



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

Psp1406I (203) **HindIII (245)** **Bsu36I (291)**
EcoNI (287)
201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACCGCCGCCCGCCCTACCTGAGGCC
301 GCCATCCACGCGGTTGAGTGCCTGCTGCCGCTCCCGCTGTGGTGCCTCTGAAGTGCCTCCGCGCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
NaeI (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCAACTCTACGTCTTTGTTTCGTTT

KasI (535) **AgeI (552)** **SphI (560)** **BstXI (571)**
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCGCTACCTGAGATCACCGGTGAGCATGCCCGTGGCCAGCCTCTGGCCCCACCTTCCTAGTCC
601 TTTCTGCTGATGACGCTACTGCTGGGAGACTCACAGAGTGGCAGGTGAGGACGAGCTACAGGTGATTACGCTGAAAAGTCCGATTCAGTTGCAGCT
13▶ F L L M T L L L G R L T G V A G E D E L Q V I Q P E K S V S V A A
701 GGAGAGTCGGCCACTCTGCGCTGTGCTATGACGTCCCTGATCCCTGTGGGCCCATCATGTGTTTAGAGGAGCTGGAGCAGGCCGGGAATTAATCTACA
47▶ G E S A T L R C A M T S L I P V G P I M W F R G A G A G R E A L I Y
801 ATCAGAAAGAGGCCACTTCCACGGTAACTGTTTCCAGAACTCACAAAGAGAAACACCTGGACTTTTCCATCAGCATCAGTAACACCCCGC
80▶ N Q K E G H F P R V T T V S E L T K R N N L D F S I S I S N I T P A
NgoMIV (904)
NaeI (904) **BspEI (929)** **BssHII (990)**
901 AGACGCCGGCACCTACTACTGTGTGAAGTTCGGAAAAGGGAGCCCTGACGACGTGAGGTTAAGTCTGGAGCAGGCAGCTGAGCTGTCTGTGGCGCCAAA
113▶ D A G T Y Y C V K F R K G S P D D V E F K S G A G T E L S V R A K
DraIII (1048) **NcoI (1074)**
1001 CCCTTGCCCCCGTGGTATCGGGCCCTGCGGTGAGGGCCACACCTGAGCACACAGTGAAGCTTACCTGCGAGTCCCATGGCTTCTCTCCAGAGACATCA
147▶ P S A P V V S G P A V R A T P E H T V S F T C E S H G F S P R D I
XmnI (1104)
1101 CCCTGAAATGTTCAAAAATGGGAATGAGCTCTCAGACTTCCAGACCAACGTGGACCCCGCAGGAGACAGTGTGCTTACAGCATCCACAGCACAGCCAG
180▶ T L K W F K N G N E L S D F Q T N V D P A G D S V S Y S I H S T A R
SandI (1268)
1201 GGTGGTGTGACCCGTGGGACGTTCACTCTCAAGTCATCTGCGAGATGGCCACATCACCTTGCAGGGGACCTCTTCGTTGGGACTGCCAAGTGTCT
213▶ V V L T R G D V H S Q V I C E M A H I T L Q G D P L R G T A N L S
XmaI (1397)
1301 GAGGCCATCCGAGTTCACCCACCTTGGAGTTACTCAACAGCCATGAGGGCAGAGAACCAGGCAAACGTCACCTGCCAGGTGAGCAATTTCTACCCCC
247▶ E A I R V P P T L E V T Q Q P M R A E N Q A N V T C Q V S N F Y P
1401 GGGGACTACAGCTGACCTGGTTGGAGAATGGAATGTGTCGGACAGAAACAGCTTCGACCCATAGAGAACAAGGATGGCACCTACAAGTGGATGAG
280▶ R G L Q L T W L E N G N V S R T E T A S T L I E N K D G T Y N W M S
1501 CTGGCTCCTGGTGAACACCTGTGCCACAGGGACGATGTGGTGTCTCACCTGTGAGGTGGAGCATGATGGGAGCAAGCAGTCAGAAAAGCTATGCCCTG
313▶ W L L V N T C A H R D D V V L T C Q V E H D G Q Q A V S K S Y A L

BglII (1601) **EcoRV (1633)** **Eco47III (1650)** **AfeI (1650)** **XcmI (1697)**
1601 GAGATCTCAGCAACCAGAAAGGAGCAGGGCTCAGATATCACCCATGAACAGCGCTGGCTCCTACTGCTCCACTCCTCGTAGCTCTCTCTGGGCCCA
347▶ E I S A H Q K E H G S D I T H E P A L A P T A P L L V A L L L G P
MscI (1788)
1701 AGCTGCTACTGGTGGTGGTGTCTCTGCCATCTACATCTGCTGGAACAGAAGGCTGACTGACCTCAGTCTCTGCTGCCTGCTAGCTGGCCAGACATG
380▶ K L L L V V G V S A I Y I C W K Q K A •
1801 ATAAGATACATTGATGAGTTGGACAAACCACAAGTGAATGCAGTGAATAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCA

HpaI (1920) MfeI (1931)
1901 TTATAAGCTGCAATAAACAAGTTAAACAACAATTGCATTATTTATGTTTCAGGTTCAAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCT

EcoRI (2016)
2001 CTACAATGTGGTATGGAATCTAAAATACAGCATAGCAAACCTTAACTCCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCAT
2101 AGGCATCAGGGGCTGTGCCAATGTGCATTAGCTTTGCAGCCTCACCTTCTTCATGGAGTTAAGATATAGTGTATTTTCCCAAGTTTGAAGTACG

SspI (2255) **SwaI (2269)**
2201 TCTTCATTCTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTATGTAATAATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAAT
2301 GTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTCATAATATCCCCAGTTTAGTAGTTGAGCTTAGGGAACAAAGAACCTTTAATAGAAATTGG
2401 ACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTCTCAATGAG
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
BstXI (2559)
2501 CACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGC
116▶ V F C D 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

2601 CTGACAGCCACAATGGTGTCAAAGTCTTCTGCCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTACCCTGCCAATGTAGGCCT
 82 R V A V 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
 2701 CAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCTGTGGCCGCCCGACATGGTGCTTGTTCCTCATAGAGCATGGTGATCTTCTCAGTGGC
 49 I H V A 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

BspHI (2844)

XmnI (2836)
 2801 GACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGATGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGA
 16 V E V L E L D Q Q S I N F T K M

AseI (2902)

2901 TGATTAATTGTCAAACACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCCACCGTACACGCCTACCG

SpeI (3057)

3001 CCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCCTGTGATTTACTAGTCAAACAAACTCCCATTGACGTCAATGGGGTGGAGA

SnaBI (3185)

3100 CTTGGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACT

NdeI (3290)

3200 GCCAAGTAGGAAAGTCCCATAAGGTCATGTACTGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATA

3300 CACTTGATGTACTGCCAAGTGGGAGTTTACCGTAAATACTCCACCCATTGACGTCAATGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCATT

PstI (3469)

SdaI (3468)PacI (3476) BspLU11I (3486)

3400 ATTGACGTCAATGGGCGGGGTCGTTGGGCGGTACGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCCTGCAGGTTAA TTAAGAACATGTGAGCA

3498 AAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAA

3598 GTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGG

3698 ATACCTGTCCGCTTTCTCCCTTCGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCCGGTGTAGGTCTGCTCCAAGCTGGGC

ApaLI (3800)

3798 TGTGTGCACGAACCCCCGTTCCAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAG

3898 CAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCTAACTACGGCTACACTAGAAGAACAGTATT

3998 TGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGT

4098 TGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAG

EagI (4236)

PacI (4216) Swal (4225) NotI (4235)

4198 GGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCGCAATAAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCG

4298 TAACTAACATACGCTCTCCATCAAAAACAAAACAAAACAAAACAAAACAAAACAAAACAAAACAAAACAAAACAAAACAAAACAAAACAAAACAAAACAAAAC

4398 GAA