

(Circular) MAP of: Peaw118.Seq check: 7314 from: 1 to: 7169

>>>pJS39

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With 198 enzymes: \*

MaxCuts: 3

May 4, 1994 15:03 ..

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E      c      N      X      C      d
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R      p      a      a      I
I      V      I      I      I
gaattcgaagttcctatactttctagagaataggaacttccgggatcggcccatcgataa
1 -----+-----+-----+-----+-----+-----+ 60
cttaagcttcaaggatatgaaagatctcttatccttgaaggccctagccgggtagctatt

      P
      K  v
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      I  I
gcttggtacccAGCTGGCACGACAGGTTTCCCGACTGGAAAGCGGGCAGTGAGCGCAACG
61 -----+-----+-----+-----+-----+ 120
cgaacctatgggTCGACCGTGCTGTCCAAAGGGCTGACCTTTCGCCCGTCACTCGCGTTGC

CAATTAATGTGAGTTAGCTCACTCATTAGGCACCCCAGGCTTTACACTTTATGCTTCCGG
121 -----+-----+-----+-----+-----+ 180
GTTAATTACACTCAATCGAGTGAGTAATCCGTGGGGTCCGAAATGTGAAATACGAAGGCC

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CTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATGACC
181 -----+-----+-----+-----+-----+ 240
GAGCATAACAACACACCTTAACACTCGCCTATTGTTAAAGTGTGTCCTTTGTCGATACTGG

ATGATTATTAATAATCTTCGTTAGTTTCTGCTACGCCTTCGCTATCATCTACAGAGAAAT
241 -----+-----+-----+-----+-----+ 300
TACTAATAATTTTTAGAAGCAATCAAAGACGATGCGGAAGCGATAGTAGATGTCTCTTTA

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CCGGCGTTGAGTTCGGGTTGCTCAGCAGCAACTCACGTACTTTCTTCTCGATCTCTTTTCG
301 -----+-----+-----+-----+-----+ 360
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GGCCGCAACTCAAGCCCAACGAGTCGTCGTTGAGTGCATGAAAGAAGAGCTAGAGAAAGC
CGGTTTCCGGGTTATCTTTCAGCCAGGCAGTCGCATTTCGCTTTACCCTGACCGATCTTCT
361 -----+-----+-----+-----+-----+-----+ 420
GCCAAAGGCCCAATAGAAAGTCGGTCCGTACGCGTAAGCGAAATGGGACTGGCTAGAAGA

CACCTTTGTAGCTGTACCACGCGCCTGCTTTCTCGATCAGCTTCTCTTTTACGCCCAGGT
421 -----+-----+-----+-----+-----+-----+ 480
GTGGAAACATCGACATGGTGCGCGGACGAAAGAGCTAGTCTGAAGAGAAAATGCGGGTCCA

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CAACCAGTTCGCCGTAGAAGTTGATACCTTCGCCGTAGAGGATCTGGAATTCAGCCTGTT
481 -----+-----+-----+-----+-----+-----+ 540
GTTGGTCAAGCGGCATCTTCAACTATGGAAGCGGCATCTCCTAGACCTTAAGTCGGACAA

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TAAACGGCGCAGCGATTTTGTTCCTTACCACCTTTCACGCGGGTTTCGCTACCCACCACGT
541 -----+-----+-----+-----+-----+-----+ 600
ATTTGCCGCGTCGCTAAAACAAGAAGTGGTGAAGTGCGCCCAAAGCGATGGGTGGTGCA

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TTTCGCCCTCTTTCACCGCGCCGATACGACGGATGTCGAGACGAACAGAGGCGTAGAATT
601 -----+-----+-----+-----+-----+-----+ 660
AAAGCGGGAGAAAGTGGCGCGGCTATGCTGCCTACAGCTCTGCTTGTCTCCGCATCTTAA

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TCAGCGGTTACCACCGGTAGTGGTTTCCGGGTTACCGAACATCACACCAATTTTCATAC
661 -----+-----+-----+-----+-----+-----+ 720
AGTCGCGCAATGGTGGCCATCACCAAAGGCCCAATGGCTTGTAGTGTGGTTAAAAGTATG

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GGATCTGGTTGATGAAGATCAGCAGCGTGTGGACTGCTTCAGGTTACCCGCCAGCTTAC
721 -----+-----+-----+-----+-----+-----+ 780
CCTAGACCAACTACTTCTAGTCGTCGCACAACCTGACGAAGTCCAATGGGCGGTGCAATG

GCATCGCCTGGCTCATCATACGTGCCGCAAGGCCCATGTGAGAGTCGCCGATTTTCGCCTT
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781 -----+-----+-----+-----+-----+-----+ 840  
CGTAGCGGACCGAGTAGTATGCACGGCGTTCCGGGTACACTCTCAGCGGCTAAAGCGGAA

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CGATTTCCGCTTTTCGGCGTCAGTGCCGCCACGGAGTCAACGACGATAACGTCTACTGCGC  
841 -----+-----+-----+-----+-----+-----+ 900  
GCTAAAGGCGAAAGCCGCAGTCACGGCGGTGCCTCAGTTGCTGCTATTGCAGATGACGCG

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CAGAACGCGCCAGGGCGTCACAGATTTCCAGTGCCTGCTCGCCGGTGTCCGGCTGGGAGC  
901 -----+-----+-----+-----+-----+-----+ 960  
GTCTTGCGCGGTCCCGCAGTGTCTAAAGGTCACGGACGAGCGGCCACAGGCCGACCCTCG

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ACAGCAGGTTGTCGATATCGACGCCAGTTTACGTGCGTAGATTGGGTCCAGCGCGTGT  
961 -----+-----+-----+-----+-----+-----+ 1020  
TGTCGTCCAACAGCTATAGCTGCGGGTCAAATGCACGCATCTAACCAGGTGCGGCACAA

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CAGCATCGATAAACGCACAGGTTTTACCTTCACGCTGCGCTGCGGCGATCACCTGCAGCG  
1021 -----+-----+-----+-----+-----+-----+ 1080  
GTCGTAGCTATTTGCGTGTCCAAAATGGAAGTGCACGCGACGCCGCTAGTGGACGTCGC

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TCAGCGTGGTTTTACCGGAAGATTCCGGTCCGTAGATTTTCGACGATACGGCCCATCGGCA  
1081 -----+-----+-----+-----+-----+-----+ 1140  
AGTCGCACCAAAATGGCCTTCTAAGGCCAGGCATCTAAAGCTGCTATGCCGGGTAGCCGT

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GACCACCTGCCCCAAGCGCGATATCCAGTGAAAGCGAACCGGTAGAGATGGTTTTCCACAT  
1141 -----+-----+-----+-----+-----+-----+ 1200  
CTGGTGGACGGGGTTTCGCGCTATAGGTCACTTTTCGCTTGGCCATCTCTACCAAAGGTGTA

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1201 CCATGGAACGGTCTTCACCCAGGCGCATGATGGAGCCTTTACCAAATTGTTTCTCAATCT 1260  
 -----+-----+-----+-----+-----+-----+  
 GGTACCTTGCCAGAAGTGGGTCCGCGTACTACCTCGGAAATGGTTTAACAAAGAGTTAGA  
  
 GGCCCAGTGTGCCGCCAACGCTTTCTGTTTGTTCGTCGATAGCCATttttactcctg  
 1261 -----+-----+-----+-----+-----+-----+ 1320  
 CCGGGTCACGACGGCGGTTGCGAAAGACAAACAAAAGCAGCTATCGGTAaaaatgaggac

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1321 tcatggatcctaataccggatagtcaatatgttctgttgaagcaattatactgtatgctc 1380  
 -----+-----+-----+-----+-----+-----+  
 agtacctaggattatggcctatcagttatacaagacaacttcgттаатatgacatacgag

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1381 atacagtatcaagtcgactctagcagatctagcttATGATAGTGATGTGCTTAAAAACTT 1440  
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 tatgtcatagttcagctgagatcgtctagatcgaaTACTATCACTACACGAATTTTTGAA

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1441 ACTCAATGGCTGGTTTATGCATATCGCAATACATGCGAAAAACCTAAAAGAGCTTGCCGA 1500  
 -----+-----+-----+-----+-----+-----+  
 TGAGTTACCGACCAAATACGTATAGCGTTATGTACGCTTTTTGGATTTTCTCGAACGGCT

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1501 TAAAAAAGGCCAATTTATTGCTATTTACCGCGGCTTTTTATTGAGCTTGAAAGATAAATA 1560  
 -----+-----+-----+-----+-----+-----+  
 ATTTTTTCCGGTTAAATAACGATAAATGGCGCCGAAAAATAACTCGAACTTTCTATTTAT  
  
 AAATAGATAGTTTTTTTGAAGCTAAATCTTCTTTATCGTAAAAAATGCCCTCTTGGGT  
 1561 -----+-----+-----+-----+-----+-----+ 1620  
 TTTATCTATCCAAAATAAACTTCGATTTAGAAGAAATAGCATTTTTTTACGGGAGAACCCA  
  
 TATCAAGAGGGTCATTATATTTTCGCGGAATAACATCATTTGGTGACGAAATAACTAAGCA  
 1621 -----+-----+-----+-----+-----+-----+ 1680  
 ATAGTTCTCCAGTAATATAAAGCGCCTTATTGTAGTAAACCACTGCTTTATTGATTCTGT

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1681 CTTGTCTCCTGTTTACTCCCCTGAGCTTGAGGGGTAAACATGAAGGTCATCGATAGCAGG  
-----+-----+-----+-----+-----+-----+ 1740  
GAACAGAGGACAAATGAGGGGACTCGAACTCCCAATTGTACTTCCAGTAGCTATCGTCC

1741 ATAATAATACAGTAAAACGCTAAACCAATAATCCAAATCCAGCCATCCCAAATTGGTAGT  
-----+-----+-----+-----+-----+-----+ 1800  
TATTATTATGTCATTTTTCGATTTGGTTATTAGGTTTAGGTCGGTAGGGTTTAAACATCA

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1801 GAATGATTATAAATAACAGTAAACAGTAATGGGCCAATAACACCGGTTGCATTGGTAAGG  
-----+-----+-----+-----+-----+-----+ 1860  
CTTACTAATATTTATTGTCATTTGTCATTACCCGGTTATTGTGGCCAACGTAACCATTCC

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1861 CTCACCAATAATCCCTGTAAAGCACCTTGCTCATGACTCTTTGTTTGGATAGACATCACT  
-----+-----+-----+-----+-----+-----+ 1920  
GAGTGGTTATTAGGGACATTTTCGTGGAACGAGTACTGAGAAACAAACCTATCTGTAGTGA

1921 CCCTGTAATGCAGGTAAAGCGATCCCACCACCAGCCAATAAAATTTAAAACAGGGAAATCT  
-----+-----+-----+-----+-----+-----+ 1980  
GGGACATTACGTCCATTTTCGCTAGGGTGGTGGTTCGGTTATTTTAATTTTGTCCCTTTAGA

1981 AACCAACCTTCAGATATAAACGCTAAAAAGGCAAATGCACTACTATCTGCAATAAATTCG  
-----+-----+-----+-----+-----+-----+ 2040  
TTGGTTGGAAGTCTATATTTTCGATTTTTCCGTTTACGTGATGATAGACGTTATTTAAGC

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2041 AGCAGTACTGCCGTTTTTTTCGCCCCATTTAGTGGCTATTCTTCTGCCACAAAGGCTTGG  
-----+-----+-----+-----+-----+-----+ 2100  
TCGTCATGACGGCAAAAAGCGGGTAAATCACCGATAAGAAGGACGGTGTTCGGAACC

2101 AATACTGAGTGTAAGACCAAGACCCGCTAATGAAAAGCCAACCATCATGCTATTCCAT  
-----+-----+-----+-----+-----+-----+ 2160  
TTATGACTCACATTTTCTGGTTCTGGGCGATTACTTTTTCGGTTGGTAGTACGATAAGGTA

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2161 CCAAAACGATTTTCGGTAAATAGCACCCACACCGTTGCGGGAATTTGGCCTATCAATTGC 2220  
-----+-----+-----+-----+-----+-----+-----+  
GGTTTTGCTAAAAGCCATTTATCGTGGGTGTGGCAACGCCCTTAAACCGGATAGTTAACG

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2221 GCTGAAAAATAAATAATCAACAAAATGGGCATCGTTTTAAATAAAGTGATGTATACCGAA 2280  
-----+-----+-----+-----+-----+-----+-----+  
CGACTTTTTATTTATTAGTTGTTTTACCCGTAGCAAAATTTATTTCACTACATATGGCTT

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2281 TTCGATTGCGTCTCAACCCCTACTTCGGTATCTGTATTATCACGTGTATTTTTGGTTTTCA 2340  
-----+-----+-----+-----+-----+-----+-----+  
AAGCTAACGCAGAGTTGGGGATGAAGCCATAGACATAATAGTGCACATAAAAAACCAAAGT

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2341 CGGAACCAAAACATAACCACAAGGAAAGTGACAATATTTAGCAACGCAGCGATAAAAAAG 2400  
-----+-----+-----+-----+-----+-----+-----+  
GCCTTGGTTTTGTATTGGTGTTCCCTTTCCTACTGTTATAAATCGTTGCGTCGCTATTTTTTC

2401 GGACTATGCGGTGAAATCTCTCCTGCAAAACCACCAATAATAGGCCCCGCTATTTAAACCA 2460  
-----+-----+-----+-----+-----+-----+-----+  
CCTGATACGCCACTTTAGAGAGGACGTTTTGGTGGTTATTATCCGGGGCGATAATTTGGT

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2461 AGCCAAAACCTTGCCCCTAACCAACCGAACCCTTACGCGTTGAGAAGCTGAGGTGGTA 2520  
-----+-----+-----+-----+-----+-----+-----+  
TCGGGTTTTGAACGGGGATTGGTTGGCTTGGTGAAGTGCGCAACTCTTCGACTCCACCAT

2521 TCGGCAATGACCGATGCCGCGACAGCCCCAGTAGCTCCTGTGATCCCTGAAAGCAAACGG 2580  
-----+-----+-----+-----+-----+-----+-----+

AGCCGTTACTGGCTACGGCGCTGTCTGGGGTTCATCGAGGACACTAGGGACTTTTCGTTTGCC  
 CCTAAATACAGCATCCAAAGCGCACTTGAAAAAGCCAGCAATAAGTAATCCAGCGATGCG  
 2581 -----+-----+-----+-----+-----+-----+ 2640  
 GGATTTATGTCGTAGGTTTCGCGTGAACTTTTTCGGTCGTTATTCATTAGGTCGCTACGC  
 CCTATTAATGACAACAACAGCACTGGGCGCCGACCAAATCGGTCAGACATTTTTTCCAAGC  
 2641 -----+-----+-----+-----+-----+-----+ 2700  
 GGATAATTACTGTTGTTGTCGTGACCCGCGGCTGGTTTTAGCCAGTCTGTAAAAAGGTTTCG  
 CAAGGAGCAAAGATAACCTGCATTAACGCATAAAGTGCAAGCAATACGCCAAAGTGGTTA  
 2701 -----+-----+-----+-----+-----+-----+ 2760  
 GTTCCTCGTTTTCTATTGGACGTAATTGCGTATTTACGTTTCGTTATGCGGTTTCACCAAT  
  
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 GCGATATCTTCCGAAGCAATAAATTCACGTAATAACGTTGGCAAGACTGGCATGATAAGG  
 2761 -----+-----+-----+-----+-----+-----+ 2820  
 CGCTATAGAAGGCTTCGTTATTTAAGTGCATTATTGCAACCGTTCTGACCGTACTATTCC  
  
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 CCAATCCCCATGGCATCGAGTAACGTAATTACCAATGCGATCTTTGTGCGAATATTTCATT  
 2821 -----+-----+-----+-----+-----+-----+ 2880  
 GGTTAGGGGTACCGTAGCTCATTGCATTAATGGTTACGCTAGAAACAGCTTGATAAGTAA  
 TCACTTTTTCTCTATCACTGATAGGGAGTGGTAAAATAACTCTATCAATGATAGAGTGTCA  
 2881 -----+-----+-----+-----+-----+-----+ 2940  
 AGTGAAAAGAGATAGTGACTATCCCTCACCATTTTATTGAGATAGTTACTATCTCACAGT  
  
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 ACAAAAATTAGGAATTAATGATGTCTAGATTAGATAAAAAGTAAAGTGATTAACAGCGCAT  
 2941 -----+-----+-----+-----+-----+-----+ 3000  
 TGTTTTTAATCCTTAATTACTACAGATCTAATCTATTTTCATTTCACTAATTGTCGCGTA  
 TAGAGCTGCTTAATGAGGTCGGAATCGAAGGTTTAAACAACCCGTAAACTCGCCCAGAAGC  
 3001 -----+-----+-----+-----+-----+-----+ 3060  
 ATCTCGACGAATTACTCCAGCCTTAGCTTCCAAATTGTTGGGCATTTGAGCGGGTCTTCG  
 TAGGTGTAGAGCAGCCTACATTGTATTGGCATGTAAAAATAAGCGGGCTTTGCTCGACG  
 3061 -----+-----+-----+-----+-----+-----+ 3120  
 ATCCACATCTCGTCGGATGTAACATAACCGTACATTTTTTTATTGCCCCGAAACGAGCTGC

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CCTTAGCCATTGAGATGTTAGATAGGCACCATACTCACTTTTGCCCTTTAGAAGGGGAAA  
3121 -----+-----+-----+-----+-----+-----+ 3180  
GGAATCGGTAACCTCTACAATCTATCCGTGGTATGAGTGAAAACGGGAAATCTTCCCCTTT

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GCTGGCAAGATTTTTTACGTAATAACGCTAAAAGTTTTAGATGTGCTTTACTAAGTCATC  
3181 -----+-----+-----+-----+-----+-----+ 3240  
CGACCGTTCTAAAAAATGCATTATTGCGATTTTCAAATCTACACGAAATGATTCAGTAG

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GCGATGGAGCAAAGTACATTTAGGTACACGGCCTACAGAAAAACAGTATGAAACTCTCG  
3241 -----+-----+-----+-----+-----+-----+ 3300  
CGCTACCTCGTTTTTCATGTAAATCCATGTGCCGGATGTCTTTTTGTGCATACTTTGAGAGC

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AAAATCAATTAGCCTTTTTATGCCAACAAAGTTTTTCTACTAGAGAATGCATTATATGCAC  
3301 -----+-----+-----+-----+-----+-----+ 3360  
TTTTAGTTAATCGGAAAAATACGGTTGTTCCAAAAAGTGATCTCTTACGTAATATACGTG

TCAGCGCTGTGGGGCATTTTACTTTAGGTTGCGTATTGGAAGATCAAGAGCATCAAGTCG  
3361 -----+-----+-----+-----+-----+-----+ 3420  
AGTCGCGACACCCCGTAAAATGAAATCCAACGCATAACCTTCTAGTTCTCGTAGTTCAGC  
CTAAAGAAGAAAGGGAAACACCTACTACTGATAGTATGCCGCCATTATTACGACAAGCTA  
3421 -----+-----+-----+-----+-----+-----+ 3480  
GATTTCTTCTTTCCCTTTGTGGATGATGACTATCATACGGCGGTAATAATGCTGTTTCGAT

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TCGAATTATTTGATCACCAAGGTGCAGAGCCAGCCTTCTTATTGGCCTTGAATTGATCA  
3481 -----+-----+-----+-----+-----+-----+ 3540  
AGCTTAATAAACTAGTGGTTCCACGTCTCGGTCGGAAGAATAAGCCGGAACCTTAAGTAGT

TATGCGGATTAGAAAAACAACCTTAAATGTGAAAGTGGGTCTTAAAAGCAGCATAACCTTT  
3541 -----+-----+-----+-----+-----+-----+ 3600  
ATACGCCTAATCTTTTTGTTGAATTTACTTTTACCCAGAATTTTCGTCGTATTGGAAA

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3601 -----+-----+-----+-----+-----+-----+ 3660  
 TTCCGTGATGGTAACTTCACGGTAACCAAGATGTCGAGTTAACCACCCTTTAGATTTCATA  
 AAGGCACTACCATTGAAGTGCCATTGGTTCTACAGCTCAATTGGTGGGAAATCTAAGTAT

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3661 -----+-----+-----+-----+-----+ 3720  
 AAGCGAAAATAATGCGGCTCCAACGTACCCACCTAAATGGAAACGGCGTTCACTCCAATC  
 TTCGCTTTTATTACGCCGAGGTTGCATGGGTGGATTTACCTTTGCCGCAAGTGAGGTTAG

3721 -----+-----+-----+-----+-----+ 3780  
 TAAACACGCACAACAGATTTTACGTGAATGTTTGGAAAGGAACGTCAATTCCCATTTTCATG  
 ATTTGTGCGTGTTGTCTAAAATGCACTTACAAACCTTCCTTGCGAGTTAAGGGTAAAGTAC

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3781 -----+-----+-----+-----+-----+ 3840  
 AAAATATTGAATACCACTTAATGTGATCATTGAACCATTTTCAGTGATCCATTGCTGTTG  
 TTTTATAACTTATGGTGAATTACACTAGTAACCTTGGTAAAAGTCACTAGGTAACGACAAC

3841 -----+-----+-----+-----+-----+ 3900  
 ACAAAGGGAATCATAGATCCTGCAAGCCTCGTCGTCCTGGCCGGACCACGCTATCTGTGC  
 TGTTTCCCTTAGTATCTAGGACGTTTCGGAGCAGCAGGACCGGCCTGGTGCATAGACACG

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3901 -----+-----+-----+-----+-----+ 3960  
 AAGGTCCCCGGCCCCGGACGCGCGCTCCATGAGCAGAGCGCCCGCCGAGGCGAAGAC  
 TTCCAGGGGCCGGGCCTGCGCGCGAGGTAICTCGTCTCGCGGGCGGCGGCTCCGCTTCTG

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3961 -----+-----+-----+-----+-----+ 4020  
 TCGGGCGGCGCCCTGCCCCTCCACCAGGTCAACAGGCGGTAACCGGCCTTTCATCGGG  
 AGCCCCGCCGGGACGGGCAGGGTGGTCCAGTTGTCCGCCATTGGCCGGAGAAGTAGCCC

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AATGCGCGGACCTTCAGCATCGCCGGCATGTCCCCCTGGCGGACGGGAAGTATCCAGCT  
4021 -----+-----+-----+-----+-----+-----+ 4080  
TTACGCGCGCTGGAAGTCGTAGCGGCCGTACAGGGGGACCGCCTGCCCTTCATAGGTCTGA

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CGAGTGGGTGGTGGAGCAGCTCGCCGTGCGCGAGCAGGCGCCAGCGCTCCATCCACGCAGT  
4081 -----+-----+-----+-----+-----+-----+ 4140  
GCTCACCCACCACTCGTCGAGCGGCAGCGCGTCTCGCGGTGCGGAGGTAGGTGCGTCA

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GACCTCAGGCGGAAAACGGGAAGACACACTCATGAGATGCCTGCAAGCAATTCGTTCTGT  
4141 -----+-----+-----+-----+-----+-----+ 4200  
CTGGAGTCCGCCTTTTGCCCTTCTGTGTGAGTACTCTACGGACGTTTCGTTAAGCAAGACA

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ATCAGGCGCAGGAGCGTCCCGTCCGGTTCGAtcgaccaattcgaagttcctatactttct  
4201 -----+-----+-----+-----+-----+-----+ 4260  
TAGTCCGCGTCTCGCAGGGCAGGCCAGCTagctggttaagcttcaaggatatgaaaga

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agagaataggaacttcgggatccTCTACGCCGGACGCATCGTGGCCGGCATCACCGGCGC  
4261 -----+-----+-----+-----+-----+-----+ 4320  
tctcttatccttgaagccctaggAGATGCGGCCTGCGTAGCACCGGCCGTAGTGGCCGCG

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CACAGGTGCGGTTGCTGGCGCCTATATCGCCGACATCCACCGATGGGGAAGATCGGGCTC  
4321 -----+-----+-----+-----+-----+-----+ 4380  
GTGTCCACGCCAACGACCGCGGATATAGCGGCTGTAGGTGGCTACCCCTTCTAGCCCGAG

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4381 -----+-----+-----+-----+-----+-----+ 4440  
GCCACTTCGGGCTCATGAGCGCTTGTTCGGCGTGGGTATGGTGGCAGGCCCGTGGCCG  
CGGTGAAGCCCGAGTACTCGCGAACAAAGCCGCACCCATACCACCGTCCGGGGCACCGGC

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4441 -----+-----+-----+-----+-----+-----+ 4500  
GGGGACTGTTGGGCGCCATCTCCTTGCATGCACCATTCTTGCGGCGGGCGGTGCTCAACG  
CCCCTGACAACCCGCGGTAGAGGAACGTACGTGGTAAGGAACGCCGCCACGAGTTGC

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4501 -----+-----+-----+-----+-----+-----+ 4560  
GCCTCAACCTACTACTGGCGCTGCTTCCTAATGCAGGAGTCGCATAAGGGAGAGCGTCGA  
CGGAGTTGGATGATGACCGCGACGAAGGATTACGTCTCAGCGTATTCCCTCTCGCAGCT

4561 -----+-----+-----+-----+-----+-----+ 4620  
CCGATGCCCTTGAGAGCCTTCAACCCAGTCAGCTCCTTCCGGTGGGCGCGGGGCATGACT  
GGCTACGGGAACCTCTCGGAAGTTGGGTACGTAGGAAGGCCACCCGCGCCCCGTACTGA

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4621 -----+-----+-----+-----+-----+-----+ 4680  
ATCGTCGCCGCACTTATGACTGTCTTCTTTATCATGCAACTCGTAGGACAGGTGCCGGCA  
TAGCAGCGGCGTGAATACTGACAGAAGAAATAGTACGTTGAGCATCCTGTCCACGGCCGT

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4681 -----+-----+-----+-----+-----+-----+ 4740  
GCGCTCTGGGTCATTTTTCGGCGAGGACCGCTTTCGCTGGAGCGCGACGATGATCGGCCTG  
CGCGAGACCCAGTAAAAGCCGCTCCTGGCGAAAGCGACCTCGCGCTGCTACTAGCCGGAC

4741 -----+-----+-----+-----+-----+-----+ 4800  
TCGCTTGGGTATTTCGGAATCTTGCACGCCCTCGCTCAAGCCTTCGTCAGTGGTCCCGCC  
AGCGAACGCCATAAGCCTTAGAACGTGCGGGAGCGAGTTCGGAAGCAGTGACCAGGGCGG

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4801 -----+-----+-----+-----+-----+-----+ 4860  
ACCAAACGTTTTTCGGCGAGAAGCAGGCCATTATCGCCGGCATGGCGGCCGACGCGCTGGGC

TGGTTTGCAAAGCCGCTCTTCGTCCGTAATAGCGGCCGTACCGCCGGCTGCGCGACCCG

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ATGCAGAACGACCGCAAGCGCTGCGCTCCGACCTACCGGAAGGGGTAATACTAAGAAGAG

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4921 GCTTCCGGCGGCATCGGGATGCCCGCTTGCAGGCCATGCTGTCCAGGCAGGTAGATGAC 4980  
-----+-----+-----+-----+-----+-----+  
CGAAGGCCCGCCGTAGCCCTACGGGCGCAACGTCCGGTACGACAGGTCCGTCCATCTACTG

4981 GACCATCAGGGACAGCTTCAAGGATCGCTCGCGGCTCTTACCAGCCTAACTTCGATCACT 5040  
-----+-----+-----+-----+-----+-----+  
CTGGTAGTCCCTGTGCGAAGTTCCTAGCGAGCGCCGAGAATGGTTCGGATTGAAGCTAGTGA

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5041 GGACCGCTGATCGTACGCGGATTTATGCCGCCTCGGCGAGCACATGGAACGGGTTGGCA 5100  
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CCTGGCGACTAGCAGTGCCGCTAAATACGGCGGAGCCGCTCGTGTACCTTGCCCAACCGT

5101 TGGATTGTAGGCGCCGCCCTATACCTTGTCTGCCTCCCCGCGTTGCGTCGCGGTGCATGG 5160  
-----+-----+-----+-----+-----+-----+  
ACCTAACATCCGCGGCGGGATATGGAACAGACGGAGGGGCGCAACGCAGCGCCACGTACC

5161 AGCCGGGCCACCTCGACCTGAATGGAAGCCGGCGGCACCTCGCTAACGGATTACCACTC 5220  
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TCGGCCCGGTGGAGCTGGACTTACCTTCGGCCCGCTGGAGCGATTGCCTAAGTGGTGAG

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5221 CAAGAATTGGAGCCAATCAATTCTTGCGGAGAAGTGTGAATGCGCAAACCAACCCTTGGC 5280  
-----+-----+-----+-----+-----+-----+  
GTTCTTAACCTCGGTTAGTTAAGAACGCCTCTTGACACTTACGCGTTTGGTTGGGAACCG

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5281 AGAACATATCCATCGCGTCCGCCATCTCCAGCAGCCGCACGCGGCATCGCGTTGCTGG 5340  
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TCTTGTATAGGTAGCGCAGGCGGTAGAGGTCGTCGGCGTGCGCCGCTAGCGCAACGACC

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CGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGA  
5341 -----+-----+-----+-----+-----+-----+-----+ 5400  
GCAAAAAGGTATCCGAGGCGGGGGACTGCTCGTAGTGTTTTTAGCTGCGAGTTCAGTCT

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GGTGGCGAAACCCGACAGGACTATAAAGATAACCAGGCGTTTCCCCCTGGAAGCTCCCTCG  
5401 -----+-----+-----+-----+-----+-----+ 5460  
CCACCGCTTTGGGCTGTCCTGATATTTCTATGGTCCGCAAAGGGGGACCTTCGAGGGAGC

TGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGG  
5461 -----+-----+-----+-----+-----+-----+ 5520  
ACGCGAGAGGACAAGGCTGGGACGGCGAATGGCCTATGGACAGGCGAAAGAGGGGAAGCC

GAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTT  
5521 -----+-----+-----+-----+-----+-----+ 5580  
CTTCGCACCGCGAAAGAGTATCGAGTGCGACATCCATAGAGTCAAGCCACATCCAGCAAG

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GCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTTCAGCCCGACCGCTGCGCCTTATCCG  
5581 -----+-----+-----+-----+-----+-----+ 5640  
CGAGGTTTCGACCCGACACACGTGCTTGGGGGGCAAGTCGGGCTGGCGACGCGGAATAGGC

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GTA ACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCA  
5641 -----+-----+-----+-----+-----+-----+ 5700  
CATTGATAGCAGAACTCAGGTTGGGCCATTCTGTGCTGAATAGCGGTGACCGTCTGTCGGT

CTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGT  
5701 -----+-----+-----+-----+-----+-----+ 5760  
GACCATTGTCCTAATCGTCTCGCTCCATACATCCGCCACGATGTCTCAAGAACTTCACCA

GGCCTAACTACGGCTACACTAGAAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAG  
5761 -----+-----+-----+-----+-----+-----+ 5820  
CCGGATTGATGCCGATGTGATCTTCTGTGTCATAAACCATAGACGCGAGACGACTTCGGTC

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5821 TTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCG 5880  
 -----+-----+-----+-----+-----+-----+  
 AATGGAAGCCTTTTTCTCAACCATCGAGAACTAGGCCGTTTGTGGTGGCGACCATCGC

5881 GTGGTTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATC 5940  
 -----+-----+-----+-----+-----+-----+  
 CACCAAAAAAACAACGTTTCGTCTAATGCGCGTCTTTTTTCTTAGAGTTCTTCTAG

5941 CTTTGATCTTTTCTACGGGTCTGACGCTCAGTGGAACGAAAACCTCACGTTAAGGGATTT 6000  
 -----+-----+-----+-----+-----+-----+  
 GAAACTAGAAAAGATGCCCCAGACTGCGAGTCACCTTGCTTTTGAGTGCAATTCCTAAA

6001 TGGTCATGAGATTATCAAAAAGGATCTTACCTAGATCCTTTTAAATTAATAATGAAGTT 6060  
 -----+-----+-----+-----+-----+-----+  
 ACCAGTACTCTAATAGTTTTTCTAGAAAGTGGATCTAGGAAAATTTAATTTTACTTCAA

6061 TTAAATCAATCTAAAGTATATATGAGTAACTTGGTCTGACAGTTACCAATGCTTAATCA 6120  
 -----+-----+-----+-----+-----+-----+  
 AATTTAGTTAGATTTTCATATATACTCATTTGAACCAGACTGTCAATGGTTACGAATTAGT

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6121 GTGAGGCACCTATCTCAGCGATCTGTCTATTTTCGTTTCATCCATAGTTGCCTGACTCCCCG 6180  
 -----+-----+-----+-----+-----+-----+  
 CACTCCGTGGATAGAGTCGCTAGACAGATAAAGCAAGTAGGTATCAACGGACTGAGGGGC

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6181 TCGTGTAGATAACTACGATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATAC 6240  
 -----+-----+-----+-----+-----+-----+  
 AGCACATCTATTGATGCTATGCCCTCCCGAATGGTAGACCGGGGTCACGACGTTACTATG

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6241 CGCGAGACCCACGCTCACCGGCTCCAGATTTATCAGCAATAAACCAGCCAGCCGGAAGGG 6300  
 -----+-----+-----+-----+-----+-----+  
 GCGCTCTGGGTGCGAGTGGCCGAGGTCTAAATAGTCGTTATTTGGTCGGTCGGCCTTCCC

6301 CCGAGCGCAGAAGTGGTCCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCC 6360  
-----+-----+-----+-----+-----+-----+  
GGCTCGCGTCTTCACCAGGACGTTGAAATAGGCGGAGGTAGGTGAGATAATTAACAACGG

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6361 GGAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTGCACAACGTTGTTGCCATTGCTG 6420  
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CCCTTCGATCTCATTTCATCAAGCGGTCAATTATCAAACGCGTTGCAACAACGGTAACGAC

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6421 CAGGCATCGTGGTGTACGCTCGTCGTTTGGTATGGCTTCATTGAGCTCCGGTTCCCAAC 6480  
-----+-----+-----+-----+-----+-----+  
GTCCGTAGCACACAGTGCGAGCAGCAAACCATACCGAAGTAAGTCGAGGCCAAGGGTTG

6481 GATCAAGGCGAGTTACATGATCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTC 6540  
-----+-----+-----+-----+-----+-----+  
CTAGTTCGGCTCAATGTACTAGGGGTACAACACGTTTTTTTCGCCAATCGAGGAAGCCAG

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6541 CTCCGATCGTTGTCAGAAGTAAGTTGGCCGAGTGTATCACTCATGGTTATGGCAGCAC 6600  
-----+-----+-----+-----+-----+-----+  
GAGGCTAGCAACAGTCTTCATTCAACCGGCGTCACAATAGTGAGTACCAATACCGTCGTG

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6601 TGCATAATTCTCTTACTGTCATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACT 6660  
-----+-----+-----+-----+-----+-----+  
ACGTATTAAGAGAATGACAGTACGGTAGGCATTCTACGAAAAGACACTGACCACTCATGA

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6661 CAACCAAGTCATTCTGAGAATAGTGTATGCGGCGACCGAGTTGCTCTTGCCCGGCGTCAA 6720  
-----+-----+-----+-----+-----+-----+  
GTTGGTTCAGTAAGACTCTTATCACATACGCCGCTGGCTCAACGAGAACGGGCCGAGTT

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6721 CACGGGATAATACCGCGCCACATAGCAGAACTTTAAAAGTGCTCATCATTGAAAACGTT 6780  
-----+-----+-----+-----+-----+-----+  
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GTGCCCTATTATGGCGCGGTGTATCGTCTTGAAATTTTCACGAGTAGTAACCTTTTGCAA  
 CTTTCGGGGCGAAAACCTCTCAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAACCCA  
 6781 -----+-----+-----+-----+-----+-----+-----+ 6840  
 GAAGCCCCGCTTTTGAGAGTTCCTAGAAATGGCGACAACCTCTAGGTCAAGCTACATTGGGT  
  
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 CTCGTGCACCCAACTGATCTTCAGCATCTTTTACTTTTACCAGCGTTTCTGGGTGAGCAA  
 6841 -----+-----+-----+-----+-----+-----+ 6900  
 GAGCACGTGGGTTGACTAGAAGTCGTAGAAAATGAAAGTGGTTCGCAAAGACCCACTCGTT  
  
 AAACAGGAAGGCAAAATGCCGCAAAAAAGGGAATAAGGGCGACACGGAAATGTTGAATAC  
 6901 -----+-----+-----+-----+-----+-----+ 6960  
 TTTGTCCTTCCGTTTTACGGCGTTTTTTCCCTTATTCCCGCTGTGCCTTTACAACCTTATG  
  
  
  
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 TCATACTCTTCCTTTTTCAATATTATTGAAGCATTATCAGGGTTATTGTCTCATGAGCG  
 6961 -----+-----+-----+-----+-----+-----+ 7020  
 AGTATGAGAAGGAAAAAGTTATAATAACTTCGTAAATAGTCCCAATAACAGAGTACTCGC  
  
 GATACATATTTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCC  
 7021 -----+-----+-----+-----+-----+-----+ 7080  
 CTATGTATAAACTTACATAAATCTTTTTATTTGTTTATCCCCAAGGCGCGTGTAAGGGG  
  
  
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 GAAAAGTGCCACCTGACGTCTAAGAAACCATTATTATCATGACATTAACCTATAAAAATA  
 7081 -----+-----+-----+-----+-----+-----+ 7140  
 CTTTTACGGTGGACTGCAGATTCTTTGGTAATAATAGTACTGTAATTGGATATTTTTAT  
  
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 GGCGTATCACGAGGCCCTTTCGTCTTCAA  
 7141 -----+-----+-----+-----+-----+ 7169  
 CCGCATAGTGCTCCGGGAAAGCAGAAGTT

Enzymes that do cut:

AatII	AccI	AciI	AflIII	AgeI	AluI	AlwI	Alw21I
Alw44I	AlwNI	ApaBI	ApoI	AvaI	AvaII	BaeI	BamHI
BanI	BanII	BbsI	BbvI	BccI	Bce83I	BcefI	BcgI
BcgI	BclI	BfaI	BglI	BglII	BpmI	Bpu10I	Bpu1102I
BsaI	BsaAI	BsaBI	BsaHI	BsaJI	BsaWI	BsBI	BscGI



BsgI	BsiI	BsiEI	BslI	BsmI	BsmAI	BsmBI	BsmFI
BsoFI	Bsp24I	Bsp24I	Bsp1286I	BspGI	BspMI	BsrI	BsrBI
BsrDI	BsrFI	BssHII	Bst1107I	BstEII	BstXI	BstYI	Bsu36I
Cac8I	CjeI	CjeI	CjePI	CjePI	ClaI	CviJI	CviRI
DdeI	DpnI	DraI	DraIII	DrdI	DrdII	DsaI	EaeI
EagI	Eam1105I	EarI	EciI	Eco47III	Eco57I	EcoNI	EcoO109I
EcoRI	EcoRII	EcoRV	FauI	FokI	FspI	GdiII	HaeI
HaeII	HaeIII	HgaI	HgiEII	HhaI	HincII	HindIII	HinfI
HpaI	HphI	KpnI	MaeII	MaeIII	MboII	MluI	MmeI
MnlI	MseI	MslI	MspI	MspAI	MunI	MwoI	NarI
NciI	NcoI	NdeI	NgoAIV	NlaIII	NlaIV	NruI	NsiI
NspI	NspV	Pfl1108I	PflMI	PleI	PmeI	PmlI	PshAI
Psp5II	Psp1406I	PstI	PvuI	PvuII	RcaI	RleAI	RsaI
RsrII	SacII	SalI	Sau96I	Sau3AI	ScaI	ScrFI	SexAI
SfaNI	SfcI	SgrAI	SnaBI	SphI	SspI	StyI	TaqI
TaqII	TaqII	TfiI	ThaI	TseI	Tsp45I	Tsp509I	Tth111II
VspI	XbaI	XcmI	XhoI	XmnI			

Enzymes that do not cut:

AflII	ApaI	AscI	AvrII	BseRI	BspEI	BspLU11I	BsrGI
FseI	MscI	NheI	NotI	PacI	SacI	SapI	SfiI
SgfI	SmaI	SpeI	SrfI	Sse8387I	StuI	SunI	SwaI
Tth111I							

Enzymes excluded; MinCuts: 1 MaxCuts: 3

AccI	AciI	AluI	AlwI	Alw21I	ApaBI	ApoI	AvaII
BanI	BbsI	BbvI	BccI	Bce83I	BcefI	BcgI	BcgI
BfaI	BglI	BsaAI	BsaHI	BsaJI	BsaWI	BscGI	BsiEI
BslI	BsmI	BsmAI	BsmFI	BsoFI	Bsp24I	Bsp24I	Bsp1286I
BspMI	BsrI	BsrDI	BsrFI	BstEII	BstYI	Cac8I	CjeI
CjeI	CjePI	CjePI	CviJI	CviRI	DdeI	DpnI	DraI
DsaI	EaeI	EciI	Eco47III	Eco57I	EcoO109I	EcoRII	FauI
FokI	GdiII	HaeI	HaeII	HaeIII	HgaI	HhaI	HincII
HinfI	HphI	MaeII	MaeIII	MboII	MmeI	MnlI	MseI
MslI	MspI	MspAI	MwoI	NarI	NciI	NgoAIV	NlaIII
NlaIV	NspI	PleI	Psp1406I	RcaI	RsaI	Sau96I	Sau3AI
ScrFI	SfaNI	SfcI	StyI	TaqI	TaqII	TaqII	TfiI
ThaI	TseI	Tsp45I	Tsp509I	Tth111II	VspI		