



PvuI (7)
SgfI (6) 1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
MfeI (82) EcoNI (96)

101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTACTGGCTCCGCCTTTTCCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203) **HindIII (245)** **Bsu36I (291)**
PvuII (239) **EcoNI (287)**
201 GTGAACGTTCTTTTTCGCAACGGGTTTGGCCGAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACAGCGCCCGCCCTACCTGAGGCC
301 GCCATCCACGCGGTTGAGTCGCGTCTGCCGCTCCCGCCTGTGGTGCCTCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTGGCTGACCCTGCTTGTCTAACTCTACGTCTTTGTTTCGTTT

AgeI (552) **SphI (568)**
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCGCCTACCTGAGATCACCGGTAGGAGGCCAGCATGCGCCGCGCCAGCAGAGACTACACCAAG
1 M R R A S R D Y T K

Bsp120I (650)
601 TACCTGCGTGGCTCGGAGGAGATGGGCGGCGGCCCGAGCCCCGACGAGGGCCCCCTGCACGCCCGCCGCGCCTGCGCCGACCCAGCCCCCTGCCG
11 Y L R G S E E M G G G P G A P H E G P L H A P P P A P H Q P P A

BstXI (709) **BsrBI (704)** **PstI (752)** **BamHI (791)**
701 CCTCCCGCTCCATGTTCTGTGGCCCTCTGGGGCTGGGGCTGGGCCAGGTTGTCTGCAGCGTCGCCCTGTTCTTCTATTTTCAGAGCGCAGATGGATCCTAA
44 A S R S M F V A L L G L G L G Q V V C S V A L F F Y F R A Q M D P N

BstAPI (817)
801 TAGAATATCAGAAGATGGCACTCACTGCATTTATAGAATTTTGGAGCTCCATGAAAATGCAGATTTTCAAGACACAACCTGGAGAGTCAAGATACAAAA
77 R I S E D G T H C I Y R I L R L H E N A D F Q D T T L E S Q D T K

StuI (931)
901 TTAATACCTGATTATGTAGGAGAATTAACAGGCCTTTCAAGAGCTGTGCAAAAGGAATTACAACATATCGTTGGATCACAGCACATCAGAGCAGAGA
111 L I P D S C R R I K Q A F Q G A V Q K E L Q H I V G S Q H I R A E

MscI (1030) **BglIII (1025)** **HindIII (1044)**
1001 AAGCGATGGTGGATGGCTCATGGTTAGATCTGGCCAAGAGGAGCAAGCTGAAGCTCAGCCTTTTGTCTACTCTACTATTAATGCCACCGACATCCCATC
144 K A M V D G S W L D L A K R S K L E A Q P F A H L T I N A T D I P S

Acc65I (1129) **BglIII (1153)**
1101 TGGTCCCATAAAGTGGTCTGTCTCTTGGTACCATGATCGGGGTTGGGCCAAGATCTCCAACATGACTTTTAGCAATGGAAAACTAATAGTTAATCAG
177 G S H K V S L S S W Y H D R G W A K I S N M T F S N G K L I V N Q

BspHI (1241)
1201 GATGGCTTTTATTACCTGTATGCCAACATTTGCTTTTCGACATCATGAACTTCAGGAGACCTAGCTACAGAGTATCTTCAACTAATGGTGTACGTCACTA
211 D G F Y Y L Y A N I C F R H H E T S G D L A T E Y L Q L M V Y V T

Psp1406I (1395)
1301 AAACCAGCATCAAAATCCCAAGTCTCATACCCTGATGAAAGGAGGAAGCACCAAGTATTGGTCAGGGAATTCTGAATCCATTTTTATTCCATAAACGT
244 K T S I K I P S S H T L M K G G S T K Y W S G N S E F H F Y S I N V

BspEI (1469) **BsaBI (1467)** **BamHI (1466)**
1401 TGTTGGATTTTTAAGTTACGGTCTGGAGAGGAAATCAGCATCGAGGTCTCCAACCCCTCTTACTGGATCCGGATCAGGATGCAACATACTTTGGGGCT
277 G G F F K L R S G E E I S I E V S N P S L L D P D Q D A T Y F G A

MscI (1576) **NheI (1570)**
1501 TTTAAAGTTCGAGATATAGATTGAGCCCGAGTTTTTGGAGTGTATGTATTTCTGGATGTTTGGAAACAGCTAGCTGGACAGATGATAAGATACATT
311 F K V R D I D •

1601 GATGAGTTTGGACAAACCACAACCTAGAATCGAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCA

HpaI (1708) **MfeI (1719)**
1701 ATAAACAAGTTAAACAACAACAAATTGCATTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGTTTTTTAAAGCAAGTAAACCTCTACAAATGTGG
1801 TATGGAATTCTAAAAACAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGG

SapI (1986)
1901 CTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTTAAAGATATAGTGTATTTCCCAAGGTTTGAAGTACTCTTCTTCTTCTT

SspI (2043) **SwaI (2057)**
2001 TATGTTTTAAATGCACTGACCTCCACATTCCTTTTTAGTAAAAATTCAGAAATAATTTAAATACATCATTGCAATGAAAAATAATGTTTTTTATTAG
2101 GCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATGGACAGCAAGAAAG
2201 CGAGCTTCTAGCTTTAGTCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAAGCAGTC
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

SacI (2318) **BstXI (2347)**
2301 AGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACA
112 P A 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

StuI (2482)

2401 ATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAG
78 I T 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
2501 CAGAGATGATCTCCCAGTCTTGGTCTGATGGCCGCCCGACATGGTCTTGTGTCTCATAGAGCATGGTGTCTTCTCAGTGGCGACCTCCACCG
45 S 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

BbsI (2628)

XmnI (2624)

2601 CTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCTATAGTGAGTCTATTATACTATGCCGATATACTATGCCGATGATTAATTGTC
12 E L D Q Q S I N F T K M

SacI (2747)

2701 AAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTCGCTC

SpeI (2845)

2801 AATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCCATTTGACGTCAATGGGGTGGAGACTTGGAAATCCCC

SnaBI (2973)

2901 GTGAGTCAAACCGTATCCACGCCATTGATGTACTGCCAAAACGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAA

NdeI (3078)

3001 GTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGTACT

3101 GCCAAGTGGCGAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGTCAATG

PacI (3264)

PstI (3257)

SdaI (3256)

BspLU11I (3274)

3201 GCGGGGGTCTTGGCGGTGAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAAATAAGAACATGTGAGCAAAAGGCCAGCAAAAG

3301 GCCAGAACCGTAAAAAGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCAGAAAAATCGACGCTCAAGTCAGAGGTGGCGAA

3401 ACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTT

ApaLI (3588)

3501 TCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCAAGCTGGGCTGTGTGCACGAACCC

3601 CCGTTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGTAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACA

3701 GGATTAGCAGAGCGAGGTATGTAGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCT

3801 GCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAACAAACCACCGCTGGTAGCGGTGGTTTTTTGTTTGAAGCAGCAGATT

3901 ACGCGCAGAAAAAAGGATCTCAAGAAGATCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAACTCACGTTAAGGGATTTTGGTCATGG

EagI (4024)

PacI (4004) SwaI (4013)

NotI (4023)

4001 CTAGTTAATTAACATTTAAATCAGCGGCCCAATAAAATATCTTTATTTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCT

4101 CTCCATCAAAACAAAACGAAACAAAACAAACTAGCAAAATAGGCTGTCCCAAGTGAAGTGCAGGTGCCAGAACATTTCTCTATCGAA