

(Circular) MAP of: Peaw116.Seq check: 4303 from: 1 to: 5850

>>>pJS39

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With 191 enzymes: \*

MaxCuts: 3

January 26, 1994 13:42 ..

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gaattcgaagttcctatacttttctagagaataggaacttcggggatcggcccatcgataa
1  -----+-----+-----+-----+-----+-----+-----+ 60
cttaagcttcaaggatatgaaagatctcttatccttgaaggccctagccgggtagctatt

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gcttgggtaccggggcggccgctagcagatctagcttATGATAGTGATGTGCTTAAAAACT
61  -----+-----+-----+-----+-----+-----+ 120
cgaaccatggggcccgccggcgatcgtctagatcgaaTACTATCACTACACGAATTTTTGA

                N
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TACTCAATGGCTGGTTTTATGCATATCGCAATACATGCGAAAAACCTAAAAGAGCTTGCCG
121 -----+-----+-----+-----+-----+-----+ 180
ATGAGTTACCGACCAAATACGTATAGCGTTATGTACGCTTTTTGGATTTTCTCGAACGGC

                S
                D a
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ATAAAAAAGGCCAATTTATTGCTATTTACCGCGGCTTTTTATTGAGCTTGAAAGATAAAT
181 -----+-----+-----+-----+-----+-----+ 240
TATTTTTTCCGGTTAAATAACGATAAATGGCGCCGAAAAATAACTCGAACTTTCTATTTA

AAAATAGATAGGTTTTATTTGAAGCTAAATCTTCTTTATCGTAAAAAATGCCCTCTTGGG
241 -----+-----+-----+-----+-----+-----+ 300
TTTTATCTATCCAAAATAAACTTCGATTTAGAAGAAATAGCATTTTTTTACGGGAGAACCC

TTATCAAGAGGGTCATTATATTTTCGCGGAATAACATCATTTGGTGACGAAATAACTAAGC
301 -----+-----+-----+-----+-----+-----+ 360
AATAGTTCTCCCAGTAATATAAAGCGCCTTATTGTAGTAAACCACTGCTTTATTGATTTCG

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361 -----+-----+-----+-----+-----+-----+ 420  
 ACTTGTCTCCTGTTTACTCCCCTGAGCTTGAGGGGTTAACATGAAGGTCATCGATAGCAG  
 TGAACAGAGGACAAATGAGGGGACTCGAACTCCCCAATTGTA CTCCAGTAGCTATCGTC

421 -----+-----+-----+-----+-----+-----+ 480  
 GATAATAATACAGTAAAACGCTAAACCAATAATCCAAATCCAGCCATCCCAAATTGGTAG  
 CTATTATTATGTCATTTTGC GATTTGGTTATTAGGTTTAGGTCGGTAGGGTTTAACCATC

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481 -----+-----+-----+-----+-----+-----+ 540  
 TGAATGATTATAAATAACAGTAAACAGTAATGGGCCAATAACACCGGTTGCATTGGTAAG  
 ACTTACTAATATTTATTGTCATTTGTCATTACCCGGTTATTGTGGCCAACGTAACCATTC

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541 -----+-----+-----+-----+-----+-----+ 600  
 GCTCACCAATAATCCCTGTAAAGCACCTTGCTCATGACTCTTTGTTTGGATAGACATCAC  
 CGAGTGGTTATTAGGGACATTTTCGTGGAACGAGTACTGAGAAACAAACCTATCTGTAGTG

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601 -----+-----+-----+-----+-----+-----+ 660  
 TCCCTGTAATGCAGGTAAAGCGATCCCACCACCAGCCAATAAAAATTAAAACAGGGAAATC  
 AGGGACATTACGTCCATTTTCGCTAGGGTGGTGGTTCGGTTATTTTAATTTTGTCCCTTTAG

661 -----+-----+-----+-----+-----+-----+ 720  
 TAACCAACCTTCAGATATAAACGCTAAAAAGGCAAATGCACTACTATCTGCAATAAATTC  
 ATTGTTGGAAGTCTATATTTGCGATTTTCCGTTTACGTGATGATAGACGTTATTTAAG

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721 -----+-----+-----+-----+-----+-----+ 780  
 GAGCAGTACTGCCGTTTTTTTCGCCCCATTTAGTGGCTATTCTTCTGCCACAAAGGCTTG  
 CTCGTCATGACGGCAAAAAAGCGGGTAAATCACCGATAAGAAGGACGGTGTTC CGAAC

781 -----+-----+-----+-----+-----+-----+ 840  
 GAATACTGAGTGTA AAAAGACCAAGACCCGCTAATGAAAAGCCAACCATCATGCTATTCCA  
 CTTATGACTCACATTTTCTGGTTCTGGGCGATTACTTTTCGGTTGGTAGTACGATAAGGT

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841 TCCAAAACGATTTTCGGTAAATAGCACCCACACCGTTGCGGGAATTTGGCCTATCAATTG 900  
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AGGTTTTGCTAAAAGCCATTTATCGTGGGTGTGGCAACGCCCTTAAACCGGATAGTTAAC

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901 CGCTGAAAAATAAATAATCAACAAAATGGGCATCGTTTTAAATAAAGTGATGTATACCGA 960  
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GCGACTTTTTATTTATTAGTTGTTTTACCCGTAGCAAAATTTATTTCACTACATATGGCT

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961 ATTCGATTGCGTCTCAACCCCTACTTCGGTATCTGTATTATCACGTGTATTTTTGGTTTT 1020  
-----+-----+-----+-----+-----+-----+  
TAAGCTAACGCAGAGTTGGGGATGAAGCCATAGACATAATAGTGCACATAAAAACCAAAG

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1021 ACGGAACCAAAACATAACCACAAGGAAAGTGACAATATTTAGCAACGCAGCGATAAAAAA 1080  
-----+-----+-----+-----+-----+-----+  
TGCCTTGGTTTTGTATTGGTGTTCCTTTCACTGTTATAAATCGTTGCGTCGCTATTTTTT

1081 GGGACTATGCGGTGAAATCTCTCCTGCAAAACCACCAATAATAGGCCCGCTATTAACC 1140  
-----+-----+-----+-----+-----+-----+  
CCCTGATACGCCACTTTAGAGAGGACGTTTTGGTGGTTATTATCCGGGGCGATAATTTGG

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1141 AAGCCCAAACTTGCCCCTAACCAACCGAACCCTTACGCGTTGAGAAGCTGAGGTGGT 1200  
-----+-----+-----+-----+-----+-----+  
TTCGGGTTTTGAACGGGGATTGGTTGGCTTGGTGAAGTGCGCAACTCTTCGACTCCACCA

1201 ATCGGCAATGACCGATGCCGCGACAGCCCCAGTAGCTCCTGTGATCCCTGAAAGCAAACG 1260  
-----+-----+-----+-----+-----+-----+  
TAGCCGTTACTGGCTACGGCGCTGTCGGGGTCATCGAGGACACTAGGGACTTTTCGTTTTGC

GCCTAAATACAGCATCCAAAGCGCACTTGAAAAAGCCAGCAATAAGTAATCCAGCGATGC  
1261 -----+-----+-----+-----+-----+-----+ 1320  
CGGATTTATGTCGTAGGTTTCGCGTGAACTTTTTCGGTTCGTTATTCATTAGGTCGCTACG

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GCCTATTAATGACAACAACAGCACTGGGCGCCGACCAAATCGGTCAGACATTTTTTCCAAG  
1321 -----+-----+-----+-----+-----+-----+ 1380  
CGGATAATTACTGTTGTTGTCGTGACCCGCGGCTGGTTTTAGCCAGTCTGTAAAAAGGTTTC

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CCAAGGAGCAAAGATAACCTGCATTAACGCATAAAGTGCAAGCAATACGCCAAAGTGGTT  
1381 -----+-----+-----+-----+-----+-----+ 1440  
GGTTCCTCGTTTTCTATTGGACGTAATTGCGTATTTACGTTTCGTTATGCGGTTTTACCAA

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AGCGATATCTTCCGAAGCAATAAATTCACGTAATAACGTTGGCAAGACTGGCATGATAAG  
1441 -----+-----+-----+-----+-----+-----+ 1500  
TCGCTATAGAAGGCTTCGTTATTTAAGTGCATTATTGCAACCGTTCTGACCGTACTATTC

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GCCAATCCCCATGGCATCGAGTAACGTAATTACCAATGCGATCTTTGTCGAACTATTCAT  
1501 -----+-----+-----+-----+-----+-----+ 1560  
CGGTTAGGGGTACCGTAGCTCATTGCATTAATGGTTACGCTAGAAACAGCTTGATAAGTA

TTCACTTTTTCTCTATCACTGATAGGGAGTGGTAAAATAACTCTATCAATGATAGAGTGTC  
1561 -----+-----+-----+-----+-----+-----+ 1620  
AAGTGAAAAGAGATAGTGACTATCCCTCACCATTTTATTGAGATAGTTACTATCTCACAG

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AACAAAAATTAGGAATTAATGATGTCTAGATTAGATAAAAAGTAAAGTGATTAACAGCGCA  
1621 -----+-----+-----+-----+-----+-----+ 1680  
TTGTTTTTAAATCCTTAATTACTACAGATCTAATCTATTTTCATTTCACTAATTGTCGCGT

TTAGAGCTGCTTAATGAGGTCGGAATCGAAGGTTTAAACAACCCGTAAACTCGCCCAGAAG  
1681 -----+-----+-----+-----+-----+-----+ 1740  
AATCTCGACGAATTACTCCAGCCTTAGCTTCCAAATTGTTGGGCATTTGAGCGGGTCTTC

CTAGGTGTAGAGCAGCCTACATTGTATTGGCATGTAAAAATAAGCGGGCTTTGCTCGAC  
1741 -----+-----+-----+-----+-----+-----+ 1800  
GATCCACATCTCGTCGGATGTAACATAACCGTACATTTTTTTATTTCGCCCGAAACGAGCTG

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GCCTTAGCCATTGAGATGTTAGATAGGCACCATACTCACTTTTGGCCCTTTAGAAGGGGAA  
1801 -----+-----+-----+-----+-----+-----+ 1860  
CGGAATCGGTAACTCTACAATCTATCCGTGGTATGAGTGAAAACGGGAAATCTTCCCCTT

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AGCTGGCAAGATTTTTTACGTAATAACGCTAAAAGTTTTAGATGTGCTTTACTAAGTCAT  
1861 -----+-----+-----+-----+-----+-----+ 1920  
TCGACCGTTCTAAAAAATGCATTATTGCGATTTTCAAAATCTACACGAAATGATTCAGTA

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CGCGATGGAGCAAAAGTACATTTAGGTACACGGCCTACAGAAAAACAGTATGAAACTCTC  
1921 -----+-----+-----+-----+-----+-----+ 1980  
GCGCTACCTCGTTTTTCATGTAAATCCATGTGCCGGATGTCTTTTTGTCATACTTTGAGAG

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GAAAATCAATTAGCCTTTTTATGCCAACAAAGTTTTTCACTAGAGAATGCATTATATGCA  
1981 -----+-----+-----+-----+-----+-----+ 2040  
CTTTTAGTTAATCGGAAAAATACGGTTGTTCCAAAAAGTGATCTCTTACGTAATATACGT

CTCAGCGCTGTGGGGCATTTTACTTTAGGTTGCGTATTGGAAGATCAAGAGCATCAAGTC  
2041 -----+-----+-----+-----+-----+-----+ 2100  
GAGTCGCGACACCCCGTAAAATGAAATCCAACGCATAACCTTCTAGTTCTCGTAGTTCAG

GCTAAAGAAGAAAGGGAAACACCTACTACTGATAGTATGCCGCCATTATTACGACAAGCT  
2101 -----+-----+-----+-----+-----+-----+ 2160  
CGATTTCTTCTTTCCCTTTGTGGATGATGACTATCATAACGGCGGTAATAATGCTGTTCTGA

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ATCGAATTATTTGATCACCAAGGTGCAGAGCCAGCCTTCTTATTCGGCCTTGAATTGATC  
2161 -----+-----+-----+-----+-----+-----+ 2220  
TAGCTTAATAAACTAGTGGTTCCACGTCTCGGTCGGAAGAATAAGCCGGAACCTTAAGTAACTAG

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2221 ATATGCGGATTAGAAAAACAACCTTAAATGTGAAAGTGGGTCTTAAAAGCAGCATAACCTT 2280  
-----+-----+-----+-----+-----+-----+  
TATACGCCTAATCTTTTTGTTGAATTTACACTTTCACCCAGAATTTTCGTCGTATTGGAA

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2281 TTTCCGTGATGGTAACTTCACGGTAACCAAGATGTCGAGTTAACCACCTTTAGATTCAT 2340  
-----+-----+-----+-----+-----+-----+  
AAAGGCACTACCATTGAAGTGCCATTGGTTCTACAGCTCAATTGGTGGGAAATCTAAGTA

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2341 AAAGCGAAAATAATGCGGCTCCAACGTACCCACCTAAATGGAAACGGCGTTCCTCAAT 2400  
-----+-----+-----+-----+-----+-----+  
TTTCGCTTTTATTACGCCGAGGTTGCATGGGTGGATTTACCTTTGCCGCAAGTGAGGTTA

2401 CTAAACACGCACAACAGATTTTACGTGAATGTTTGAAGGAACGTCAATTCCCATTTTCAT 2460  
-----+-----+-----+-----+-----+-----+  
GATTTGTGCGTGTTGTCTAAAATGCACTTACAAACCTTCCTTGCAGTTAAGGGTAAAGTA

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2461 GAAAATATTGAATACCACTTAATGTGATCATTGAACCATTTTCAGTGATCCATTGCTGTT 2520  
-----+-----+-----+-----+-----+-----+  
CTTTTATAACTTATGGTGAATTACACTAGTAACTTGGTAAAAGTCACTAGGTAACGACAA

2521 GACAAAGGGAATCATAGATCCTGCAAGCCTCGTCGTCCTGGCCGGACCACGCTATCTGTG 2580  
-----+-----+-----+-----+-----+-----+  
CTGTTTCCCTTAGTATCTAGGACGTTCCGGAGCAGCAGGACCGGCCTGGTGCGATAGACAC

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2581 CAAGGTCCCCGGCCCCGGACGCGCGCTCCATGAGCAGAGCGCCCCGCCGCGAGGCGAAGA 2640  
-----+-----+-----+-----+-----+-----+  
GTTCCAGGGGCCGGGCCTGCGCGCGAGGTAICTGTCGCGGGCGGCGGCTCCGCTTCT

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2641 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2700

CTCGGGCGGGCGCCCTGCCCCGTCCCACCAGGTCAACAGGCGGTAAACCGGCCTCTTCATCGG  
GAGCCCCGCCGCGGGACGGGCAGGGTGGTCCAGTTGTCCGCCATTGGCCGGAGAAGTAGCC

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2701 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 2760

GAATGCGCGCGACCTTCAGCATCGCCGGCATGTCCCCCTGGCGGACGGGAAGTATCCAGC  
CTTACGCGCGCTGGAAGTCGTAGCGGCCGTACAGGGGGACCGCCTGCCCTTCATAGGTCG

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2761 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 2820

TCGAGTGGGTGGTGAGCAGCTCGCCGTCGCGCAGCAGGCGCCAGCGCTCCATCCACGCAG  
AGCTCACCCACCACTCGTCGAGCGGCAGCGCGTCGTCCGCGGTTCGCGAGGTAGGTGCGTC

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2821 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 2880

TGACCTCAGGCGGAAAACGGGAAGACACACTCATGAGATGCCTGCAAGCAATTCGTTCTG  
ACTGGAGTCCGCCTTTTGCCTTCTGTGTGAGTACTCTACGGACGTTTCGTTAAGCAAGAC

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2881 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 2940

TATCAGGCGCAGGAGCGTCCCGTCCGGGTCGAtcgaccaattcgaagttcctatactttc  
ATAGTCCGCGTCCTCGCAGGGCAGGCCAGCTagctggttaagcttcaaggatatgaaag

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2941 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 3000

tagagaataggaacttcgggatccTCTACGCCGACGCATCGTGGCCGGCATCACCGGCG  
atctcttatccttgaagccctaggAGATGCGGCCTGCGTAGCACCGGCCGTAGTGGCCGC

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3001 -----+-----+-----+-----+-----+-----+-----+ 3060  
 CCACAGGTGCGGTTGCTGGCGCCTATATCGCCGACATCCACCGATGGGGAAGATCGGGCT  
 GGTGTCCACGCCAACGACCGCGGATATAGCGGCTGTAGGTGGCTACCCCTTCTAGCCCGA

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3061 -----+-----+-----+-----+-----+-----+ 3120  
 CGCCACTTCGGGCTCATGAGCGCTTGTTTTCGGCGTGGGTATGGTGGCAGGCCCCGTGGCC  
 GCGGTGAAGCCCGAGTACTCGCGAACAAAGCCGCACCCATAACCACCGTCCGGGGCACC

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3121 -----+-----+-----+-----+-----+-----+ 3180  
 GGGGACTGTTGGGCGCCATCTCCTTGATGCACCATTCTTGCGGGCGGCTGCTCAAC  
 CCCCCTGACAACCCGCGGTAGAGGAACGTACGTGGTAAGGAACGCCGCCACGAGTTG

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3181 -----+-----+-----+-----+-----+-----+ 3240  
 GGCCTCAACCTACTACTGGCGCTGCTTCTTAATGCAGGAGTCGCATAAGGGAGAGCGTCG  
 CCGGAGTTGGATGATGACCGCGACGAAGGATTACGTCCTCAGCGTATTCCCTCTCGCAGC

3241 -----+-----+-----+-----+-----+-----+ 3300  
 ACCGATGCCCTTGAGAGCCTTCAACCCAGTCAGCTCCTTCCGGTGGGCGCGGGGCATGAC  
 TGGCTACGGGAACCTCTCGGAAGTTGGGTGAGTCGAGGAAGGCCACCCGCGCCCCGTACTG

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3301 -----+-----+-----+-----+-----+-----+ 3360  
 TATCGTCGCCGCACTTATGACTGTCTTCTTTATCATGCAACTCGTAGGACAGGTGCCGGC  
 ATAGCAGCGGCGTGAATACTGACAGAAGAAATAGTACGTTGAGCATCCTGTCCACGGCCG



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3361 AGCGCTCTGGGTCATTTTCGGCGAGGACCGCTTTTCGCTGGAGCGCGACGATGATCGGCCT 3420  
 -----+-----+-----+-----+-----+-----+-----+  
 TCGCGAGACCCAGTAAAAGCCGCTCCTGGCGAAAGCGACCTCGCGCTGCTACTAGCCGGA

3421 GTCGCTTGCGGTATTTCGGAATCTTGCACGCCCTCGCTCAAGCCTTCGTCACTGGTCCCGC 3480  
 -----+-----+-----+-----+-----+-----+-----+  
 CAGCGAACGCCATAAGCCTTAGAACGTGCGGGAGCGAGTTTCGGAAGCAGTGACCAGGGCG

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3481 CACCAAACGTTTCGGCGAGAAGCAGGCCATTATCGCCGGCATGGCGGGCCGACGCGCTGGG 3540  
 -----+-----+-----+-----+-----+-----+-----+  
 GTGGTTTGCAAAGCCGCTCTTCGTCCGGTAATAGCGGCCGTACCGCCGGCTGCGCGACCC

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3541 CTACGTCTTGCTGGCGTTTCGCGACGCGAGGCTGGATGGCCTTCCCCATTATGATTCTTCT 3600  
 -----+-----+-----+-----+-----+-----+-----+  
 GATGCAGAACGACCGCAAGCGCTGCGCTCCGACCTACCGGAAGGGGTAATACTAAGAAGA

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3601 CGCTTCCGGCGGCATCGGGATGCCCGCCTTGCAGGCCATGCTGTCCAGGCAGGTAGATGA 3660  
 -----+-----+-----+-----+-----+-----+-----+  
 GCGAAGGCCCGCCGTAGCCCTACGGGCGCAACGTCCGGTACGACAGGTCCGTCCATCTACT

3661 CGACCATCAGGGACAGCTTCAAGGATCGCTCGCGGCTCTTACCAGCCTAACTTCGATCAC 3720  
 -----+-----+-----+-----+-----+-----+-----+  
 GCTGGTAGTCCCTGTGCGAAGTTCCTAGCGAGCGCCGAGAATGGTTCGGATTGAAGCTAGTG

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3721 TGGACCGCTGATCGTACGGCGATTTATGCCGCCTCGGCGAGCACATGGAACGGGTTGGC 3780  
 -----+-----+-----+-----+-----+-----+-----+  
 ACCTGGCGACTAGCAGTGCCGCTAAATACGGCGGAGCCGCTCGTGTACCTTGCCCAACCG

3781 ATGGATTGTAGGCGCCGCTTATACTTGTCTGCCTCCCCGCGTTGCGTCGCGGTGCATG 3840  
 -----+-----+-----+-----+-----+-----+-----+  
 TACCTAACATCCGCGGCGGGATATGGAACAGACGGAGGGGCGCAACGCAGCGCCACGTAC

3841 GAGCCGGGCCACCTCGACCTGAATGGAAGCCGGCGGCACCTCGCTAACGGATTCACTACT 3900  
 -----+-----+-----+-----+-----+-----+-----+  
 CTCGGCCCGGTGGAGCTGGACTTACCTTCGGCCCGCTGGAGCGATTGCCTAAGTGGTGA

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3901 CCAAGAATTGGAGCCAATCAATTCTTGC GGAGAACTGTGAATGCGCAAACCAACCCTTGG  
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 GGTTCTTAACCTCGGTTAGTTAAGAACGCCTCTTGACACTTACGCGTTTGGTTGGGAACC

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3961 CAGAACATATCCATCGCGTCCGCCATCTCCAGCAGCCGCACGCGGCATCGCGTTGCTG  
 -----+-----+-----+-----+-----+-----+-----+ 4020  
 GTCTTGTATAGGTAGCGCAGGCGGTAGAGGTCGTCGGCGTGCGCCGCGTAGCGCAACGAC

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4021 GCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAG  
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 CGCAAAAAGGTATCCGAGGCGGGGGACTGCTCGTAGTGTTTTTAGCTGCGAGTTCAGTC

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4081 AGGTGGCGAAACCCGACAGGACTATAAAGATAACCAGGCGTTTCCCCCTGGAAGCTCCCTC  
 -----+-----+-----+-----+-----+-----+-----+ 4140  
 TCCACCGCTTTGGGCTGTCCTGATATTTCTATGGTCCGCAAAGGGGGACCTTCGAGGGAG

4141 GTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACTGTCCGCCTTTCTCCCTTCG  
 -----+-----+-----+-----+-----+-----+-----+ 4200  
 CACGCGAGAGGACAAGGCTGGGACGGCGAATGGCCTATGGACAGGCGGAAAGAGGGGAAGC

4201 GGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTT  
 -----+-----+-----+-----+-----+-----+-----+ 4260  
 CCTTCGCACCGCGAAAGAGTATCGAGTGCGACATCCATAGAGTCAAGCCACATCCAGCAA

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4261 CGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTTCAGCCCGACCGCTGCGCCTTATCC  
 -----+-----+-----+-----+-----+-----+-----+ 4320  
 GCGAGGTTTCGACCCGACACACGTGCTTGGGGGGCAAGTCGGGCTGGCGACGCGGAATAGG

4321 GGTAACATATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCC  
 -----+-----+-----+-----+-----+-----+-----+ 4380  
 CCATTGATAGCAGAACTCAGGTTGGGCCATTCTGTGCTGAATAGCGGTGACCGTTCGTCGG

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4381 ACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGG 4440  
-----+-----+-----+-----+-----+-----+  
TGACCATTGTCCTAATCGTCTCGCTCCATACATCCGCCACGATGTCTCAAGAACTTCACC  
  
TGGCCTAACTACGGCTACACTAGAAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCA  
4441 -----+-----+-----+-----+-----+-----+ 4500  
ACCGGATTGATGCCGATGTGATCTTCTGTGCATAAACCATAGACGCGAGACGACTTCCGGT

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GTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGC  
4501 -----+-----+-----+-----+-----+-----+ 4560  
CAATGGAAGCCTTTTTCTCAACCATCGAGAAGTCCGCTTTGTTTGGTGGCGACCATCG  
  
GGTGGTTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGAT  
4561 -----+-----+-----+-----+-----+-----+ 4620  
CCACCAAAAAAACAACGTTTCGTCTAATGCGCGTCTTTTTTCTTAGAGTTCTTCTA  
  
CCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAAACGAAAACTCACGTTAAGGGATT  
4621 -----+-----+-----+-----+-----+-----+ 4680  
GGAAACTAGAAAAGATGCCCCAGACTGCGAGTCACCTTGCTTTTGAGTGCAATTCCTAA  
  
TTGGTCATGAGATTATCAAAAAGGATCTTACCTAGATCCTTTTAAATTAATAATGAAGT  
4681 -----+-----+-----+-----+-----+-----+ 4740  
AACCAGTACTCTAATAGTTTTTCTAGAAAGTGGATCTAGGAAAATTTAATTTTTACTTCA  
  
TTTAAATCAATCTAAAGTATATATGAGTAACTTGGTCTGACAGTTACCAATGCTTAATC  
4741 -----+-----+-----+-----+-----+-----+ 4800  
AAATTTAGTTAGATTTTCATATATACTCATTTGAACCAGACTGTCAATGGTTACGAATTAG

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AGTGAGGCACCTATCTCAGCGATCTGTCTATTTTCGTTTCATCCATAGTTGCCTGACTCCCC  
4801 -----+-----+-----+-----+-----+-----+ 4860  
TCACTCCGTGGATAGAGTCGCTAGACAGATAAAGCAAGTAGGTATCAACGGACTGAGGGG

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4861 GTCGTGTAGATAACTACGATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATA  
-----+-----+-----+-----+-----+-----+ 4920  
CAGCACATCTATTGATGCTATGCCCTCCCGAATGGTAGACCGGGGTCACGACGTTACTAT

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4921 CCGCGAGACCCACGCTCACCGGCTCCAGATTTATCAGCAATAAACCCAGCCAGCCGGAAGG  
-----+-----+-----+-----+-----+-----+ 4980  
GGCGCTCTGGGTGCGAGTGGCCGAGGTCTAAATAGTCGTTATTTGGTCGGTCGGCCTTCC

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4981 GCCGAGCGCAGAAGTGGTCCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGC  
-----+-----+-----+-----+-----+-----+ 5040  
CGGCTCGCGTCTTCACCAGGACGTTGAAATAGGCGGAGGTAGGTCAGATAATTAACAACG

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5041 CGGGAAGCTAGAGTAAGTAGTTCCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCT  
-----+-----+-----+-----+-----+-----+ 5100  
GCCCTTCGATCTCATTTCATCAAGCGGTCAATTATCAAACGCGTTGCAACAACGGTAACGA

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5101 GCAGGCATCGTGGTGTACGCTCGTCGTTTGGTATGGCTTCATTTCAGCTCCGGTTCCCAA  
-----+-----+-----+-----+-----+-----+ 5160  
CGTCCGTAGCACACAGTGCAGCAGCAAACCATAACCGAAGTAAGTCGAGGCCAAGGGTT

5161 CGATCAAGGCGAGTTACATGATCCCCATGTTGTGCAAAAAGCGGTTAGCTCCTTCGGT  
-----+-----+-----+-----+-----+-----+ 5220  
GCTAGTTCGGCTCAATGTACTAGGGGTACAACACGTTTTTTTCGCCAATCGAGGAAGCCA

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5221 CCTCCGATCGTTGTGTCAGAAGTAAGTTGGCCGAGTGTTATCACTCATGGTTATGGCAGCA  
-----+-----+-----+-----+-----+-----+ 5280  
GGAGGCTAGCAACAGTCTTCATTCAACCGGCGTCACAATAGTGAGTACCAATACCGTCGT



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CGAAAAGTGCCACCTGACGTCTAAGAAACCATTATTATCATGACATTAACCTATAAAAAAT  
 5761 -----+-----+-----+-----+-----+ 5820  
 GCTTTTTCACGGTGGACTGCAGATTCTTTGGTAATAATAGTACTGTAATTGGATATTTTTTA

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AGGCGTATCACGAGGCCCTTTCGTCTTCAA  
 5821 -----+-----+-----+ 5850  
 TCCGCATAGTGCTCCGGGAAAGCAGAAGTT

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	Bpul0I	BsaI
BsaAI	BsaBI	BsaHI	BsaJI	BsaWI	BscGI	BsgI	BsiI
BsiEI	BslI	BsmI	BsmAI	BsmFI	Bsp24I	Bsp1286I	BspGI
BspMI	BsrI	BsrBI	BsrDI	BsrFI	BssHII	Bst1107I	BstEII
BstXI	BstYI	Bsu36I	Cac8I	ClaI	CviJI	CviRI	DdeI
DpnI	DraI	DraIII	DrdI	DrdII	DsaI	EaeI	EagI
Eam1105I	EarI	EciI	Eco47III	Eco57I	EcoNI	EcoO109I	EcoRI
EcoRII	EcoRV	Esp3I	FauI	FokI	FspI	GdiII	HaeI
HaeII	HaeIII	HgaI	HgiEII	HhaI	HincII	HindIII	HinfI
HpaI	HphI	ItaI	KpnI	MaeII	MaeIII	MboII	MluI
MmeI	MnlI	MseI	MslI	MspI	MspAI	MunI	MwoI
NarI	NciI	NcoI	NdeI	NgoAIV	NheI	NlaIII	NlaIV
NotI	NruI	NsiI	NspI	NspV	Pfl1108I	PflMI	PleI
PmlI	PshAI	Psp5II	Psp1406I	PstI	PvuI	RcaI	RleAI
RsaI	SacII	SalI	Sau96I	Sau3AI	ScaI	ScrFI	SexAI
SfaNI	SfcI	SgrAI	SmaI	SnaBI	SphI	SspI	StyI
TaqI	TaqII	TaqII	TfiI	ThaI	Tsp45I	Tsp509I	Tth111II
VspI	XbaI	XhoI	XmnI				

Enzymes that do not cut:

AflII	ApaI	AscI	AvrII	Bpu1102I	BseRI	BspEI	BspLU11I
BsrGI	FseI	MscI	PacI	PmeI	PvuII	RsrII	SacI
SapI	SfiI	SgfI	SpeI	SrfI	Sse8387I	StuI	SunI
SwaI	Tth111I	XcmI					

Enzymes excluded; MinCuts: 1 MaxCuts: 3

AciI	AluI	AlwI	Alw21I	ApaBI	ApoI	AvaII	BanI
BbsI	BbvI	BccI	Bce83I	BcefI	BcgI	BcgI	BfaI
BglI	BsaAI	BsaHI	BsaJI	BsaWI	BscGI	BsiEI	BslI
BsmAI	BsmFI	Bsp24I	Bsp1286I	BsrI	BsrDI	BsrFI	BstYI
Cac8I	CviJI	CviRI	DdeI	DpnI	DraI	EaeI	EciI
Eco47III	Eco57I	EcoO109I	EcoRII	FauI	FokI	GdiII	HaeI
HaeII	HaeIII	HgaI	HhaI	HincII	HinfI	HphI	ItaI

MaeII	MaeIII	MboII	MmeI	MnlI	MseI	MslI	MspI
MspAII	MwoI	NarI	NciI	NgoAIV	NlaIII	NlaIV	NspI
PleI	Psp1406I	RcaI	RsaI	Sau96I	Sau3AI	ScrFI	SfaNI
SfcI	StyI	TaqI	TaqII	TaqII	TfiI	ThaI	Tsp45I
Tsp509I	Tth111II						