



PvuI (7)
SgfI (6) MfeI (82)
1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
101 GAGAAAGTGGCGGGGTAACGGAAAGTGTGCTGTACTGGTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203) HindIII (245) Bsu36I (291)
201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCCTTACGCGCCCGCCCTACCTGAGGCC
301 GCCATCCACGCGGGTTGAGTCGCGTTTCTGCCGCCTCCCGCTGTGGTGCCTCCTGAAGTGCCTCCGCCGTCTAGGTAAGTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

NcoI (560)
BstEII (555)
KasI (535) AgeI (552)
501 TCTGTTCTGCGCGGTTACAGATCCAAGCTGTGACCGCGGCTACCTGAGATCACCGGTACCATTGGTTTCCCACGGTCTCGCCCTCCCTCCTGGAGGC
601 CCTGAGCAGCGACTTCTGGCCTGTAATACTGCTGAGCAGCTGCGGGCACCAAGACTGCCCTGCCTGCATACCTACTGCAAGACTGCCTGGCA
130 M V S H G S S P S L L E A
131 L S S D F L A C K I C L E Q L R A P K T L P C L H T Y C Q D C L A

EagI (714)
NotI (713)
701 CAGCTGGCGGATGGCGGCCGCTCCGCTGCCCGAGTCCCGGAGACAGTGCCTGTGCCGCCGAGGGTGTGGCCTCCTCAAGACCAACTTCTTCGTCA
47 Q L A D G G R V R C P E C R E T V P V P P E G V A S F K T N F F V

SrfI (823)
801 ATGGGCTGCTGGACCTGGTGAAGGCCGGGCTGTGGAGACCTGCGTCCGGGAAGCCAGCCTGTGCCCTGTGTCCCCTGGTGGGTGGCACCAGCACC
80 N G L L D L V K A R A C G D L R A G K P A C A L C P L V G G T S T G

NgoMIV (903) DraIII (991)
901 GGGCCCGCCACGGCCGGTGCCTGGACTGTGCCGATGACTTGTGCCAGGCTGTGCCGACGGGACCCGCTGCACCCGCCAGACCCACCCACCGCGT
113 G P A T A R C L D C A D D L C Q A C A D G H R C T R Q T H T H R V
1001 GTGGACCTGGTGGCTACAGGGCCGGTGGTATGATGAGGAGGCCGGGAGCGCAAGCGGCCAGTGTCCCAGCACCCTGGGAGGACTGCGCTTCC
147 V D L V G Y R A G W Y D E E A R E R Q A A Q C P Q H P G E A L R F
1101 TGTGCCAGCCTGCTCACAGTTGCTGTGCAGAGAGTGGCCCTAGACCCACCTGGACCACCCTGCCTGCCTTGGCTGAAGTGTGCGTGGCCGGAG
180 L C Q P C S Q L L C R E C R L D P H L D H P C L P L A E A V R A R R

NheI (1281)
1201 GCCGGCCTGGAGGACTGCTGGCCGGTGTGGACAATAAAGTGGAGTGGAGGCAGCGGGAGGGTGGAGAAGGAGGCGTAGCCCGGCTGCGGGAG
213 P G L E G L L A G V D N N L V E L E A A R R V E K E A L A R L R E

SfiI (1353) BbrPI (1399)
1301 CAGCGGCCCGGGTGGGACTCAGTGGAGGAGCGGCTGAGGGCTCCTCCGGCCCTGTGGCCAGAAAGCAGGAGGTGCTGGGCGAGCTACGAGCCC
247 Q A A R V G T Q V E E A A E G V L R A L L A Q K Q E V L G Q L R A
1401 ACGTGGAGGCTGCCGAAGAAGCTGCTCGGAGAGGCTGGCGGAGCTTGGAGGCCGGGAGCAGGTGGCCAGGGCGCAGCGCCTTCGCCCGCGGGTACT
280 H V E A A E E A A R E R L A E L E G R E Q V A R A A A A F A R R V L

PvuI (1541)
SgfI (1540)
1501 CAGCTGGGCGAGAGGCCGAGATCCTCTCCCTGGAAGGGCGATCGCACAGCGGCTCAGGCAGTGCAGGGTGCCTGGGACCAGGCCGGCCCC
313 S L G R E A E I L S L E G A I A Q R L R Q L Q G C P W A P G P A P
1601 TGCCTGCTCCACAGCTGGAGCTCCATCCTGGGCTCCTGGACAAGAAGTCCACCTTCTCGGCTGTCTTTGAGGAGCAGCAGCCCCAGAAGGATGGTG
347 C L L P Q L E L H P G L L D K N C H L L R L S F E E Q Q P Q K D G

Acc65I (1714) BbsI (1761)
1701 GAAAGACGGAGCTGGTACCCAGGAGGTGAGGAGAGCCAGAGCCGGAGGAGGATGAGCCGAAGACTGAGAGACAGGGTGGAGTCCAGCCCCAGGCTGG
380 G K D G A G T Q G G E E S Q S R R E D E P K T E R Q G G V Q P Q A G
1801 AGATGGAGCCAGACCCAAAAGAGGAAAAGCCAGACAACCCGAGAAGAGGAGGCCAGACCTTGGAGGAGACAGGGCCAGACCCACCCAGGAGT
413 D G A Q T P K E E K A Q T T R E E G A Q T L E E D R A Q T P H E D
1901 GGAGGACCCAGCCACAGGGTGGCAGACCAACAAGAAGAAAAGTTCAAAGGCAGGCTCAAGTCAATTTCCGGGAGCCAGCCAGCCCTGGGGC
447 G G P Q P H R G G R P N K K K K F K G R L K S I S R E P S P A L G
2001 CGAATCTGGACGGCTTGGCCTCCTCCAGACCCATCTTTACTGCAGTTTCCACGCGGATGCCTGGAGACAAGCGGTCCCCCGGATCACCAGGGCT
480 P N L D G S G L L P R P I F Y C S F P T R M P G D K R S P R I T G L
2101 CTGTCCCTTCGGTCCCGGAGATCCTGGTGGCGGATGAGCAGAACCAGGCACTGAAACGCTTCCCTCAACGGCGACTACAAGGGCAGCGTCCCGGCT
513 C P F G P R E I L V A D E Q N R A L K R F S L N G D Y K G T V P V

Bsu36I (2200) NheI (2257)
2201 CCTGAGGGTGTCTCCCTTGCAGCGTGGCCGCCCTGCAGAGCGCGGTGGCCTTCTCCGCTAGCGCAGGCTCTATCTCATCAACCCCAACGGCGAAGTGC
547 P E G C S P C S V A A L Q S A V A F S A S A R L Y L I N P N G E V

DraIII (2335) BbrPI (2389) BsrGI
2301 AGTGGCGCAGGGCCTGAGCCTCTCCAGGCCAGCCAGCGGTGGCGGCACTGCCTAGCGGGACCGGCTGGCTGTCAGCGTGGCGGGCCAGTGGAGGT
580 Q W R R A L S L S Q A S H A V A A L P S G D R V A V S V A G H V E V
2401 GTACAATATGAAGGAGCTGGCCACCCGGTTCTTCTGGAGGCAAGGCCAGCCGGGCTGCGGGCGTGGTGTCTGACCACCCAGCCCGGGG
613 Y N M E G S L A T R F I P G G K A S R G L R A L V F L T T S P Q G
2501 CATTTCGTGGGTCGACTGGCAGCAGAATAGTGTGTAATCTGTGATGGGCTGGCCAGGTGGTGGGGAGTACAAGGGCCAGGCTGCATGGCTGCC
647 H F V G S D W Q Q N S V V I C D G L G Q V V G E Y K G P G L H G C

SandI (2686)
2601 AGCCGGGCTCCGTGTCTGTGGATAAGAAGGCTACATCTTTCTGACCCCTCGAGAAGTCAACAAGGTGGTGTCTGGACCCGAGGGTCCCTCCTTGG
680 Q P G S V S V D K K G Y I F L T L R E V N K V V I L D P K G S L L G

NcoI (2747) BstEII (2739) Acc65I (2762)
2701 AGACTTCCTGACAGCCTACCACGGCCTGAAAAAGCCCGGTTACCACCATGGTGGATGGCAGGTACCTGGTCGTGCCCTCAGTAACGGGACCATCCAC
713▷ D F L T A Y H G L E K P R V T T M V D G R Y L V V S L S N G T I H

BspEI (2817) AvrII (2853)
2801 ATCTTTCCGGTCCGTTCTCCGGACAGTTAAAGGGGCTAGGACTAGGCTGAGAGCCTAGGTCTAGCTGGCCAGACATGATAAGTACATTGATGAGTTGG
747▷ I F R V R S P D S •

HpaI (2997)
2901 ACAAACCACAAGTGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACATTATAAGCTGCAATAAACAAGTT

MfeI (3008) EcoRI (3093)
3001 AACAACAACAATTGCATTCATTTTATGTTTCAGGTTCCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCT
3101 AAAATACAGCATAGCAAACTTTAACCTCCAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTGCCAAT
3201 GTGCATTAGCTGTTTGCAGCCTCACCTTCTTCATGGAGTTAAAGATATAGTGTATTTTCCCAAGTTTGAAC TAGCTCTTCATTTCTTTATGTTTTAAA

SspI (3332) SmaI (3346)
3301 TGCACTGACCTCCACATTCCTTTTGTAGTAAATATTAGAAATAATTTAAATACATCATTGCAATGAAAAAATGTTTTTATTAGGCAGAAATCCAG
3401 ATGCTCAAGGCCCTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAG
3501 CTTTAGTTCCTGGTGACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTATCTCAATGAGCACAAAGCAGTCAGGAGCATAGT
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 Y D
3601 CAGAGATGAGCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAA
108◀ 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 D F
3701 GTCCTTCTGCCCGTTCACAGCAGACCAATGGCAATGGCTTCAGCACAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATC
75◀ 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 I I
3801 TCCCCAGTCTGGTCTGATGGCCGCCGACATGGTCTGTGTCTCATAGAGCATGGTGTCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCT
41◀ 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 D Q

BspHI (3921) BbsI (3917) AseI (3979)
3901 GCTGAGAGATGTTGAAGGCTTCATGATGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTG
8◀ Q S I N F T K M
4001 GATGGCGTCTCCAGCTTATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTGCGTCAATGGGGCGGA

SpeI (4134)
4101 GTTGTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAACAACTCCCATGACGTCATGGGGTGGAGACTTGGAAATCCCCGTGAGTCAA

SnaBI (4262)
4200 CCGCTATCCACGCCATTGATGTACTGCCAAAACGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCCATAG

NdeI (4367)
4300 GTCATGTACTGGGATAATGCCAGGCGGCCATTTACCGTATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGTGACTGCCAAGTGGG
4400 CAGTTTACCGTAAATACTCCACCATTGACGTCAATGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGTCAATGGGCGGGGTC

SdaI (4545) PacI (4553) BspLU11I (4563)
4500 GTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAAGTTATGTAACGCCCTGCAGGTTAA TTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAA
4598 CCGTAAAAAGGCCGCTTGTGGCGTTTTTCCATAGGCTCCGCCCTGACGAGCATCAAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACA
4698 GGACTATAAAGATACCAGCGTTTTCCCCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTT

ApaLI (4877)
4798 CGGGAAGCGTGGCGCTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTCA
4898 GCCCGACCCTGCGCTTATCCGGTAACTATCGTCTTGTAGTCCAAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGC
4998 AGAGCGAGGTATGTAGCGGTGCTACAGAGTCTTGAAGTGGTGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGC
5098 CAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGTATCCGCAAAACACCCTGGTACGGGTGGTTTTTTTGTGTAAGCAGCAGATTACGCGCAG

PacI (5293)
5198 AAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGCTGACGCTCAGTGGAAACGAAAACTCACGTTAAGGGATTTTGGTCAATGGCTAGTTAA

EagI (5313) NotI (5312) SmaI (5302)
5298 TTAACATTTAAATC AGCGGCCGAATAAAATATCTTTATTTTATTACATCTGTGTGGTTTTTTGTGTAATCGTAACATAACGCTCTCCATCA
5398 AAACAAAACGAAACAAAACAACTAGCAAAATAGGCTGTCCCGAGTGAAGTGCAGGTGCCAGAACATTTCTCTATCGAA