



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

Psp1406I (203) HindIII (245) Bsu36I (291) EcoNI (287)
201 GTGAACGTTCTTTTTTCGCAACGGGTTTCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACACGCCGCCCGCCCTACCTGAGGCC
301 GCCATCCACGCCGGTTGAGTGCAGTCTGCCGCTCCCGCCTGTGGTGCCTCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTAACTCTACGTCTTTGTTTCGTTT

AgeI (552) NcoI (560) XbaI (573)
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCCTACCTGAGATCACCGGTACCATTGGCTGAATTTCTAGATGACCAGGAACTCGACTGTG
1 M A E F L D D Q E T R L C

XmnI (691)
601 TGACAACCTGCAAAAAAGAAATTCCTGTGTTAACTTTACCATCCATGAGATCCACTGTCAAAGGAACATTGGTATGTGTCTACCTGTAAGGAACATT
13 D N C K K E I P V F N F T I H E I H C Q R N I G M C P T C K E P F

XcmI (701)
701 CCCAAATCTGACATGGAGACTCACATGGCTGCAGAACACTGTCAGGTGACCTGCAAATGTAACAAGAAGTTGGAGAAGAGGCTGTTAAAGAAGCATGAGG
47 P K S D M E T H M A A E H C Q V T C K C N K K L E K R L L K K H E
801 AGACTGAGTGCCTTTGCGGCTTGTCTGCTGCCAGCACTGTGATTTAGAACTTTCCATTCTCAAATGAAGGAACATGAAGATTATTGTGGTCCCGGAC
80 E T E C P L R L A V C Q H C D L E L S I L K L K E H E D Y C G A R T

BglII (939)
901 GGAACATGTGGCAACTGTGGTCGCAATGTCCTTGTGAAAGATCTGAAGACTCACCTGAAGTTTGTGGGAGAGAGGGGGAGGAAAAGAGAAATGAGGTT
113 E L C G N C G R N V L V K D L K T H P E V C G R E G E E K R N E V

NdeI (1016)
1001 GCCATACCTCCTAATGCATATGATGAATCTTGGGGTCCAGGATGGAATCTGGATTGCATCCCAACTCCTCAGACAAATTGAGGCTCTGGACCCACCCATGA
147 A I P P N A Y D E S W G Q D G I W I A S Q L L R Q I E A L D P P M
1101 GGCTGCCGCAAGGCCCTGAGAGCCTTTGAATCAGATGTTTTCCACAATAGAATACCAACCAAGGAACATTACAGCCAGGTTTCAATTCAGAATAA
180 R L P R R P L R A F E S D V F H N R T T N Q R N I T A Q V S I Q N N
1201 TCTGTTTGAAGAACAAGAGAGGCAAGGAATGAGAGCCAAACAGCCCCCAAGAGGGTGGTGAAGAGAGTCAAACCTGGACTTCATGTTGGCCCTA
213 L F E E Q E R Q E R N R G Q Q P P K E G G E E S A N L D F M L A L
1301 AGTCTGCAAAAAGAGCCCAAGCTCCAGTGTGGCAGAGCAGGACTTCTGGAGGGCGTATGTGAGGCCGACCACTCATGGCGTCCCAGGCTCTCA
247 S L Q N E G Q A S S V A E Q D F W R A V C E A D Q S H G G P R S L
1401 GTGACATAAAGGGTGCAGCTGACGAGATCATGTTGCCTTGTGAATTTGTGAGGAGCTTACCAGAGGAACTGCTGATTGACCATCAGACAAGCTGTAA
280 S D I K G A A D E I M L P C E F C E E L Y P E E L L I D H Q T S C N

BbrPI (1505) SapI (1535)
1501 CCCTTCAGTGCCTTACCTTCACTCAACTGGCAGCTTCCCGCAGAGGGGTGGAGGAACCTGATGTCATCTTCCAGAACTTCTTGAACAGGCTGCA
313 P S R A L P S L N T G S S T S P R G V E E P D V I F Q N F L Q Q A A

DraIII (1639)
1601 AGTAACCAAGTACTCTTTGATGGGCTGAGCAATTCACACCTGTGGAGGAGAGCATCATTATCCCATGTGAATCTGTGGGTACAGTGGAAAGAGG
347 S N Q L L D S L M G L S N S H P V E E S I I I P C E F C G V Q L E E
1701 AGTGCTGTTCCATCACCAGGACAGTGTGACCAACGCCAGCACTGCAACCAACATGTGACAGAGGGGATTCCTAGACTGGATTCCAGCCTCAAGA
380 E V L F H H Q D Q C D Q R P A T A T N H V T E G I P R L D S Q P Q E

Bsp120I (1891)
1801 GACCTCACCAGAGCTGCCAGGAGGCGTGTGACACACCAGGGAGACCTGTCTTCTGGTTACCTGGATGATACTAAGCAGGAAACAGCTAATGGGCCACC
413 T S P E L P R R R V R H Q G D L S S G Y L D D T K Q E T A N G P T

BsaBI (1961)
1901 TCCTGTCTGCCTCCAGCCGACCCATTAACAATATGACAGTACCTATAACCAGTATCGAGATCAACATCAGGCCCCAGACCTGGGTGCCAGCCAGCT
447 S C L P P S R P I N N M T A T Y N Q L S R S T S G P R P G C Q P S
2001 CTCCTTGTGTGCCAAGCTCAGCAACTCAGACAGCCAGGACATCCAGGGGCGGAATCGAGACAGCCAGAAATGGGGCCATAGCCCTGGGCACGTTTCACT
480 S P C V P K L S N S D S Q D I Q G R N R D S Q N G A I A P G H V S V
2101 GATTCCGCCTCCTCAAAATCTCTACCCAGAAAACATTTGCCCTTTTCTCCCTGGGCTTCCAGGGAGATACGGAGTAGTGGTAGGAGTGAAGGTGGC
513 I R P P Q N L Y P E N I V P S F S P G P S G R Y G A S G R S E G G

XmaI (2207)
2201 AGGAATTCGGGGTACCCTGCAGCTGCCAACTACCGCAGCAGAACTGCAAAGGCAAAGCCTTCCAAGCAACAGGGAGCTGGGGATGCAGAAGAGGAAG
547 R N S R V T P A A A N Y R S R T A K A K P S K Q Q G A G D A E E E

MscI (2348) NheI (2342)
2301 AGGAGGAGTAATGGTGTCTCCAGAGACTTTACATCGGTTCTGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAA
580 E E E •

HpaI (2480) MfeI (2491)
2401 TGCAGTGAATAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAACATTGCAT
2501 TCATTTTATGTTTCAGGTTACAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAAACCTTACAAATGTGGTATGGAATCTAAAATACAGCATAGCAA
2601 AACTTAAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGC

2701 **SapI (2758)**
AGCTCACCTTCTTTTCATGGAGTTAAGATATAGTGTATTTTCCCAAGGTTTGAAGTCTCTTCATTCTTTTATGTTTTAAATGCACTGACCTCCCACA

2801 **SspI (2815)** **SwaI (2829)**
TTCCCTTTTTAGTAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCA

2901 TAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTA
141 • N R T Y

3001 CTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTG
136 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 Y D S I L E R

3101 CACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCCGTTGC
102 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 D F D K Q G N S

3201 **StuI (3254)**
TCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCT
69 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 I I E G T K T R

3301 **XmnI (3396)**
GATGGCCGCCCCGACATGGTGTGTTGTCTCATAGAGCATGGTGTCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCTGCTGAGAGATGTTGAAG
36 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 D Q Q S I N F

3401 **AseI (3462)**
GTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACGCGTGGATGGCGTCTCCAGCTT
2 T K M

3501 ATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGCGGAGTTGTTACGACATTTTG

3601 **SpeI (3617)**
GAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATT

3701 **SnaBI (3745)**
GATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAA

3801 **NdeI (3850)**
TGCCAGGGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGCCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAATACT

3901 CCACCCATTGACGTCAATGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGTCTGTTGGCGGTGAGCCAGG

4001 **PacI (4036)** **SdaI (4028)** **BspLU11I (4046)**
CGGGCCATTTACCCTAAGTTATGTAACGCCTGCAGGTTAAATAAGAACATGTGAGCAAAGGCCAGAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGC
4101 TGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAATAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGC
4201 GTTCCCCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGCGCTTTCT

4301 **ApaLI (4360)**
CATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTGTTGCTCCAAAGTGGGCTGTGTGCACGAACCCCCGTTCCAGCCGACCGCTGCGCCTTAT

4401 CCGGTAACATATCGTCTTGTAGTCCAAACCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGG

4501 TGCTACAGAGTTCTTGAAGTGGTGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGA

4601 GTTGGTAGCTCTTGATCCGGCAAACAAACACCGCTGGTAGCGGTGGTTTTTTTGTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAG

4701 **EagI (4796)** **PacI (4776)** **SwaI (4785)** **NotI (4795)**
ATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAAACGAAAACCTACGTTAAGGGATTTGGTTCATGGCTAGTTAATTAACATTTAAATCAGCGGC

4801 CGCAATAAATATCTTTATTTTTCATTACATCTGTGTGGTTTTTTGTGTGAATCGTAACATAACGCTCTCCATCAAAAACAAACGAAACAAAACA

4901 AACTAGCAAATAGGCTGTCCCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA