACCTTAAACCTCCAA
 2101 ATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTTGGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTT

 2201 CATGGAGTTTAAAGATATAGTGTATTTTCCCAAGTTTGAAGTACTGCTTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTATGTA

SspI (2300) **SwaI (2314)**
 2301 AATATTCAGAAATAATTTAAATACATCATTGCAATGAAAAATAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTATAATATCCCCAGTT

2401 TAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTACTTGAGGGGGATGAG
141 • N R T Y K L P I L
SacI (2575)

2501 TTCCTCAATGGTGGTTTTGACCAGCTTGCCATTTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGG
131 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 M G C P
2601 CTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCCTTCTGCCCGTTGCTCACAGCAGACCCAA
97 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 A S G I
StuI (2739)

2701 TGGCAATGGCTTCAGCACAGACAGTGACCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCTGATGGCCGCCCGAC
64 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 A A G V
BspHI (2889)

2801 ATGGTGCTTGTTCCTCATAGAGCATGGTGATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGATGGCC
31 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 K M
XmnI (2881)

2901 CTCCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACAGCGTGATGGCGTCTCCAGCTTATCTGACGGTCACT
AseI (2947)

3001 AAACGAGCTCTGTTATATAGACCTCCACCCTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGAT
SacI (3004)

3101 T TACTAGTCAAACAAACTCCCATTGACGTCAATGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTA CTGCCAAA
SpeI (3102)

3200 ACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTA CTGCCAAGTAGGAAAGTCCCAT AAGTCATGTA CTGGGCATAATGCCAGGCGGGCCA
SnaBI (3230)

3300 TTTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGATGTA CTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGT
NdeI (3335)

3400 CAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGTCAATGGGGGGGGTCTTGGGCGGT CAGCCAGGCGGGCCATTTACCG
PstI (3514)
SdaI (3513) PaeI (3521) BspLU11I (3531)

3500 TAAGTTATGTAACGCTTGCAGGTTAA TTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGTTGCTGGCGTTTTTCC
3598 ATAGGCTCCGCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACAGGCGTTTTCCCTGG
3698 AAGCTCCCTCGTGCCTCTCTGTTCCGACCCTGCCGTTACCGGATACTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGC
ApaLI (3845)

3798 TGTAGGTATCTCAGTTCCGGTGTAGGTGCTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTT CAGCCCGACCGCTGCGCCTTATCCGGTAACTATC
3898 GTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTT
3998 CTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCT
4098 TGATCCGGCAAACAAACCACCGTGGTAGCGGTGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCT
EagI (4281)
PacI (4261) SmaI (4270) NotI (4280)

4198 TTTCTACGGGTCTGACGCTCAGTGAACGAAACTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCGCAATAAAATA
4298 TCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAAACTAGCAAAT
4398 AGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA