



PvuI (7) SgfI (6) MfeI (82) EcoNI (96)  
1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA  
101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGATGCTGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCC

Psp1406I (203) HindIII (245) Bsu36I (291) EcoNI (287)  
201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACACGCCGCCGCCCTACCTGAGGCC  
301 GCCATCCACGCCGGTTGAGTCGCGTTTCTGCCGCTCCCGCCTGTGGTGCTCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)  
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTAACTCTACGTCTTTGTTTCGTTT

BspLU11I (560) AgeI (552) Acc65I (576)  
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCCTACCTGAGATCACCGGTCAACATGTGGGTCCGGCAGGTACCCTGGTCATTCACTTGGGC  
1 M W V R Q V P W S F T W A

XbaI (633) Bsp120I (649)  
601 TGTGCTGCAGTTGAGCTGGCAATCAGGGTGGCTTCTAGAGTCCCAATGGCCCTGGAGGTCCCTCACCTTCTACCCAGCCTGGCTCACAGTGTGAGAG  
13 V L Q L S W Q S G W L L E V P N G P W R S L T F Y P A W L T V S E  
701 GGAGCAAATGCCACCTTACCTGCAGTGTCCAAGTGGTCCGAGGATCTTATGCTGAAGTGAACCCGCTGAGTCCCAGCAACCAGACTGAAAAACAGG  
47 G A N A T F T C S L S N W S E D L M L N W N R L S P S N Q T E K Q  
801 CCGCCTTCTGTAATGGTTTGGCAACCCGTCAGGATGCCGCTTCCAGATCATAACAGCTGCCAACAGGCATGACTTCCACATGAACATCCTTGACAC  
80 A A F C N G L S Q P V Q D A R F Q I I Q L P N R H D F H M N I L D T  
901 ACGGCGCAATGACAGTGGCATCTACCTCTGTGGGGCCATCTCCCTGCACCCCAAGGCAAAAATCGAGGAGAGCCCTGGAGCAGAGCTCGTGGTAAACAGAG  
113 R R N D S G I Y L C G A I S L H P K A K I E E S P G A E L V V T E

EcoRV (1022) BspHI (1079)  
1001 AGAATCCTGGAGACCTCAACAAGATATCCAGCCCTCGCCCAAACAGAAAGCCGGTTTCAAGGCATGGTCATTGGTATCATGAGTGCCTAGTGGGTA  
147 R I L E T S T R Y P S P K P E G R F Q G M V I G I M S A L V G

Bsp120I (1124)  
1101 TCCCTGTATTGCTGCTGCTGGCCTGGGCCCTAGCTGTCTTCTGCTCAACAAGTATGTCAGAGGCCAGAGGAGCTGGAAGCAAGGACGACTCTGAAGGA  
180 I P V L L L L A W A L A V F C S T S M S E A R G A G S K D D T L K E

ApaI (1291)  
1201 GGAGCCTTACAGCAGCACCTGTCCCTAGTGTGGCCTATGAGGAGCTGGACTTCCAGGGACGAGAGAAGACACCAGAGCTCCCTACCGCCTGTGTGCACACA  
213 E P S A A P V P S V A Y E E L D F Q G R E K T P E L P T A C V H T

NcoI (1343) SdaI (1371)  
1301 GAATATGCCACCATTGTCTTCACTGAAGGGCTGGGTGCCTCGGCCATGGGACGTAGGGGCTCAGCTGATGGCTGCAGGGTCTCGGCCTCAAGACATG  
247 E Y A T I V F T E G L G A S A M G R R G S A D G L Q G P R P P R H

NheI (1452) SphI (1448) MscI (1458)  
1401 AGGATGGACATTGTTCTTGGCCTCTTTGACCAGATTCTTACGCCATTAGCATGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACC  
280 E D G H C S W P L •

HpaI (1590)  
1501 ACAACTAGAATGCAGTGAATAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACA

MfeI (1601) EcoRI (1686)  
1601 ACAATTGCATTATTTTATGTTTCAGGTTACAGGGGAGGTGTGGGAGTTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCTAAAATAC  
1701 AGCATAGCAAACCTTAACTCCAAATCAAGCCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATT

SapI (1868)  
1801 AGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGTATTTTCCCAAGTTTGAAGTACTAGCTCTTCATTCTTTTATGTTTTAAATGCAGCTG

SspI (1925) SmaI (1939)  
1901 ACCTCCACATTCCTTTTTAGTAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCA  
2001 AGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGAACCTTTAATAGAAATTGGACAGCAAGAAAGCAGCTTCTAGCTTTAGT  
141 • N  
2101 TCCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGAT  
139 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 S I

BstXI (2229)  
2201 GAGCTCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTC  
106 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 D K

StuI (2364)  
2301 TGCCCGTTGCTCACAGCAGACCAATGGCAATGGCTTACAGCACAGACAGTACCCTGCCAATGTAGGCCTAATGTGGACAGCAGAGATGATCTCCCCAG  
72 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 E G T  
2401 TCTTGGTCTGATGGCCGCCGACATGGTGTCTTGTCTCATAGAGCATGGTGTCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGA  
39 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 Q S

XmnI (2506) AseI (2572)  
2501 GATGTTGAAGGCTTTCATGGTGGCCCTCTATAGTGAGTCTATTATACTATGCGGATATACTATGCCGATGATTAATTGTCAAACACAGCGTGGATGGCG  
6 I N F T K M  
2601 TCTCCAGCTTATCTGACGGTTCACATAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTA

2701 CGACATTTTGAAAAGTCCCGTTGATTTACTAGTCAAAACAAACTCCATTGACGTCAATGGGGTGGAGACTTGAAAATCCCCGTGAGTCAAACCGCTATC  
SpeI (2727)  


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 2801 CACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCATGTA  
SnaBI (2855)  


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 2901 CTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTAC  
NdeI (2960)  


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 3001 CGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCG  


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 3101 GTCAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCTGCAGGTTAATTAAGAACATGTGAGCAAAAGGCCAGAAAAGGCCAGGAACCGTAAAAAG  
SdaI (3138) PacI (3146) BspLU11I (3156)  


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 3201 GCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCAGAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAA  
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 3301 GATACCAGGCGTTTCCCCTGGAAGCTCCCTCGTGGCTCTCCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGT  


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 3401 GGGCCTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTTACGCCGACCGC  
ApaLI (3470)  


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 3501 TGGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGT  


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 3601 ATGTAGGCGGTGTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTT  


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 3701 CGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGA  


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 3801 TCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACCTACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTA  
PacI (3886) SmaI (3895)  


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EagI (3906)  
NotI (3905)  
 3901 AATC AGCGGCCGCAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTAATCGTAACTAACATACGCTCTCCATCAAAACAAAACG  
 4001 AAACAAAACAACTAGCAAAATAGGCTGTCCCCAGTGAAGTGCAGGTGCCAGAACATTTCTCTATCGAA