



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

Psp1406I (203) **HindIII (245)** **Bsu36I (291)**
PvuII (239) EcoNI (287)
201 GTGAACGTTCTTTTTCGCAACGGGTTTGGCCGAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACCGCCGCCCGCCCTACCTGAGGCC
301 GCCATCCACGCGGTTGAGTGCAGTCTGCCGCTCCCGCTGTGGTGCTCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC
401 GGGCCTTTGTCCGGGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

KasI (535) **SphI (560)**
AgeI (552)
501 TCTGTTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCGCTACCTGAGATCACCGGTGAGCATGCTGGCCCGGAGGAAGCCGGTGTACCGGCACTCAC
148▶ M L A R R K P V L P A L T
601 TATCAACCTACCATCGCCGAGGGGCCCTCCCCACCAGCGAGGGCGCCTCTGAGGCAAACCTGGTGGACCTCCAGAAGAAGCTGGAAGAGCTGGACCTG
148▶ I N P T I A E G P S P T S E G A S E A N L V D L Q K L E E L D L
701 GATGAGCAGCAAAGGAAGCGGCTTCCCTTACCAGAAAGGCTAAGGTCGGTGAAGTCAAGGACGACGACTTTGAGAGGATCTCAGAGCTGGGTG
48▶ D E Q Q R K R L E A F L T Q K A K V G E L K D D D F E R I S E L G

Bsp120I (621) **KasI (643)** **FspI (893)**
801 CCGCAATGGCGGAGTGGTACCAAGGCCCGGCATAGGCCGTACGGCCTCATCATGGCCAGAAAGCTGATCCACTGGAGATCAAACCGCCGTGCGCAA
81▶ A G N G G V V T K A R H R P S G L I M A R K L I H L E I K P A V R N
901 CCAGATCATCCGGGAGCTGCAGGTGCTGCACGAGTGAACCTCGCCTACATCGTGGGCTTCTATGGGCCTTCTACAGCGACGGCGAGATCAGCATCTGC
114▶ Q I I R E L Q V L H E C N S P Y I V G F Y G A F Y S D G E I S I C
1001 ATGGAGCACATGGATGGTGGCTCACTGGACCAGGTAAGGAGGCCAAGCGGATTCCTGAAGACATCTGGGAAGGTGAGCATTGCGGTGCTCCGGG
148▶ M E H M D G G S L D Q V L K E A K R I P E D I L G K V S I A V L R

BstEII (816) **EagI (887)**
BsaBI (987)
1101 GCCTGGCTACCTCCGAGAGAAGCACCAGATCATGCACAGAGATGTGAAGCCCTCAAACATCCTGGTGAACCTCTCGCGGGGAGATTAAGCTGTGTGACTT
181▶ G L A Y L R E K H Q I M H R D V K P S N I L V N S R G E I K L C D F

BsrBI (1206) **NotI (1226)** **BspLU11I (1259)**
1201 CGGGGTGAGCGGCCAGCTGATCGACTCCATGGCCAACTCGTTTGTAGGGACGCGCTCTACATGTCCTCCAGAGCGGCTGCAGGGCACCCTACTCTGTG
214▶ G V S G Q L I D S M A N S F V G T R S Y M S P E R L Q G T H Y S V
1301 CAGTCGGACATCTGGAGCATGGGCTGTGCTGGTGGAGCTGGCCATCGGGAGGTATCCCATCCCCACCTGATGCCAAGGAAGTACAGGGCCAGCTTTG
248▶ Q S D I W S M G L S L V E L A I G R Y P I P P P D A K E L E A S F
1401 GCCGGCCTGTGGTGGACGGGCGAGCGGAGAACCCATAGTGTCTCCCGAGGGCCAGGCCCTGGACGCCCATCAGTGGTCAATGGATGGACAGCCG
281▶ G R P V V D G A D G E P H S V S P R P R P P G R P I S G H G M D S R

NcoI (1505) **BsrBI (1270)**
1501 ACCGGCCATGGCCATCTTTGAGCTGCTGGACTACATAGTGAACGAGCCACCTCCAAGCTGCCAGTGGTGTGTTGAGCTCAGACTTCCAGGAGTTTGTG
314▶ P A M A I F E L L D Y I V N E P P P K L P S G V F S S D F Q E F V

BglIII (1635) **Eco47III (1670)**
AfeI (1670)
1601 AATAAATGTCTCATTAAAGAACCCAGCAGAGCGAGCAGATCTGAAGCTGCTGATGAACCACGCCTTCATCAAGCGCTCTGAGGGGGAGGAAGTGGACTTCG
348▶ N K C L I K N P A E R A D L K L L M N H A F I K R S E G E E V D F
1701 CCGGCTGGCTGTGAGAACCCTGCGGCTGAAGCAGCCAGCACACCCACGCGACTGCAGTGTGACAGCCAGCGCCGCTAGCTGGCCAGACATGATAAGA
381▶ A G W L C R T L R L K Q P S T P T R T A V •
1801 TACATTGATGAGTTGGACAACCACTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAA

HpaI (1914) MfeI (1925)
1901 GCTGCAATAAACAAGTTAAACAACAATTGCATTCTTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAA

EcoRI (2010)
2001 ATGTGGTATGGAATCTAAAATACAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCAT
2101 CAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTCTTTCATGGAGTTTAAAGATATAGTATTTTCCCAAGGTTTGAAGTACTCTTCA

SspI (2249) **Swal (2263)**
2201 TTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTTAGTAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTT
2301 TATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCA
2401 AGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAA
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
2501 GCAGTCAGGAGCATAGTCAGAGATGAGCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACA
114▶ 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 R V

2601 GCCACAATGGTGTCAAAGTCTTCTGCCGTTGGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGT
 801 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 I H
 2701 GGACAGCAGAGATGATCTCCCCAGTCTTGGTCTGTATGGCCGCCCGACATGGTGCTTGTTCCTCATAGAGCATGGTGATCTTCTCAGTGGCGACCTC
 471 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 V E

BspHI (2838)
 BbsI (2834)

2801 CACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCATGATGGCCCTCCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTA
 141 V L E L D Q Q S I N F T K M

AseI (2896)

2901 ATTGTCAAACACAGCTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCCAT

SpeI (3051)

3000 TTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCGTTGATTTACTAGTCAAACAAACTCCATTGACGTCAATGGGGTGGAGACTTGG

SnaBI (3179)

3099 AAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTAAGTCCGCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTAAGTCCAA

NdeI (3284)

3199 GTAGGAAAGTCCATAAGGTCATGTAAGTCCGCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTAAGTCCAA

3299 GATGTAAGTCCATAAGGTCATGTAAGTCCGCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTAAGTCCAA

SdaI (3462) Pacl (3470) BspLU11I (3480)

3399 CGTCAATGGGCGGGGCTGTTGGGCGGTGAGCCAGGCGGGCCATTACCGTAAGTTATGTAACGCTGCGAGGTTAA TTAAGAACATGTGAGCAAAAGG

3497 CCAGCAAAAGGCCAGGAACCGTAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAG

3597 AGGTGGCGAAACCGACAGGACTATAAAGATACAGGCGTTTTCCCTGGAAGCTCCCTGTCGCTCTCCTGTTCCGACCTGCCGTTACCGGATACC

ApaLI (3794)

3697 TGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTGCTCCAAGCTGGGCTGTGT

3797 GCACGAACCCCCGTTCCAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGTAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCC

3897 ACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTA

3997 TCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGTACCGCAAACAAACCACCGTGGTAGCGGTGGTTTTTTTTGTTGCAA

4097 GCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATT

EagI (4230)

PacI (4210) SwaI (4219) **NotI (4229)**

4197 TTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCCAATAAAATATCTTTATTTTATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACT

4297 AACATACGCTCTCCATCAAACAAACGAAACAAACAAACTAGCAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA