

(Circular) MAP of: Peaw127.Seq check: 8385 from: 1 to: 7978

PBR322 with the amp.R region reversed

With 212 enzymes: \*

MaxCuts: 2

July 15, 1999 17:04 ..

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TTCTCATGTTTGACAGCTTATCATCGATAAGCTTGGATCAATTCCTGTAACAATAGCAAT
1 -----+-----+-----+-----+-----+-----+ 60
AAGAGTACAAACTGTCTGAATAGTAGCTATTTCGAACCTAGTTAAGGACATTGTTATCGTTA

ACCCCAAATACCTAATGTAGTTCCAGCAAGCAAGCTAAAAAGTAAAGCAACAACATAACC
61 -----+-----+-----+-----+-----+-----+ 120
TGGGGTTTATGGATTACATCAAGGTCGTTTCGTTTCGATTTTTTCATTTTCGTTGTTGATTGG

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TGACTCTTATACACAAGTAGCGTCCTGAACGGAACTTTCCCGTTTTCCAGGATCCcgga
121 -----+-----+-----+-----+-----+-----+ 180
ACTGAGAATATGTGTTTCATCGCAGGACTTGCCTTGGAAAGGGCAAAGGTCCTAGGgcct

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agttcctatttctctagaaagtataggaacttcgaattggtcgaaattcgttgcgggccgca
181 -----+-----+-----+-----+-----+-----+ 240
tcaaggataagagatctttcatatccttgaagcttaaccagctttaagcaacgccggcgt

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acggtacccgggggatcggggAAAGCCACGTTGTGTCTCAAAATCTCTGATGTTACATTG
241 -----+-----+-----+-----+-----+-----+ 300
tgccatggggccccctagccccTTTCGGTGCAACACAGAGTTTTAGAGACTACAATGTAAC

CACAAAGATAAAAATATATCATCATGAACAATAAAACTGTCTGCTTACATAAACAGTAATA
301 -----+-----+-----+-----+-----+-----+ 360
GTGTTCTATTTTTATATAGTAGTACTTGTTATTTTTGACAGACGAATGTATTTGTCATTAT

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361 CAAGGGGTGTTATGAGCCATATTCAACGGGAAACGTCTTGCTCGAGGCCGCGATTAAATT 420  
-----+-----+-----+-----+-----+-----+  
GTTCCCCACAATACTCGGTATAAGTTGCCCTTTGCAGAACGAGCTCCGGCGCTAATTTAA

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421 CCAACATGGATGCTGATTTATATGGGTATAAATGGGCTCGCGATAATGTCTGGGCAATCAG 480  
-----+-----+-----+-----+-----+-----+  
GGTTGTACCTACGACTAAATATACCCATATTTACCCGAGCGCTATTACAGCCCGTTAGTC

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481 GTGCGACAATCTATCGATTGTATGGGAAGCCCGATGCGCCAGAGTTGTTTCTGAAACATG 540  
-----+-----+-----+-----+-----+-----+  
CACGCTGTTAGATAGCTAACATAACCCTTCGGGCTACGCGGTCTCAACAAAGACTTTGTAC

541 GCAAAGGTAGCGTTGCCAATGATGTTACAGATGAGATGGTCAGACTAAACTGGCTGACGG 600  
-----+-----+-----+-----+-----+-----+  
CGTTTCCATCGCAACGGTTACTACAATGTCTACTCTACCAGTCTGATTTGACCGACTGCC

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601 AATTTATGCCTCTTCCGACCATCAAGCATTTTATCCGTACTCCTGATGATGCATGGTTAC 660  
-----+-----+-----+-----+-----+-----+  
TTAAATACGGAGAAGGCTGGTAGTTTCGTAAAATAGGCATGAGGACTACTACGTACCAATG

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661 TCACCACTGCGATCCCCGGGAAAACAGCATTCCAGGTATTAGAAGAATATCCTGATTTCAG 720  
-----+-----+-----+-----+-----+-----+  
AGTGGTGACGCTAGGGGCCCTTTTGTCTGTAAGGTCCATAATCTTCTTATAGGACTAAGTC

721 GTGAAAATATTGTTGATGCGCTGGCAGTGTTCCTGCGCCGGTTGCATTCGATTCTGTTT 780  
-----+-----+-----+-----+-----+-----+  
CACTTTTATAACAACACTACGCGACCGTCAACAAGGACGCGGCAACGTAAGCTAAGGACAAA

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781 GTAATTGTCCTTTTAAACAGCGATCGCGTATTTTCGTCTCGCTCAGGCGCAATCACGAATGA 840  
-----+-----+-----+-----+-----+-----+  
CATTAAACAGGAAAATTGTCTGCTAGCGCATAAAGCAGAGCGAGTCCGCGTTAGTGCTTACT

841 ATAACGGTTTGGTTGATGCGAGTGATTTTGTGACGAGCGTAATGGCTGGCCTGTTGAAC 900  
-----+-----+-----+-----+-----+-----+

TATTGCCAAACCAACTACGCTCACTAAAACACTACTGCTCGCATTACCGACCGGACAACCTTG

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901 AAGTCTGGAAAGAAATGCATAAGCTTTTGCCATTCTCACCGGATTTCAGTCGTCACTCATG 960  
 -----+-----+-----+-----+-----+-----+-----+  
 TTCAGACCTTTCTTTACGTATTTCGAAAACGGTAAGAGTGGCCTAAGTCAGCAGTGAGTAC

961 GTGATTTCTCACTTGATAACCTTATTTTTGACGAGGGGAAATTAATAGTTGTATTGATG 1020  
 -----+-----+-----+-----+-----+-----+-----+  
 CACTAAAGAGTGAACCTATTGGAATAAAAACTGCTCCCCTTTAATTATCCAACATAACTAC

1021 TTGGACGAGTCGGAATCGCAGACCGATAACCAGGATCTTGCCATCCTATGGAACCTGCCTCG 1080  
 -----+-----+-----+-----+-----+-----+-----+  
 AACCTGCTCAGCCTTAGCGTCTGGCTATGGTCCTAGAACGGTAGGATACCTTGACGGAGC

1081 GTGAGTTTTCTCCTTCATTACAGAAACGGCTTTTTCAAAAATATGGTATTGATAATCCTG 1140  
 -----+-----+-----+-----+-----+-----+-----+  
 CACTCAAAGAGGAAGTAATGTCTTTGCCGAAAAGTTTTTATACCATAACTATTAGGAC

1141 ATATGAATAAATTGCAGTTTCATTTGATGCTCGATGAGTTTTTCTAATCAGAATTGGTTA 1200  
 -----+-----+-----+-----+-----+-----+-----+  
 TATACTTATTTAACGTCAAAGTAAACTACGAGCTACTCAAAAAGATTAGTCTTAACCAAT

1201 ATTGGTTGTAACACTGGCAGAGCATTACGCTGACTTGACGGGACGGCGGCTTTGTTGAAT 1260  
 -----+-----+-----+-----+-----+-----+-----+  
 TAACCAACATTGTGACCGTCTCGTAATGCGACTGAACTGCCCTGCCGCCGAAACAACCTTA

1261 AAATCGAACTTTTGCTGAGTTGAAGGATCAGATCACGCATCTTCCCACAAACGCAGACCG 1320  
 -----+-----+-----+-----+-----+-----+-----+  
 TTTAGCTTGAAAACGACTCAACTTCCTAGTCTAGTGCCTAGAAAGGGCTGTTGCGTCTGGC

1321 TTCCGTGGCAAAGCAAAGTTCAAATCACCAACTGGTCCACCTACAACAAAGCTCTCAT 1380  
 -----+-----+-----+-----+-----+-----+-----+  
 AAGGCACCGTTTTCGTTTTCAAGTTTTAGTGGTTGACCAGGTGGATGTTGTTTTCGAGAGTA

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1381 CAACCGTGGCTCCCTCACTTTCTGGCTGGATGATGGGGCGATTTCAGGCCTGGTATGAGTC 1440  
 -----+-----+-----+-----+-----+-----+-----+  
 GTTGGCACCGAGGGAGTGAAAGACCGACCTACTACCCCGCTAAGTCCGGACCATACTCAG

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1441 AGCAACACCTTCTTACGAGGCAGACCTCAGCGCTAagatcctctagagtcgaggatccT 1500  
 -----+-----+-----+-----+-----+-----+-----+  
 TCGTTGTGGAAGAAGTGCTCCGTCTGGAGTCGCGATgctaggagatctcagctcctaggA

GGAAAACGGGAAAGGTTCCGTTCCAGGACGCTACTTGTGTATAAGAGTCAGGTTATGTTGT

1501 -----+-----+-----+-----+-----+-----+ 1560  
CCTTTTGGCCCTTTCCAAGGCAAGTCCTGCGATGAACACATATTCTCAGTCCAATACAACA  
TGCTTTACTTTTTAGCTTGCTTGCTGGAACACATTAGGTATTTGGGGTATTGCTATTGT  
1561 -----+-----+-----+-----+-----+-----+ 1620  
ACGAAATGAAAAATCGAACGAACGACCTTGATGTAATCCATAAACCCATAACGATAACA  
TACAGGAATTGATCCTCGACCGATGCCCTTGAGAGCCTTCAACCCAGTCAGCTCCTTCCG  
1621 -----+-----+-----+-----+-----+-----+ 1680  
ATGTCCTTAACTAGGAGCTGGCTACGGGAACCTCTCGGAAGTTGGGTGAGTCGAGGAAGGC

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GTGGGCGCGGGGCATGACTATCGTCGCCGCACTTATGACTGTCTTCTTTATCATGCAACT  
1681 -----+-----+-----+-----+-----+-----+ 1740  
CACCCGCGCCCCGTACTGATAGCAGCGGCGTGAATACTGACAGAAGAAATAGTACGTTGA  
CGTAGGACAGGTGCCGGCAGCGCTCTGGGTCAATTTTCGGCGAGGACCGCTTTCGCTGGAG  
1741 -----+-----+-----+-----+-----+-----+ 1800  
GCATCCTGTCCACGGCCGTGCGGAGACCCAGTAAAGCCGCTCCTGGCGAAAGCGACCTC  
CGCGACGATGATCGGCCTGTGCTTGGCGTATTTCGGAATCTTGACAGCCCTCGCTCAAGC  
1801 -----+-----+-----+-----+-----+-----+ 1860  
GCGCTGCTACTAGCCGGACAGCGAACGCCATAAGCCTTAGAACGTGCGGGAGCGAGTTTCG  
CTTCGTCACTGGTCCC GCCACCAAACGTTTTTCGGCGAGAAGCAGGCCATTATCGCCGGCAT  
1861 -----+-----+-----+-----+-----+-----+ 1920  
GAAGCAGTGACCAGGGCGGTGGTTTTGCAAAGCCGCTCTTCGTCCGGTAATAGCGGCCGTA

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GGCGGCCGACGCGCTGGGCTACGTCTTGCTGGCGTTTCGCGACGCGAGGCTGGATGGCCTT  
1921 -----+-----+-----+-----+-----+-----+ 1980  
CCGCCGGCTGCGCGACCCGATGCAGAACGACCGCAAGCGCTGCGCTCCGACCTACCGGAA

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CCCCATTATGATTCTTCTCGCTTCCGGCGGCATCGGGATGCCCGGTTGCAGGCCATGCT  
1981 -----+-----+-----+-----+-----+-----+ 2040  
GGGGTAATACTAAGAAGAGCGAAGGCCCGCCGTAGCCCTACGGGCGCAACGTCCGGTACGA  
GTCCAGGCAGGTAGATGACGACCATCAGGGACAGCTTCAAGGATCGCTCGCGGCTCTTAC  
2041 -----+-----+-----+-----+-----+-----+ 2100  
CAGGTCCGTCCATCTACTGCTGGTAGTCCCTGTGCAAGTTCTTAGCGAGCGCCGAGAATG  
CAGCCTAACTTCGATCACTGGACCGCTGATCGTCACGGCGATTTATGCCGCTCGGCGAG  
2101 -----+-----+-----+-----+-----+-----+ 2160  
GTCGGATTGAAGCTAGTGACCTGGCGACTAGCAGTGCCGCTAAATACGGCGGAGCCGCTC

CACATGGAACGGGTTGGCATGGATTGTAGGCGCCGCCCTATACCTTGTCTGCCTCCCCGC  
 2161 -----+-----+-----+-----+-----+-----+ 2220  
 GTGTACCTTGCCCAACCGTACCTAACATCCGCGGCGGGATATGGAACAGACGGAGGGGCG  
  
 GTTTCGTCGCGGTGCATGGAGCCGGGCCACCTCGACCTGAATGGAAGCCGGCGGCACCTC  
 2221 -----+-----+-----+-----+-----+-----+ 2280  
 CAACGCAGCGCCACGTACCTCGGCCCGGTGGAGCTGGACTTACCTTCGGCCGCGGTGGAG  
  
 GCTAACGGATTCACTCACTCCAAGAATTGGAGCCAATCAATTCTTGCGGAGAACTGTGAAT  
 2281 -----+-----+-----+-----+-----+-----+ 2340  
 CGATTGCCTAAGTGGTGGAGTTCTTAACCTCGGTTAGTTAAGAACGCCTCTTGACACTTA  
  
 GCGCAAACCAACCCCTTGGCAGAACATATCCATCGCGTCCGCCATCTCCAGCAGCCGCACG  
 2341 -----+-----+-----+-----+-----+-----+ 2400  
 CGCGTTTGGTTGGGAACCGTCTTGTATAGGTAGCGCAGGCGGTAGAGGTCGTCGGCGTGC

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CGGCGCATCTCGGGCAGCGTTGGGTCTGGCCACGGGTGCGCATGATCGTGCTCCTGTCTG  
 2401 -----+-----+-----+-----+-----+-----+ 2460  
 GCCGCGTAGAGCCCGTTCGCAACCCAGGACCGGTGCCACGCGTACTAGCACGAGGACAGC

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TTGAGGACCCGGCTAGGCTGGCGGGGTTGCCTTACTGGTTAGCAGAATGAATCACCGATA  
 2461 -----+-----+-----+-----+-----+-----+ 2520  
 AACTCCTGGGCCGATCCGACCGCCCCAACGGAATGACCAATCGTCTTACTTAGTGGCTAT

CGCGAGCGAACGTGAAGCGACTGCTGCTGCAAAACGTCTGCGACCTGAGCAACAACATGA  
 2521 -----+-----+-----+-----+-----+-----+ 2580  
 GCGCTCGCTTGCCTTCGCTGACGACGACGTTTTGCGAGACGCTGGACTCGTTGTTGTACT

ATGGTCTTCGGTTTTCCGTGTTTTCGTAAAGTCTGGAAACGCGGAAGTCAGCGCCCTGCACC  
 2581 -----+-----+-----+-----+-----+-----+ 2640  
 TACCAGAAGCCAAAGGCACAAAGCATTTCAGACCTTTGCGCCTTCAGTCGCGGGACGTGG

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ATTATGTTCCGGATCTGCATCGCAGGATGCTGCTGGCTACCCTGTGGAACACCTACATCT  
 2641 -----+-----+-----+-----+-----+-----+ 2700  
 TAATACAAGGCCTAGACGTAGCGTCTACGACGACCGATGGGACACCTTGTGGATGTAGA

GTATTAACGAAGCGCTGGCATTGACCCTGAGTGATTTTTCTCTGGTCCCGCCGCATCCAT  
 2701 -----+-----+-----+-----+-----+-----+ 2760  
 CATAATTGCTTCGCGACCGTAACTGGGACTCACTAAAAAGAGACCAGGGCGGCGTAGGTA

ACCGCCAGTTGTTTTACCCTCACAAAGTTCCAGTAACCGGGCATGTTTCATCATCAGTAACC  
2761 -----+-----+-----+-----+-----+-----+ 2820  
TGGCGGTCAACAAATGGGAGTGTTCGAAGGTCATTGGCCCCGTACAAGTAGTAGTCATTGG

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CGTATCGTGAGCATCCTCTCTCGTTTTATCGGTATCATTACCCCCATGAACAGAAATTCC  
2821 -----+-----+-----+-----+-----+-----+ 2880  
GCATAGCACTCGTAGGAGAGAGCAAAGTAGCCATAGTAATGGGGTACTTGTCTTTAAGG

CCCTTACACGGAGGCATCAAGTGACCAAACAGGAAAAAACCGCCCTTAACATGGCCCGCT  
2881 -----+-----+-----+-----+-----+-----+ 2940  
GGGAATGTGCCTCCGTAGTTCCTGTTTGTCTTTTTTGGCGGGAATTGTACCGGGCGA

TTATCAGAAGCCAGACATTAACGCTTCTGGAGAACTCAACGAGCTGGACGCGGATGAAC  
2941 -----+-----+-----+-----+-----+-----+ 3000  
AATAGTCTTCGGTCTGTAATTGCGAAGACCTCTTTGAGTTGCTCGACCTGCGCCTACTTG

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AGGCAGACATCTGTGAATCGCTTCACGACCACGCTGATGAGCTTTACCGCAAGATCTTGA  
3001 -----+-----+-----+-----+-----+-----+ 3060  
TCCGTCTGTAGACACTTAGCGAAGTGCTGGTGCGACTACTCGAAATGGCGTTCTAGAACT

TCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCAGGGCTT  
3061 -----+-----+-----+-----+-----+-----+ 3120  
AGGGGACGCGGTAGTCTAGGAACCGCGTTCTTTTCGGTAGGTCAAATGAAACGTCCCGAA

CCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAAAC  
3121 -----+-----+-----+-----+-----+-----+ 3180  
GGGTTGGAATGGTCTCCCGGGGTGACCGTTAAGGCCAAGCGAACGACAGGTATTTTG

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CGCCCAGTCTAGCTATCGCCATGTAAGCCCACTGCAAGCTACCTGCTTTCTCTTTGCGCT  
3181 -----+-----+-----+-----+-----+-----+ 3240  
GCGGGTCAGATCGATAGCGGTACATTCGGGTGACGTTTCGATGGACGAAAGAGAAACGCGA

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TGCGTTTTCCCTTGTCCAGATAGCCCAGTAGCTGACATTCATCCGGGGTCAGCACCGTTT  
3241 -----+-----+-----+-----+-----+-----+ 3300  
ACGCAAAAGGGAACAGGTCTATCGGGTCATCGACTGTAAGTAGGCCCCAGTCGTGGCAAA

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3301 CTGCGGACTGGCTTTCTACGTGTTCCGCTTCCTTTAGCAGCCCTTGCGCCCTGAGTGCTT 3360  
-----+-----+-----+-----+-----+-----+-----+  
GACGCCTGACCGAAAGATGCACAAGGCGAAGGAAATCGTCGGGAACGCGGGACTCACGAA  
GCGGCAGCGTGAAGCTTTCTCTGAGCTGTAACAGCCTGACCGCAACAAACGAGAGGATCG  
3361 -----+-----+-----+-----+-----+-----+ 3420  
CGCCGTGCACTTCGAAAGAGACTCGACATTGTGCGACTGGCGTTGTTTGCTCTCCTAGC  
AGACCATCCGCTCCAGATTATCCGGCTCCTCCATGCGTTGCCTCTCGGCTCCTGCTCCGG  
3421 -----+-----+-----+-----+-----+-----+ 3480  
TCTGGTAGGCGAGGTCTAATAGGCCGAGGAGGTACGCAACGGAGAGCCGAGGACGAGGCC  
TTTTCCATGCCTTATGGAACCTCTCGATCCGCCAGCGATGGGTATAAATGTCGATGACGC  
3481 -----+-----+-----+-----+-----+-----+ 3540  
AAAAGGTACGGAATACCTTGAGGAGCTAGGCGGTGCTACCCATATTTACAGCTACTGCG

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3541 GCAAGGCTTGGGCTAGCGACTCGACCGGTTGCGCCGGTCAGCAACAACCATTTCAACGGGG 3600  
-----+-----+-----+-----+-----+-----+  
CGTTCGGAACCCGATCGCTGAGCTGGCCAAGCGGCCAGTCGTTGTTGGTAAAGTTGCCCC  
TCTCACCTTGGGCGGGTTAATCTCCTCGGCCAGCACCGCGTTGAGCGTGATATTCCCCT  
3601 -----+-----+-----+-----+-----+-----+ 3660  
AGAGTGGGAACCCGCCAATTAGAGGAGCCGGTTCGTGGCGCAACTCGCACTATAAGGGGA  
GTTTTAGCGTGATGCGCCACTGCGCAGGCTCAAGCTCGCCTTGCGGGCTGGTTCGATTTT  
3661 -----+-----+-----+-----+-----+-----+ 3720  
CAAAATCGCACTACGCGGGTACGCGTCCGAGTTCGAGCGGAACGCCCGACCAGCTAAAA  
TACGTTTACCGCGTTTATCCACCACGCCCTTTTGCGGAATGCTGATCTGATAGCCACCCA  
3721 -----+-----+-----+-----+-----+-----+ 3780  
ATGCAAATGGCGCAAATAGGTGGTGCGGGAAAACGCCTTACGACTAGACTATCGGTGGGT

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3781 ACTCCGGTTGGTTCTTCAGATGGTTCGATCAGATACAACCCAGACTCTACGTCCTTGCGTG 3840  
-----+-----+-----+-----+-----+-----+  
TGAGGCCAACCAAGAAGTCTACCAGCTAGTCTATGTTGGGTCTGAGATGCAGGAACGCAC

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GGTGCTTGGAGCGCACCACGAAGCGCTCGTTATGCGCCAGCCTGTCCTGCAGATAAGCAT  
3841 -----+-----+-----+-----+-----+-----+ 3900  
CCACGAACCTCGCGTGGTGCTTCGCGAGCAATACGCGGTTCGGACAGGACGTCTATTCGTA

GAATATCGGCTTCGCGGTACAGACCGCAATCACGTTGCTCATCATGCTGCCCATGCGTA  
3901 -----+-----+-----+-----+-----+-----+ 3960  
CTTATAGCCGAAGCGCCAGTGTCTGGCGTTAGTGCAACGAGTAGTACGACGGGTACGCAT

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ACCGGCTAGTTGCGGCCGCTGCCAGCCATTTGCCACTCTCCTTTTCATCCGCATCGGCAG  
3961 -----+-----+-----+-----+-----+-----+ 4020  
TGGCCGATCAACGCCGCGACGGTCGGTAAACGGTGAGAGGAAAAGTAGGCGTAGCCGTC

GGTCATCCGGGCGCATCCACCACTCCTGATGCAGTAATCCTACGGTGCGGAATGTGGTGG  
4021 -----+-----+-----+-----+-----+-----+ 4080  
CCAGTAGGCCCGCGTAGGTGGTGAGGACTACGTCATTAGGATGCCACGCCTTACACCACC

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CCTCGAGCAAGAGAACGGAGTGAACCCACCATCCGCGGGATTTATCCTGAATAGAGCCCA  
4081 -----+-----+-----+-----+-----+-----+ 4140  
GGAGCTCGTTCTCTTGCCTCACTTGGGTGGTAGGCGCCCTAAATAGGACTTATCTCGGGT

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GCTTGCCAAGCTCTTCGGCGACCTGGTGGCGATAACTCAAAGAGGTGGTGTCTCAATGG  
4141 -----+-----+-----+-----+-----+-----+ 4200  
CGAACGGTTTCGAGAAGCCGCTGGACCACCGCTATTGAGTTTCTCCACCACAGGAGTTACC

CCAGCAGTTCGGGAAACTCCTGAGCCAACTTGACTGTTTGCATGGCGCCAGCCTTTCTGA  
4201 -----+-----+-----+-----+-----+-----+ 4260  
GGTCGTCAAGCCCTTTGAGGACTCGGTTGAACTGACAAACGTACCGCGGTTCGGAAAGACT

TGCCTCGGCAGAAACGTTGGGATTGCGGTAAAATCGGTAAGCGCCTTCTGCATGGCTT  
4261 -----+-----+-----+-----+-----+-----+ 4320  
AGCGGAGCCGTCTTTGCAACCCTAACGCCATTTTAGCCATTTCGCGGAAGGACGTACCGAA

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CACTACCCTCTGATGAGATGGTTATTGATTTACCAGAATATTTTGCCAATTGGGCGGCGA  
4321 -----+-----+-----+-----+-----+-----+ 4380  
GTGATGGGAGACTACTCTACCAATAACTAAATGGTCTTATAAAACGGTTAACCCGCGCT

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4381 CGTTAACCAAGCGGGCAGTACGGCGAGGATCACCCAGCGCCGCCGAAGAGAACACAGATT 4440  
 -----+-----+-----+-----+-----+-----+  
 GCAATTGGTTTCGCCCCTCATGCCGCTCCTAGTGGGTCGCGGGCTTCTCTTGTGTCTAA

4441 TAGCCCAGTCGGCCGCACGATGAAGAGCAGAAGTTATCATGCTGCCTCGCGGTTTTCGGT 4500  
 -----+-----+-----+-----+-----+-----+  
 ATCGGGTCAGCCGGCGTGCTACTTCTCGTCTTCAATAGTACGACGGAGCGCGCAAAGCCA

4501 GATGACGGTGAAAACCTCTGACACATGCAGCTCCCGGAGACGGTCACAGCTTGTCTGTAA 4560  
 -----+-----+-----+-----+-----+-----+  
 CTA CTACTGCCACTTTTGGAGACTGTGTACGTCGAGGGCCTCTGCCAGTGTGCAACAGACATT

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4561 GCGGATGCCGGGAGCAGACAAGCCCGTCAGGGCGCGTCAGCGGGTGTGGCGGGTGTTCGG 4620  
 -----+-----+-----+-----+-----+-----+  
 CGCCTACGGCCCTCGTCTGTTTCGGGCAGTCCC GCGCAGTCGCC CACAACCGCCACAGCC

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4621 GGCGCAGCCATGACCCAGTCACGTAGCGATAGCGGAGTGCACCATCGAATGGCGCAAAC 4680  
 -----+-----+-----+-----+-----+-----+  
 CCGCGTCGGTACTGGGTCAGTGCATCGCTATCGCCTCACGTGGTAGCTTACCGGTTTTG

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4681 CTTTCGCGGTATGGCATGATAGCGCCCGGAAGAGAGTCAATTCAGGGTGGTGAATGTGAA 4740  
 -----+-----+-----+-----+-----+-----+  
 GAAAGCGCCATACCGTACTATCGCGGGCCTTCTCTCAGTTAAGTCCCACCACTTACACTT

4741 ACCAGTAACGTTATACGATGTCGCAGAGTATGCCGGTGTCTCTTATCAGACCGTTTTCCCG 4800  
 -----+-----+-----+-----+-----+-----+  
 TGGTCATTGCAATATGCTACAGCGTCTCATA CGGCCACAGAGAATAGTCTGGCAAAGGGC

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4801 CGTGGTGAACCAGGCCAGCCACGTTTTCTGCGAAAACGCGGGAAAAAGTGAAGCGGCGAT 4860  
 -----+-----+-----+-----+-----+-----+  
 GCACCACTTGGTCCGGTCCGTGCAAAGACGTTTTTGCGCCCTTTTTTACCTTCGCCGCTA

GGCGGAGCTGAATTACATTCCCAACCGCGTGGCACAACA ACTGGCGGGCAAACAGTCGTT



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5461 GCTGGTTGCCAACGATCAGATGGCGCTGGGCGCAATGCGCGCCATTACCGAGTCCGGGCT 5520  
-----+-----+-----+-----+-----+-----+  
CGACCAACGGTTGCTAGTCTACCGCGACCCGCGTTACGCGCGGTAATGGCTCAGGCCCGA

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5521 GCGCGTTGGTGCGGATATCTCGGTAGTGGGATACGACGATACCGAAGACAGCTCATGTTA 5580  
-----+-----+-----+-----+-----+-----+  
CGCGCAACCACGCCTATAGAGCCATCACCTATGCTGCTATGGCTTCTGTGAGTACAAT

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5581 TATCCCGCCGTTAACACCATCAAACAGGATTTTCGCTGCTGGGGCAAACCAGCGTGGA 5640  
-----+-----+-----+-----+-----+-----+  
ATAGGGCGGCAATTGGTGGTAGTTTGTCTAAAAGCGGACGACCCCGTTTGGTGCACCT

5641 CCGCTTGCTGCAACTCTCTCAGGGCCAGGCGGTGAAGGGCAATCAGCTGTTGCCCGTCTC 5700  
-----+-----+-----+-----+-----+-----+  
GGCGAACGACGTTGAGAGAGTCCCGGTCCGCCACTTCCCGTTAGTCGACAACGGGCAGAG

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5701 ACTGGTGAAAAGAAAAACCACCCTGGCGCCAATACGCAAACCGCCTCTCCCCGCGCGTT 5760  
-----+-----+-----+-----+-----+-----+  
TGACCACTTTTCTTTTTGGTGGGACCGCGGGTTATGCGTTTGGCGGAGAGGGGCGCGCAA

5761 GGCCGATTCATTAATGCAGCTGGCACGACAGGTTTCCCGACTGGAAAGCGGGCAGTGAGC 5820  
-----+-----+-----+-----+-----+-----+  
CCGGCTAAGTAATTACGTCGACCGTGCTGTCAAAGGGCTGACCTTTCGCCCGTCACTCG

5821 GCAACGCAATTAATGTAAGTTAGCTCACTCATTAGGCTATACTGGCTTAACTATGCGGCA 5880  
-----+-----+-----+-----+-----+-----+  
CGTTGCGTTAATTACATTCAATCGAGTGAGTAATCCGATATGACCGAATTGATACGCCGT

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5881 TCAGAGCAGATTGTAAGTGCACCATAACCGAATTCCGGTATGCGGTGTGAAATAC 5940  
-----+-----+-----+-----+-----+-----+  
AGTCTCGTCTAACATGACTCTCACGTGGTATGGCCTTAAGGCCATACGCCACACTTTATG

5941 CGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCTCTTCCGCTTCTCGCTCACTG 6000  
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CGGTGTCTACGCATTCTCTTTTATGGCGTAGTCCGCGAGAAGGCGAAGGAGCGAGTGAC  
ACTCGCTGCGCTCGGTCTGTTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAA  
6001 -----+-----+-----+-----+-----+-----+ 6060  
TGAGCGACGCGAGCCAGCAAGCCGACGCCGCTCGCCATAGTCGAGTGAGTTTCCGCCATT

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TACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGC  
6061 -----+-----+-----+-----+-----+-----+ 6120  
ATGCCAATAGGTGTCTTAGTCCCCTATTGCGTCTTTCTTGTACTACTCGTTTTCCGGTCTG

AAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTTCATAGGCTCCGCCCC  
6121 -----+-----+-----+-----+-----+-----+ 6180  
TTTTCCGGTCTTGGCATTTTTTCCGGCGCAACGACCCGCAAAAAGGTATCCGAGGCGGGG

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CTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTAT  
6181 -----+-----+-----+-----+-----+-----+ 6240  
GACTGCTCGTAGTGTTTTTAGCTGCGAGTTCAGTCTCCACCGCTTTGGGCTGTCCTGATA

AAAGATAACCAGGCGTTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGC  
6241 -----+-----+-----+-----+-----+-----+ 6300  
TTTCTATGGTCCGCAAAGGGGGACCTTCGAGGGAGCACGCGAGAGGACAAGGCTGGGACG

CGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCT  
6301 -----+-----+-----+-----+-----+-----+ 6360  
GCCAATGGCCTATGGACAGGCGGAAAGAGGGGAAGCCCTTCGCACCGCGAAAGAGTATCGA

CACGCTGTAGGTATCTCAGTTCGGTGTAGGTGCTTCGCTCCAAGCTGGGCTGTGTGCACG  
6361 -----+-----+-----+-----+-----+-----+ 6420  
GTGCGACATCCATAGAGTCAAGCCACATCCAGCAAGCGAGGTTTCGACCCGACACACGTGC

AACCCCCCGTTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACC  
6421 -----+-----+-----+-----+-----+-----+ 6480  
TTGGGGGGCAAGTCGGGCTGGCGACGCGGAATAGGCCATTGATAGCAGAACTCAGGTTGG

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CGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGA  
6481 -----+-----+-----+-----+-----+-----+ 6540  
GCCATTCTGTGCTGAATAGCGGTGACCGTCGTGGTACCATTGTCCTAATCGTCTCGCT

GGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAA  
6541 -----+-----+-----+-----+-----+-----+ 6600  
CCATACATCCGCCACGATGTCTCAAGAACTTACCACCGGATTGATGCCGATGTGATCTT

GGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTA  
6601 -----+-----+-----+-----+-----+-----+ 6660  
CCTGTCATAAACCATAGACGCGAGACGACTTCGGTCAATGGAAGCCTTTTTCTCAACCAT

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GCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGCAAGCAGC  
6661 -----+-----+-----+-----+-----+-----+ 6720  
CGAGAACTAGGCCGTTTTGTTTGGTGGCGACCATCGCCACCAAAAAACAAACGTTTCGTGC

AGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTG  
6721 -----+-----+-----+-----+-----+-----+ 6780  
TCTAATGCGCGTCTTTTTTCTTAGAGTTCTTCTAGGAACTAGAAAAGATGCCCCAGAC

ACGCTCAGTGGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGA  
6781 -----+-----+-----+-----+-----+-----+ 6840  
TGCGAGTCACCTTGCTTTTGGAGTGCAATTCCTAAAACCAGTACTCTAATAGTTTTTCTC

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TCTTACCTAGATCCTTTTCCGGAATTCCAAATCAATCTAAAGTATATATGAGTAAACTT  
6841 -----+-----+-----+-----+-----+-----+ 6900  
AGAAGTGGATCTAGGAAAAGGCCTTAAGGTTTAGTTAGATTTTCATATATACTCATTTGAA

GGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTT  
6901 -----+-----+-----+-----+-----+-----+ 6960  
CCAGACTGTCAATGGTTACGAATTAGTCACTCCGTGGATAGAGTCGCTAGACAGATAAAG

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GTTTCATCCATAGTTGCCTGACTCCCCGTCGTGTAGATAACTACGATACGGGAGGGCTTAC  
6961 -----+-----+-----+-----+-----+-----+ 7020  
CAAGTAGGTATCAACGGACTGAGGGGCAGCACATCTATTGATGCTATGCCCTCCCGAATG

CATCTGGCCCCAGTGCTGCAATGATACCGCGAGACCCACGCTCACCGGCTCCAGATTTAT  
7021 -----+-----+-----+-----+-----+-----+ 7080  
GTAGACCGGGTACGACGTTACTATGGCGCTCTGGGTGCGAGTGGCCGAGGTCTAAATA

CAGCAATAAACAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGGTCCTGCAACTTTATCCG  
7081 -----+-----+-----+-----+-----+-----+ 7140  
GTCGTTATTTGGTTCGGTTCGGCCTTCCCGGCTCGCGTCTTACCAGGACGTTGAAATAGGC

7141 CCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAGTAGTTCGCCAGTTAATA 7200  
-----+-----+-----+-----+-----+-----+  
GGAGGTAGGTCAGATAATTAACAACGGCCCTTCGATCTCATTTCATCAAGCGGTCAATTAT

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7201 GTTTGCGCAACGTTGTTGCCATTGCTGCAGGCATCGTGGTGTACGCTCGTCGTTTGGTA 7260  
-----+-----+-----+-----+-----+-----+  
CAAACGCGTTGCAACAACGGTAACGACGTCCGTAGCACCACAGTGCAGCAGCAAACCAT

7261 TGGCTTCATTTCAGCTCCGGTTCCCAACGATCAAGGCGAGTTACATGATCCCCCATGTTGT 7320  
-----+-----+-----+-----+-----+-----+  
ACCGAAGTAAGTCGAGGCCAAGGGTTGCTAGTTCCGCTCAATGTACTAGGGGGTACAACA

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7321 GCAAAAAGCGGTTAGCTCCTTCGGTCTCCGATCGTTGTGAGAAGTAAGTTGGCCGCAG 7380  
-----+-----+-----+-----+-----+-----+  
CGTTTTTTCGCCAATCGAGGAAGCCAGGAGGCTAGCAACAGTCTTCATTCAACCGGCGTC

7381 TGTTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACTGTCATGCCATCCGTAA 7440  
-----+-----+-----+-----+-----+-----+  
ACAATAGTGAGTACCAATACCGTCGTGACGTATTAAGAGAATGACAGTACGGTAGGCATT

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7441 GATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAATAGTGTATGCGGC 7500  
-----+-----+-----+-----+-----+-----+  
CTACGAAAAGACACTGACCACTCATGAGTTGGTTTCAGTAAGACTCTTATCACATACGCCG

7501 GACCGAGTTGCTCTTGCCCGGCGTCAACACGGGATAATACCGCGCCACATAGCAGAACTT 7560  
-----+-----+-----+-----+-----+-----+  
CTGGCTCAACGAGAACGGGCCGAGTTGTGCCCTATTATGGCGCGGTGTATCGTCTTGAA

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7561 TAAAAGTGCTCATCATTGGAAAACGTTCTTCGGGGCGAAAACCTCTCAAGGATCTTACCGC 7620  
-----+-----+-----+-----+-----+-----+  
ATTTTCACGAGTAGTAACCTTTTGCAAGAAGCCCCGCTTTTGAGAGTTCTTAGAATGGCG

7621 TGTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAAGTATCTTCAGCATCTTTTA 7680  
-----+-----+-----+-----+-----+-----+  
ACAACCTTAGGTCAAGCTACATTGGGTGAGCACGTGGGTTGACTAGAAGTCGTAGAAAAT

7681 CTTTCACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAGGGAA 7740  
-----+-----+-----+-----+-----+-----+  
GAAAGTGGTCGAAAGACCCACTCGTTTTTGTCTTCGGTTTTACGGCGTTTTTTCCCTT

TAAGGGCGACACGGAAATGTTGAATACTCATACTCTTCCTTTTTCAATATTATTGAAGCA  
 7741 -----+-----+-----+-----+-----+-----+-----+ 7800  
 ATTCCCCTGTGCCTTTACAACCTTATGAGTATGAGAAGGAAAAAGTTATAATAACTTCGT  
  
 TTTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAAC  
 7801 -----+-----+-----+-----+-----+-----+-----+ 7860  
 AAATAGTCCCAATAACAGAGTACTCGCCTATGTATAAACTTACATAAATCTTTTTATTGG  
  
  
  
  
  
  
 AAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTCTAAGAAACCATTA  
 7861 -----+-----+-----+-----+-----+-----+-----+ 7920  
 TTTATCCCCAAGGCGCGTGTAAAGGGGCTTTTTCACGGTGGACTGCAGATTCTTTGGTAAT  
  
 TTATCATGACATTAACCTATAAAAAATAGGCGTATCACGAGGCCCTTTTCGTCTTCAAGA  
 7921 -----+-----+-----+-----+-----+-----+-----+ 7978  
 AATAGTACTGTAATTGGATATTTTTATCCGCATAGTGCTCCGGGAAAGCAGAAGTTCT

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Enzymes that do cut and were not excluded:

AatII	AhdI	AlwNI	ApaI	BamHI	BclI	BglII	BmgI
BsaAI	BsaBI	BsaXI	BspEI	BspLU11I	BspMI	BssHII	BstEII
ClaI	DraI	DraIII	DrdI	DrdII	EcoNI	EcoRI	EcoRV
HgiEII	HpaI	KpnI	MluI	MscI	MunI	NheI	NotI
NruI	NsiI	NspV	PinAI	PpuMI	PshAI	PstI	PvuI
SacII	ScaI	SexAI	SgfI	SmaI	StuI	TatI	Tth111I
UbaDI	XbaI	XhoI	XmnI				

Enzymes that do not cut:

AccI	AflIII	AscI	AvrII	BaeI	BplI	Bpu1102I	BsrGI
Bst1107I	Bsu36I	FseI	NcoI	NdeI	PacI	PmeI	PmlI
RleAI	RsrII	SalI	SanDI	SfiI	SgrAI	SnaBI	SpeI
SphI	SrfI	Sse8387I	Sse8647I	SstI	SunI	SwaI	

Enzymes excluded; MinCuts: 1 MaxCuts: 2

AceIII	AciI	AflIII	AluI	AlwI	Alw26I	ApaBI	ApaLI
ApoI	AvaI	AvaII	BanI	BanII	BbsI	BbvI	BccI
Bce83I	BcefI	BcgI	BcgI	BfaI	BfiI	BglI	BpmI
Bpu10I	BsaI	BsaHI	BsaJI	BsaWI	BsbI	BscGI	BseRI
BsgI	BsiEI	BsiHKAI	BslI	BsmI	BsmBI	BsmFI	Bsp24I
Bsp24I	Bspl286I	BspGI	BsrI	BsrBI	BsrDI	BsrFI	BssSI
BstXI	BstYI	Cac8I	CjeI	CjeI	CjePI	CjePI	CviJI
CviRI	DdeI	DpnI	DsaI	EaeI	EagI	EarI	EciI
Eco47III	Eco57I	EcoO109I	EcoRII	FauI	Fnu4HI	FokI	FspI
GdiII	HaeI	HaeII	HaeIII	HgaI	HhaI	Hin4I	HincII
HindIII	HinfI	HphI	MaeIII	MboII	MmeI	MnlI	MseI
MslI	MspI	MspA1I	MwoI	NarI	NciI	NgoAIV	NlaIII
NlaIV	NspI	Pfl1108I	PflMI	PleI	Psp1406I	PvuII	RcaI
RsaI	SapI	Sau96I	Sau3AI	ScrFI	SfaNI	SfcI	SimI
SspI	StyI	TaiI	TaqI	TaqII	TaqII	TauI	TfiI
ThaI	TseI	Tsp45I	Tsp4CI	Tsp509I	TspRI	Tth111II	VspI
XcmI							

