



PvuI (7)
SgfI (6) EcoNI (96)
1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTCGGCAATTGAACGGGTGCCTA
101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGACTGGTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245) Bsu36I (291)
Psp1406I (203) PvuII (239) EcoNI (287)
201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACCGCCGCCCGCCCTACCTGAGGCC
301 GCCATCCACGCGGGTTGAGTGCGGTTCTGCCGCCTCCCGCTGTGGTGCTCTGAACTGCCTCCGCGCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTGTCCGGCGCTCCCTTGAGCGCTACCTAGACTCAGCCGGCTCTCCACGCTTGGCTGACCCTGCTTGTCTCAACTCTACGTCTTTGTTTCGTTT

NcoI (560)
BstEII (555) NcoI (590)
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCGCCTACCTGAGATCACCGGTACCATTGGAATCCTGCCGTTCTACTGATCCCCATGGAGAG
1 M G I L P F L L I P M E S

NdeI (637) BspHI [m] (681)
601 CAACTGGACTGTCCATGTGTTCTCACGGACTTTGTCCATATGCTACTGTGGACAGCCGTGCTAAATCTTGTCTGGGACTCATGATCTTCCAAAGGCT
13 N W T V H V F S R T L C H M L L W T A V L N L A A G T H D L P K A

XhoI (709) BamHI (722) BbsI (739) SandI (766) BstXI (771)
701 GTGGTCAAACCTCGAGCCCCGTGGATCCAGGTGCTCAAGGAAGACACGGTGACACTGACATGCGAAGGGACCCACAACCTGGGAACCTTCTACCCAGT
47 V V K L E P P W I Q V L K E D T V T L T C E G T H N P G N S S T Q
801 GGTTCACAATGGGAGGTCCATCCGAGCCAGGTCCAAGCCAGCTACACGTTAAGGCCACAGTCAATGACAGTGGAGAATATCGGTGTC AAATGGAGCA
80 W F H N G R S I R S Q V Q A S Y T F K A T V N D S G E Y R C Q M E Q

BspEI (821) PvuII (964)
901 GACCCGCCTCAGCGACCCCTGTAGATCTGGGAGTGATTTCTGACTGGCTGCTGCCAGACCCCTCAGCTGGTGTTTCTGGAAGGGGAAACCATCACGCTA
113 T R L S D P V D L G V I S D W L L L Q T P Q L V F L E G E T I T L
1001 AGTGCCATAGCTGGAGGAACAACTACTGAACAGGATCTCGTCTCCATAATGAAAAATCCGTGAGGTATCATCACTACAGTAGTAATTTCTCTATCC
147 R C H S W R N K L L N R I S F F H N E K S V R Y H H Y S S N F S I

XcmI (1110) Bsp120I (1195)
1101 CAAAAGCCAAACACAGTCACAGTGGGACTACTACTGCAAAGGAGTCTAGGAAGGACTGCACCAGTCCAAGCCTGTACCATCACTGTCCAAAGGGCC
180 P K A N H S H S G D Y Y C K G S L G R T L H Q S K P V T I T V Q G P
1201 CAAGTCCAGCAGGCTTTACCAGTATTGACAATTGGCTGCTGCTGCTGCTGGATTGCTGTCGCAGCCATTTGTTATTATCTAGTATCCCTGGTCTATCTC
213 K S S R S L P V L T I V A A V T G I A V A A I V I I L V S L V Y L
1301 AAGAAAAAGCAGGTTCCAGACAATCCTCCTGATCTGGAAGAAGCTGCCAAAACCTGAGGCTGAGAATACGATCACCTACTACTTCTCAAGCATCCCGAAG
247 K K K Q V P D N P P D L E E A A K T E A E N T I T Y S L L K H P E

MscI (1471) NheI (1465)
1401 CCCTGGATGAAGAACAGAGCATGATTACCAGAACCACATTTAGTCTCCCTTGGCATTGGGAAAAGCTAGCTGGCCAGACATGATAAGATACATTGATGA
280 A L D E E T E H D Y Q N H I •

HpaI (1603) EcoRI
1501 GTTTGGACAAACCACAAC TAGAATG CAGTGA AAAAAATGCTT TATTTGTGAAATTTGTGATGCTATTGCTT TATTTGTAACCATTATAAGCTGCAATAAA

SapI (1881)
1601 CAAGTTAACACAACA AATTGCATT CATT TATGTTTCAGGTT CAGGGGAGGTGTGGGAGTTTTTAAAGCAAGTAAAACCTCTACA AATGTGGTATGG
1701 AATTCTAAAATACAGCATAGCAAACTTAACTCCAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTT

SspI (1938) SwaI (1952)
1801 GCCAATGTGCATTAGCTGTTTGAGCCTCACCTCTTTTCATGGAGTTAAGATATAGTGATTTTCCCAAGGTTTGAAGTACTTCTTCACTTTCTTTATGT
1901 TTTAAATGCACTGACCTCCACATTTCCCTTTTTAGTAAAATATT CAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGA
2001 ATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGACTTAGGGAACAAGGAACCTTAAATAGAAATGGACAGCAAGAAAGCGAGC
2101 TTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTCCATTCACTCAATGAGCACAAAGCAGTCAGGAG
— 141 • N R T Y K 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

SacI (2213) BstXI (2242)
2201 CATAGTCAGAGATGAGCTCTGTCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTCCTGACAGCCACAATGGT
110 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 H R V A V I T

StuI (2377)
2301 GTC AAAGTCTTCTGCCC GTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAG
77 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 A E I H V A S
2401 ATGATCTCCCAGTCTTGGTCTGATGGCGCCCGGACATGGTCTGTTGTCCTCATAGAGCATGGTGTCTCTCAGTGGCGACCTCCACCAAGCTCCA
43 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 T A V E V L E L

BbsI (2523) XmnI (2519) AseI (2585)
2501 GATCCTGCTGAGAGATGTTGAAGGCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGCAAAAC
10 D Q Q S I N F T K M

2601 AGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCCACGTACACGCCTACCGCCATTTCGCTCAATGG
SacI (2642)

2701 GGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAG
SpeI (2740)

2801 TCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCC
SnaBI (2868)

2901 ATAAGTCATGTACTGGCATAATGCCAGGCGGGCCATTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACTTGTACTGACAA
NdeI (2973)

3001 GTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGTCAATGGGCGG

3101 GGGTCGTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCTGCAGGTTAAATAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAG
PacI (3159)
PstI (3152)
SdaI (3151)
BspLU11I (3169)

3201 GAACCGTAAAAAGGCCGCTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCG
 3301 ACAGGACTATAAAGATACCAGGCGTTTCCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCGACCCTGCCGCTTACCGGATACCTGTCCGCTTTCTCC

3401 CTTCCGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGT
ApaLI (3483)

3501 TCAGCCCAGCGCTGCGCCTTATCCGGTAACTATCGTCTTGAAGTCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATT
 3601 AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGA
 3701 AGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCG

3801 CAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGT
PacI (3899)

3901 TAATTAACATTTAAATC AGCGGCCGCAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCA
Swal (3908)
EagI (3919)
NotI (3918)

4001 TCAAAACAAAACGAAACAAAACAAACTAGCAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA