



PvuI (7)  
SgfI (6)  
1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTCGGCAATTGAACGGGTGCCTA  
101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)  
Psp1406I (203) PvuII (239) Bsu36I (291)  
201 GTGAACGTTCTTTTTTCGCAACGGGTTTCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACAGCGCCCGCCGCCCTACCTGAGGCC  
301 GCCATCCACGCGGTTGAGTGCAGTCTGCCGCTCCCGCCTGTGGTGCCTCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)  
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTAACTCTACGCTTTTGTTCGTTT

NcoI (560)  
BstEII (555)  
AgeI (552)  
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCCCTACCTGAGATCACCGGTCACCATGGAGAATATGAAAGTCTACTGGGGCTCATTGTCT  
1 M E N M K V L L G L I C L

BsrGI (634)  
601 CATGGTGCCTCTGCTGTCGCTGGAGATTGACGTATGTACAGAATATCCAAATCAGATCGTTTTGTTTTATCTGTAATGAAATTGATATTCGCAAGTGT  
13 M V P L L S L E I D V C T E Y P N Q I V L F L S V N E I D I R K C

RsrII (773)  
701 CCTCTTACTCCAATAAAATGCACGGGACACCATAATTTGGTACAAGAATGACAGCAAGACCCCATATCAGCGGACCGGGACTCCAGGATTCATCAGC  
47 P L T P N K M H G D T I I W Y K N D S K T P I S A D R D S R I H Q  
801 AGAATGAACATCTTTGGTTTGTACTGCGCAAGTGGAGGACTCAGGATATTACTATTGTATAGTAAGAACTCAACTTACTGCCTCAAACTAAAGTAAC  
80 Q N E H L W F V P A K V E D S G Y Y Y C I V R N S T Y C L K T K V T  
901 CGTAACTGTGTAGAGAATGACCTGGCTTGTGTTACAGCACACAGGCCACCTCCACAGCGGCTCCACATTGCCGGGGATGGAAGTCTTGTGTGCCPT  
113 V T V L E N D P G L C Y S T Q A T F P Q R L H I A G D G S L V C G  
1001 TATGTGAGTTATTTAAAGATGAAAATAATGAGTTACCCGAGGTCAGTGGTATAAAGAACTGTAACCTCTGTTCTTGACAACGTGAGCTTCTTCGGAG  
147 Y V S Y F K D E N N E L P E V Q W Y K N C K P L L L D N V S F F G  
1101 TAAAAGATAAACTTTGGTGGGAATGTGGCTGAAGAGCACAGAGGGGACTATATATGCCGTATGTCTATACGTTCCGGGGGAAAGCAATATCCGGTCCAC  
180 V K D K L L V R N V A E E H R G D Y I C R M S Y T F R G K Q Y P V T

PvuI (1274)  
1201 ACGAGTAATAACAATTTATCACAATAGATGAAAAAAGAGGGACAGACCTGTTATCCTGAGCCCTCGGAATGAGACGATCGAAGCTGACCCAGGATCAATG  
213 R V I Q F I T I D E N K R D R P V I L S P R N E T I E A D P G S M

Tth111I (1336)  
1301 ATACAACCTGATCTGCAACGTGACGGGCCAGTTCTCAGACCTTGTCTAGCTGGAAGTGAATGGATCAGAAATTGAATGGAATGATCCATTTCTAGCTGAAG  
247 I Q L I C N V T G Q F S D L V Y W K W N G S E I E W N D P F L A E  
1401 ACTATCAATTTGTGGAACATCCTTCAACCAAAAAGAAAATACACACTCATTACAACACTTAACATTTGAGAAGTAAAAGCCAGTTTTATCGCTATCCGTT  
280 D Y Q F V E H P S T K R K Y T L I T T L N I S E V K S Q F Y R Y P F

Spl (1522)  
1501 TATCTGTGTTGTTAAGAACAATAATTTTTGAGTCCGGCGCATGTGCAGTTAATATACCAGTCCCTGACTTCAAGAATTACCTCATCGGGGGCTTTATC  
313 I C V V K N T N I F E S A H V Q L I Y P V P D F K N Y L I G G F I  
1601 ATCCTCACGGCTACAATTGTATGCTGTGTGCATCTATAAAGCTTCAAGGTTGACATAGTCTTTGGTACAGGGACTCCTGCTCTGGTTTTCTTCCTT  
347 I L T A T I V C C V C I Y K V F K V D I V L W Y R D S C S G F L P

HindIII (1703) BstXI (1745) EcoO109I (1762)  
1701 CAAAAGCTTCAGATGAAAAGACATACGATGCCTATATTCTTTATCCCAAGACCTGGGAGAGGGGCTTCTCAGACTTAGATACTTTTGTTTTAAACT  
380 S K A S D G K T Y D A Y I L Y P K T L G E G S F S D L D T F V F K L

Bsu36I (1804)  
1801 GTTGCCCTGAGGCTTTGGAGGGACAGTTTGGATAACAAGCTGTTCAATTTATGGAAGGGATGACTATGTTGGAGAAGATACCATCGAGGTTACTAATGAAAAT  
413 L P E V L E G Q F G Y K L F I Y G R D D Y V G E D T I E V T N E N

PvuII (1953)  
1901 GTAAGAAAAGCAGGAGGCTGATTATCATTCTAGTGAGAGATATGGGAGGCTCAGCTGGCTGGCCAGTCTGAAAGACAAATAGCCATATAACAATG  
447 V K K S R R L I I I L V R D M G G F S W L G Q S S E E Q I A I Y N  
2001 CTCTCATCCAGGAAGGAATTAATCGTCTGCTGAGTTGGAGAAAATCCAAGACTATGAGAAAATGCCAGATTCTATTGATTCATTAAGCAGAAAACA  
480 A L I Q E G I K I V L L E L E K I Q D Y E K M P D S I Q F I K Q K H

PshAI (2135)  
2101 CGGAGTCATTTGCTGGTCCAGGAGACTTTCAAGAAAAGACCACAGCTGCAAGACCAGGTTCTGAAAAACTTAAGATACCAGATGCCAGCCCAACGGAGA  
513 G V I C W S G D F Q E R P Q S A K T R F W K N L R Y Q M P A Q R R

BamHI (2232) NgoMIV (2262) MscI (2299)  
2201 TCACCATTGTCTAAACACCGCTTACTAACCTGGATCCTGTGCGGGACACTAAGGAGAACTGCCGGCAGCAACACACTTACCCTCGGCTAGGCTAGCT  
547 S P L S K H R L L T L D P V R D T K E K L P A A T H L P L G •  
2301 GGCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAAGAAAATGCTTTATTTGTGAATTTGTGATGCTATTGCTTT

HpaI (2431)  
2401 ATTTGTAACCATTATAAGCTGCAATAAACAAGTAAACAACAACAAATTGCATTCTTTTATGTTTCAGGTTTCAGGGGGAGGTGGGAGGTTTTTAAAGC

EcoRI (2527)  
2501 AAGTAAAACCTCTACAAATGTGGTATGGAATTTAAAATACAGCATAGCAAACCTTTAACCTCCAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGAT  
2601 GAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGACGCTCACCTTCTTCATGGAGTTAAGATATAGTGATTTTCCAAGG

2701 TTTGAACTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTATAGTAAAATATTCAGAAATAATTTAAATACATCATTGCAA  
SspI (2766) SwaI (2780)

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2801 TGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGAACCTTTA  
EcoO109I (2841)

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2901 ATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTACTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTC  
141 • N R T Y K L P I L E E I T T K V L K G N

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3001 ATCTCAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAG  
SacI (3041) BstXI (3070)  
 119 M E I L 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

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3101 AGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCAGACAGTGGACCTGCC  
 86 Y P H 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

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3201 AATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCGAGTCTTGGTCTGATGGCCGCCCGACATGGTGTCTGTTGTCTCATAGAGCATGGTGATC  
StuI (3205)  
 53 I Y A E 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

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3301 TTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATA  
XmnI (3347)  
 19 K E T A V E V L E L D Q Q S I N F T K M

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3401 TACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCCACCGTA  
AseI (3413) SacI (3470)

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3501 CACGCCTACCGCCCATTTGCGTCAATGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAACAAACTCCCATTGACGTCAAT  
SpeI (3568)

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3601 GGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTAAGTCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACG  
SnaBI (3696)

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3701 TAGATGTAAGTCCCAAGTAGAAAGTCCATAAGGTCATGTAAGTGGCATAATGCCAGGCGGGCCATTTACCGTCAATTGACGTCAATAGGGGGCTACTTG

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3801 GCATATGATACACTTGATGTAAGTGGCAGTTTACCCTAAATACTCCACCCATTGACGTCAATGAAAGTCCCTATTGGCGTACTATGGGAAC  
NdeI (3801)

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3901 ATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGACGGTTAATTAAGAACA  
PacI (3987) PstI (3980) SdaI (3979) BspLU11I

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4001 TGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGGTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCG

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4101 ACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCTGGAAGCTCCCTCGTGCGCTCTCTGTTCCGACCTGCCG

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4201 CTTACCGGATACCTGTCCGCTTTCTCCCTTCGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCA

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4301 AGCTGGGCTGTGTGCACGAACCCCCGTTAGCCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGTAAGACACGACTTATCGCC  
ApaLI (4311)

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4401 ACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGA

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4501 ACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAAACAAACCACCGCTGGTAGCGGTGGTT

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4601 TTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACTC

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4701 ACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCGCAATAAAATATCTTTATTTTTCATTACATCTGTGTGTTGGTTTTTGT  
EagI (4747) Pacl (4727) SwaI (4736) NotI (4746)

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4801 GTGAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAAATAGGCTGTCCCCAGTGAAGTGCAGGTGCCAGAACATT  
 4901 TCTCTATCGAA