

(Circular) MAP of: Peaw133.Seq check: 311 from: 1 to: 8044

PBR322 with the amp.R region reversed

With 212 enzymes: *

MaxCuts: 2

July 14, 1999 15:14 ..

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TTCTCATGTTTGACAGCTTATCATCGATAAGCTTGGATCAATTCCTGTAACAATAGCAAT
1 -----+-----+-----+-----+-----+-----+ 60
AAGAGTACAAACTGTGCAATAGTAGCTATTCGAACCTAGTTAAGGACATTGTTATCGTTA

ACCCCAAATACCTAATGTAGTTCAGCAAGCAAGCTAAAAAGTAAAGCAACAACATAACC
61 -----+-----+-----+-----+-----+-----+ 120
TGGGGTTTATGGATTACATCAAGGTCGTTTCGTTTCGATTTTTTCATTTTCGTTGTTGATTGG

TGACTCTTATACACAAGTAGCGTCCTGAACGGAACCTTTCCCGTTTTCCAggatcttcca
121 -----+-----+-----+-----+-----+-----+ 180
ACTGAGAATATGTGTTTCATCGCAGGACTTGCCTTGGAAGGGCAAAGGTcctagaaggt

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attcgaagttcctatactttctagagaataggaacttccgggatcgcccatcgataagct
181 -----+-----+-----+-----+-----+-----+ 240
taagcttcaaggatatgaaagatctcttatccttgaaggccctagcgggtagctattcga

tgggctgcaggtcgatcgactctagaggatcgTAGCGCTGAGGTCTGCCTCGTGAAGAAG
241 -----+-----+-----+-----+-----+-----+ 300
acccgacgtccagctagctgagatctcctagcATCGCGACTCCAGACGGGAGCACTTCTTC

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GTGTTGCTGACTCATAACAGGCCTGAATCGCCCCATCATCCAGCCAGAAAGTGAGGGAGC
301 -----+-----+-----+-----+-----+-----+ 360
CACAACGACTGAGTATGGTCCGGACTTAGCGGGGTAGTAGGTCGGTCTTTCACTCCCTCG

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CACGGTTGATGAGAGCTTTGTTGTAGGTGGACCAGTTGGTGATTTTGAACCTTTTGCTTTG
361 -----+-----+-----+-----+-----+-----+ 420
GTGCCAACTACTCTCGAAACAACATCCACCTGGTCAACCACTAAAACCTTGAAAACGAAAC

CCACGGAACGGTCTGCGTTGTGCGGAAGATGCGTGATCTGATCCTTCAACTCAGCAAAAG
421 -----+-----+-----+-----+-----+-----+ 480
GGTGCCTTGCCAGACGCAACAGCCCTTCTACGCACTAGACTAGGAAGTTGAGTCGTTTTTC

TTCGATTTATTCAACAAAGCCCGTCCCGTCAAGTCAGCGTAATGCTCTGCCAGTGTTA
481 -----+-----+-----+-----+-----+-----+ 540
AAGCTAAATAAGTTGTTTCGGCGGCAGGGCAGTTCAGTCGCATTACGAGACGGTCACAAT
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1141 CATAAATTCGGTCAGCCAGTTTGTAGTCTGACCATCTCATCTGTAACATCATTGGCAACGCT 1200
-----+-----+-----+-----+-----+-----+
GTATTTAAGGCAGTCGGTCAAATCAGACTGGTAGAGTAGACATTGTAGTAACCGTTGCGA

1201 ACCTTTGCCATGTTTCAGAAACAACCTCTGGCGCATCGGGCTTCCCATAACAATCGATAGAT 1260
-----+-----+-----+-----+-----+-----+
TGGAAACGGTACAAAGTCTTTGTTGAGACCGCGTAGCCCGAAGGGTATGTTAGCTATCTA

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1261 TGTCGCACCTGATTGCCCCGACATTATCGCGAGCCCATTTATACCCATATAAATCAGCATC 1320
-----+-----+-----+-----+-----+-----+
ACAGCGTGGACTAACGGGCTGTAATAGCGCTCGGGTAAATATGGGTATATTTAGTCGTAG

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1321 CATGTTGGAATTTAATCGCGGCCTCGAGCAAGACGTTTCCCGTTGAATATGGCTCATAAC 1380
-----+-----+-----+-----+-----+-----+
GTACAACCTTAAATTAGCGCCGGAGCTCGTTCTGCAAAGGGCAACTTATACCGAGTATTG

1381 ACCCCTTGTATTACTGTTTATGTAAGCAGACAGTTTTATTGTTTCATGATGATATATTTTT 1440
-----+-----+-----+-----+-----+-----+
TGGGGAACATAATGACAAATACATTCTGTCTGTCAAATAACAAGTACTACTATATAAAAA

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1441 ATCTTGTGCAATGTAACATCAGAGATTTTGTAGACACAACGTGGCTTTcgatccccgggta 1500
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TAGAACACGTTACATTGTAGTCTCTAAAACCTCTGTGTTGCACCGAAAgtaggggcccac

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1501 ccgagctcgaatctcgaccaattcgaagttcctatactttctagagaataggaacttcgg 1560
-----+-----+-----+-----+-----+-----+
ggctcgagcttaaagctggttaagcttcaaggatatgaaagatctcttatccttgaagcc

1561 gatccTGGAAAACGGGAAAGGTTCCGTTTCAGGACGCTACTTGTGTATAAGAGTCAGGTTA 1620
-----+-----+-----+-----+-----+-----+
ctaggACCTTTTGCCTTTCCAAGGCAAGTCTCGGATGAACACATATTCTCAGTCCAAT

1621 TGTTGTTGCTTTACTTTTTAGCTTGCTTGCTGGAACCTACATTAGGTATTTGGGGTATTGC 1680
-----+-----+-----+-----+-----+-----+
ACAACAACGAAATGAAAAATCGAACGAACGACCTTGATGTAATCCATAAACCCCATACG

1681 TATTGTTACAGGAATTGATCCTCGACCGATGCCCTTGAGAGCCTTCAACCCAGTCAGCTC 1740
-----+-----+-----+-----+-----+-----+
ATAACAATGTCCTTAACTAGGAGCTGGCTACGGGAACTCTCGGAAGTTGGGTTCAGTCGAG

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1741 CTTCCGGTGGGCGCGGGGCATGACTATCGTCGCCCACTTATGACTGTCTTCTTTATCAT 1800
-----+-----+-----+-----+-----+-----+
GAAGGCCACCCGCGCCCCGTACTIONGATAGCAGCGGCGTGAATACTGACAGAAGAAATAGTA

1801 GCAACTCGTAGGACAGGTGCCGGCAGCGCTCTGGGTCAATTTTCGGCGAGGACCGCTTTTCG 1860
-----+-----+-----+-----+-----+-----+
CGTTGAGCATCCTGTCCACGGCCGTGCGGAGACCCAGTAAAAGCCGCTCCTGGCGAAAGC

1861 CTGGAGCGCGACGATGATCGGCCTGTGCTTGCGGTATTTCGGAATCTTGCACGCCCTCGC 1920
-----+-----+-----+-----+-----+-----+
GACCTCGCGCTGCTACTAGCCGGACAGCGAACGCCATAAGCCTTAGAACGTGCGGGAGCG

1921 TCAAGCCTTCGTCACTGGTCCC GCCACCAAACGTTTTCGGCGAGAAGCAGGCCATTATCGC 1980
-----+-----+-----+-----+-----+-----+
AGTTTCGGAAGCAGTGACCAGGGCGGTGGTTTTGCAAAGCCGCTCTTCGTCCGGTAATAGCG

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1981 CGGCATGGCGGCCGACGCGCTGGGCTACGTCTTGCTGGCGTTCGCGACGCGAGGCTGGAT 2040
-----+-----+-----+-----+-----+-----+
GCCGTACCGCCGGCTGCGCGACCCGATGCAGAACGACCGCAAGCGCTGCGCTCCGACCTA

2041 GGCCTTCCCCATTATGATTCTTCTCGCTTCCGGCGGCATCGGGATGCCCGGTTGCAGGC 2100
-----+-----+-----+-----+-----+-----+
CCGGAAGGGGTAATACTAAGAAGAGCGAAGGCCCGCTAGCCCTACGGGCGCAACGTCCG

2101 CATGCTGTCCAGGCAGGTAGATGACGACCATCAGGGACAGCTTCAAGGATCGCTCGCGGC 2160
-----+-----+-----+-----+-----+-----+
GTACGACAGGTCCGTCCATCTACTGCTGGTAGTCCCTGTGCAAGTTCCTAGCGAGCGCCG

2161 TCTTACCAGCCTAACTTCGATCACTGGACCGCTGATCGTCACGGCGATTTATGCCGCCTC 2220
-----+-----+-----+-----+-----+-----+
AGAATGGTCGGATTGAAGCTAGTGACCTGGCGACTAGCAGTGCCGCTAAATACGGCGGAG

2221 GGCGAGCACATGGAACGGGTTGGCATGGATTGTAGGCGCCGCCCTATACCTTGTCTGCCT 2280
-----+-----+-----+-----+-----+-----+
CCGCTCGTGTACCTTGCCCAACCGTACCTAACATCCGCGGCGGGATATGGAACAGACGGA

2281 CCCC GCGTTGCGTCGCGGTGCATGGAGCCGGGCCACCTCGACCTGAATGGAAGCCGGCGG 2340
-----+-----+-----+-----+-----+-----+
GGGGCGCAACGCAGCGCCACGTACCTCGGCCGGTGGAGCTGGACTTACCTTCGGCCGCGC

CACCTCGCTAACGGATTCACTCAAGCAATTGGAGCCAATCAATTCTTGGCGGAGAACT

2341 -----+-----+-----+-----+-----+-----+ 2400
GTGGAGCGATTGCCTAAGTGGTGGAGGTTCTTAACCTCGGTTAGTTAAGAACGCCTCTTGA

GTGAATGCGCAAACCAACCCTTGGCAGAACATATCCATCGCGTCCGCCATCTCCAGCAGC
2401 -----+-----+-----+-----+-----+-----+ 2460
CACTTACGCGTTTGGTTGGGAACCGTCTTGTATAGGTAGCGCAGGCGGTAGAGGTCGTGC

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CGCACGCGGCGCATCTCGGGCAGCGTTGGGTCTGGCCACGGGTGCGCATGATCGTGCTC
2461 -----+-----+-----+-----+-----+-----+ 2520
GCGTGCGCCGCGTAGAGCCCCTCGCAACCCAGGACCGGTGCCACGCGTACTAGCACGAG

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CTGTCGTTGAGGACCCGGCTAGGCTGGCGGGGTTGCCTTACTGGTTAGCAGAATGAATCA
2521 -----+-----+-----+-----+-----+-----+ 2580
GACAGCAACTCCTGGGCCGATCCGACCGCCCCAACGGAATGACCAATCGTCTTACTTAGT

CCGATACGCGAGCGAACGTGAAGCGACTGCTGCTGCAAAACGTCTGCGACCTGAGCAACA
2581 -----+-----+-----+-----+-----+-----+ 2640
GGCTATGCGCTCGCTTGCCTTGCCTGACGACGACGTTTTGCAGACGCTGGACTCGTTGT

ACATGAATGGTCTTCGGTTTCCGTGTTTCGTAAAGTCTGGAAACGCGGAAGTCAGCGCCC
2641 -----+-----+-----+-----+-----+-----+ 2700
TGTACTTACCAGAAGCCAAAGGCACAAAGCATTTCAGACCTTTGCGCCTTCAGTCGCGGG

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TGCACCATTATGTTCCGGATCTGCATCGCAGGATGCTGCTGGCTACCCTGTGGAACACCT
2701 -----+-----+-----+-----+-----+-----+ 2760
ACGTGGTAATACAAGGCCTAGACGTAGCGTCTACGACGACCGATGGGACACCTTGTGGA

ACATCTGTATTAACGAAGCGCTGGCATTGACCCTGAGTGATTTTTCTCTGGTCCCGCCGC
2761 -----+-----+-----+-----+-----+-----+ 2820
TGTAGACATAATTGCTTCGCGACCGTAACCTGGGACTCACTAAAAAGAGACCAGGGCGGGC

ATCCATAACCGCCAGTTGTTTACCCTCACAACGTTCCAGTAACCGGGCATGTTTCATCATCA
2821 -----+-----+-----+-----+-----+-----+ 2880
TAGGTATGGCGGTCAACAAATGGGAGTGTTGCAAGGTCATTGGCCCGTACAAGTAGTAGT

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

CATTGGGCATAGCACTCGTAGGAGAGAGCAAAGTAGCCATAGTAATGGGGTACTTGTCT

2941 AATTCCCCCTTACACGGAGGCATCAAGTGACCAAACAGGAAAAACCGCCCTTAACATGG 3000
-----+-----+-----+-----+-----+-----+
TTAAGGGGGAATGTGCCTCCGTAGTTCACTGGTTTGTCTTTTTTGGCGGGAATTGTACC

3001 CCCGCTTTATCAGAAGCCAGACATTAACGCTTCTGGAGAAACTCAACGAGCTGGACGCGG 3060
-----+-----+-----+-----+-----+-----+
GGGCGAAATAGTCTTCGGTCTGTAATTGCGAAGACCTCTTTGAGTTGCTCGACCTGCGCC

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3061 ATGAACAGGCAGACATCTGTGAATCGCTTACGACCACGCTGATGAGCTTTACCGCAAGA 3120
-----+-----+-----+-----+-----+-----+
TACTTGTCCGTCTGTAGACACTTAGCGAAGTGCTGGTGCGACTACTCGAAATGGCGTTCT

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3121 TCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCA 3180
-----+-----+-----+-----+-----+-----+
AGAACTAGGGGACGCGGTAGTCTAGGAACCGCCGTTCTTTTCGGTAGGTCAAATGAAACGT

3181 GGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTTCGCTTGCTGTCCA 3240
-----+-----+-----+-----+-----+-----+
CCCCAAGGGTTGGAATGGTCTCCCGCGGGGTGACCGTTAAGGCCAAGCGAACGACAGGT

3241 TAAAACCGCCCAGTCTAGCTATCGCCATGTAAGCCCACTGCAAGCTACCTGCTTTCTCTT 3300
-----+-----+-----+-----+-----+-----+
ATTTTGGCGGGTCAGATCGATAGCGGTACATTTCGGGTGACGTTTCGATGGACGAAAGAGAA

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3301 TCGCCTTGCCTTTTCCCTTGTCCAGATAGCCCAGTAGCTGACATTCATCCGGGGTCAGCA 3360
-----+-----+-----+-----+-----+-----+
ACGCGAACGCAAAAGGGAACAGGTCTATCGGGTCATCGACTGTAAGTAGGCCCCAGTCGT

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3361 CCGTTTCTGCGGACTGGCTTTCTACGTGTTCCGCTTCTTTTAGCAGCCCTTGCGCCCTGA 3420
-----+-----+-----+-----+-----+-----+
GGCAAAGACGCCTGACCGAAAGATGCACAAGGCGAAGGAAATCGTCGGGAACGCGGGACT

GTGCTTGCGGCAGCGTGAAGCTTTCTCTGAGCTGTAACAGCCTGACCGCAACAAACGAGA

4561 -----+-----+-----+-----+-----+-----+ 4620
AAGCCACTACTGCCACTTTTGGAGACTGTGTACGTTCGAGGGCCTCTGCCAGTGTCTGAACA

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CTGTAAGCGGATGCCGGGAGCAGACAAGCCCGTCAGGGCGCGTCAGCGGGTGTGGCGGG
4621 -----+-----+-----+-----+-----+ 4680
GACATTCGCCTACGGCCCTCGTCTGTTTCGGGCAGTCCCGCGCAGTCGCCACAACCGCCC

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TGTCGGGGCGCAGCCATGACCCAGTCACGTAGCGATAGCGGAGTGCACCATCGAATGGCG
4681 -----+-----+-----+-----+-----+ 4740
ACAGCCCCGCGTCGGTACTGGGTACTGGGTACTGCATCGCTATCGCCTCACGTGGTAGCTTACCGC

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CAAAACCTTTTCGCGGTATGGCATGATAGCGCCCGGAAGAGAGTCAATTCAGGGTGGTGAA
4741 -----+-----+-----+-----+-----+ 4800
GTTTTGGAAAGCGCCATACCGTACTATCGCGGGCCTTCTCTCAGTTAAGTCCCACCACTT

TGTGAAACCAGTAACGTTATACGATGTTCGAGAGTATGCCGGTGTCTCTTATCAGACCGT
4801 -----+-----+-----+-----+-----+ 4860
ACACTTTGGTCATTGCAATATGCTACAGCGTCTCATACGGCCACAGAGAATAGTCTGGCA

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TTCCCGCGTGGTGAACCAGGCCAGCCACGTTTCTGCGAAAACGCGGGAAAAAGTGGGAAGC
4861 -----+-----+-----+-----+-----+ 4920
AAGGGCGCACCCTTGGTCCGGTCGGTGCAAAGACGCTTTTTCGCGCCCTTTTTCACCTTCG

GGCGATGGCGGAGCTGAATTACATTCCTCAACCGCGTGGCACAACAACCTGGCGGGCAAACA
4921 -----+-----+-----+-----+-----+ 4980
CCGCTACCGCCTCGACTTAATGTAAGGGTTGGCGCACCGTGTGTTGACCGCCCGTTTGT

GTCGTTGCTGATTGGCGTTGCCACCTCCAGTCTGGCCCTGCACGCGCCGTGCGAAATTGT
4981 -----+-----+-----+-----+-----+ 5040
CAGCAACGACTAACCAGCAACGGTGGAGGTGACACCGGGACGTGCGCGGCAGCGTTTAACA

CGCGGCGATTAAATCTCGCGCCGATCAACTGGGTGCCAGCGTGGTGGTGTGATGGTAGA
5041 -----+-----+-----+-----+-----+ 5100

GCGCCGCTAATTTAGAGCGCGGCTAGTTGACCCACGGTCGCACCACCACAGCTACCATCT

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ACGAAGCGGCGTCTGAAGCCTGTAAAGCGGCGGTGCACAATCTTCTCGCGCAACGCGTCAG
5101 -----+-----+-----+-----+-----+-----+ 5160
TGCTTCGCCGCAGCTTCGGACATTTGCGCCGCACGTGTTAGAAGAGCGCGTTGCGCAGTC

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TGGGCTGATCATTAACTATCCGCTGGATGACCAGGATGCCATTGCTGTGGAAGCTGCCTG
5161 -----+-----+-----+-----+-----+-----+ 5220
ACCCGACTAGTAATTGATAGGCGACCTACTGGTCCTACGGTAACGACACCTTCGACGGAC

CACTAATGTTCCGGCGTTATTTCTTGATGTCTCTGACCAGACACCCATCAACAGTATTAT
5221 -----+-----+-----+-----+-----+-----+ 5280
GTGATTACAAGGCCGCAATAAAGAACTACAGAGACTGGTCTGTGGGTAGTTGTCATAATA

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TTTCTCCCATGAAGACGGTACGCGACTGGGCGTGGAGCATCTGGTCGCATTGGGTACCA
5281 -----+-----+-----+-----+-----+-----+ 5340
AAAGAGGGTACTTCTGCCATGCGCTGACCCGCACCTCGTAGACCAGCGTAACCCAGTGGT

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GCAAATCGCGCTGTTAGCGGGCCCATTAAGTTCTGTCTCGGCGCGTCTGCGTCTGGCTGG
5341 -----+-----+-----+-----+-----+-----+ 5400
CGTTTAGCGCGACAATCGCCCGGGTAATTCAAGACAGAGCCGCGCAGACGCAGACCGACC

CTGGCATAAATATCTCACTCGCAATCAAATTCAGCCGATAGCGGAACGGGAAGGCGACTG
5401 -----+-----+-----+-----+-----+-----+ 5460
GACCGTATTTATAGAGTGAGCGTTAGTTTAAGTCGGCTATCGCCTTGCCCTTCCGCTGAC

GAGTGCCATGTCCGTTTTCAACAAACCATGCAAATGCTGAATGAGGGCATCGTTCCAC
5461 -----+-----+-----+-----+-----+-----+ 5520
CTCACGGTACAGGCCAAAAGTTGTTTGGTACGTTTACGACTTACTCCCCTAGCAAGGGTG

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TGCGATGCTGGTTGCCAACGATCAGATGGCGCTGGGCGCAATGCGCGCCATTACCGAGTC

5521 -----+-----+-----+-----+-----+-----+ 5580
ACGCTACGACCAACGGTTGCTAGTCTACCGCGACCCGCGTTACGCGCGGTAATGGCTCAG

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CGGGCTGCGCGTTGGTGCGGATATCTCGGTAGTGGGATACGACGATAACCGAAGACAGCTC
5581 -----+-----+-----+-----+-----+ 5640
GCCCCGACGCGCAACCACGCCTATAGAGCCATCACCCCTATGCTGCTATGGCTTCTGTGCGAG

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ATGTTATATCCCGCCGTTAACCACCATCAAACAGGATTTTCGCCTGCTGGGGCAAACCAG
5641 -----+-----+-----+-----+-----+ 5700
TACAATATAGGGCGGCAATTGGTGGTAGTTTGTCTAAAAGCGGACGACCCCGTTTGGTC

CGTGGACCGCTTGTGCAACTCTCTCAGGGCCAGGCGGTGAAGGGCAATCAGCTGTTGCC
5701 -----+-----+-----+-----+-----+ 5760
GCACCTGGCGAACGACGTTGAGAGAGTCCCGGTCCGCCACTTCCCGTTAGTCGACAACGG

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CGTCTCACTGGTGAAAAGAAAACCACCCTGGCGCCAATACGCAAACCGCCTCTCCCCG
5761 -----+-----+-----+-----+-----+ 5820
GCAGAGTGACCACTTTTCTTTTTGGTGGGACCGCGGGTTATGCGTTTGGCGGAGAGGGGC

CGCGTTGGCCGATTCAATTAATGCAGCTGGCACGACAGGTTTCCCGACTGGAAAGCGGGCA
5821 -----+-----+-----+-----+-----+ 5880
GCGCAACCGGCTAAGTAATTACGTCGACCGTGCTGTCAAAGGGCTGACCTTTCGCCCGT

GTGAGCGCAACGCAATTAATGTAAGTTAGCTCACTCATTAGGCTATACTGGCTTAACTAT
5881 -----+-----+-----+-----+-----+ 5940
CACTCGCGTTGCGTTAATTCAATTCGAGTGAGTAATCCGATATGACCGAATTGATA

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GCGGCATCAGAGCAGATTGTACTIONGAGAGTGACCATAACCGGAATTCCGGTATGCGGTGTG
5941 -----+-----+-----+-----+-----+ 6000
CGCCGTAAGTCTCGTCTAACATGACTCTCACGTGGTATGGCCTTAAGGCCATACGCCACAC

AAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCTCTTCCGCTTCTCTCGC
6001 -----+-----+-----+-----+-----+ 6060
TTTATGGCGTGTCTACGCATTCTCTTTTATGGCGTAGTCCGCGAGAAGGCGAAGGAGCG

TCACTGACTCGCTGCGCTCGGTCGTTCCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGG

6061 -----+-----+-----+-----+-----+-----+-----+ 6120
AGTGACTGAGCGACGCGAGCCAGCAAGCCGACCCGCTCGCCATAGTCGAGTGAGTTTCC

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CGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAG
6121 -----+-----+-----+-----+-----+-----+ 6180
GCCATTATGCCAATAGGTGTCTTAGTCCCCTATTGCGTCCTTTCTTGTACTACTCGTTTTTC

GCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTTCATAGGCTCC
6181 -----+-----+-----+-----+-----+-----+ 6240
CGGTCGTTTTCCGGTCCTTGGCATTTCGGCGCAACGACCCGCAAAAAGGTATCCGAGG

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GCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAG
6241 -----+-----+-----+-----+-----+-----+ 6300
CGGGGGGACTGCTCGTAGTGTTTTTAGCTGCGAGTTCAGTCTCCACCGCTTTGGGCTGTC

GACTATAAAGATAACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGA
6301 -----+-----+-----+-----+-----+-----+ 6360
CTGATATTTCTATGGTCCGCAAAGGGGGACCTTCGAGGGAGCACGCGAGAGGACAAGGCT

CCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTC
6361 -----+-----+-----+-----+-----+-----+ 6420
GGGACGGCGAATGGCCTATGGACAGGCGGAAAGAGGGGAAGCCCTTCGCACCGCGAAAGAG

ATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTGCTTCGCTCCAAGCTGGGCTGTG
6421 -----+-----+-----+-----+-----+-----+ 6480
TATCGAGTGCGACATCCATAGAGTCAAGCCACATCCAGCAAGCGAGGTTTCGACCCGACAC

TGCACGAACCCCCCGTTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGT
6481 -----+-----+-----+-----+-----+-----+ 6540
ACGTGCTTGGGGGGCAAGTCGGGCTGGCGACGCGGAATAGGCCATTGATAGCAGAACTCA

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CCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAAACAGGATTAGCA
6541 -----+-----+-----+-----+-----+-----+ 6600
GGTTGGGCCATTCTGTGCTGAATAGCGGTGACCGTCGTCGGTGACCATTGTCCTAATCGT

GAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACA
6601 -----+-----+-----+-----+-----+-----+ 6660
CTCGCTCCATACATCCGCCACGATGTCTCAAGAACTTCACCACCGGATTGATGCCGATGT

6661 CTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAG 6720
-----+-----+-----+-----+-----+-----+
GATCTTCCTGTGCATAAACCATAGACGCGAGACGACTTCGGTCAATGGAAGCCTTTTTTCTC

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6721 TTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGGCA 6780
-----+-----+-----+-----+-----+-----+
AACCATCGAGAACTAGGCCGTTTGTGGTGGCGACCATCGCCACCAAAAAACAAACGT

6781 AGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGG 6840
-----+-----+-----+-----+-----+-----+
TCGTCGTCTAATGCGCGTCTTTTTTCTAGAGTTCTTCTAGGAACTAGAAAAGATGCC

6841 GGTCTGACGCTCAGTGGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGAGATTATCAA 6900
-----+-----+-----+-----+-----+-----+
CCAGACTGCGAGTCACCTTGCTTTTGGAGTGCAATTCCTAAAACCAGTACTCTAATAGTT

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6901 AAAGGATCTTCACCTAGATCCTTTTCCGGAATTCCAAATCAATCTAAAGTATATATGAGT 6960
-----+-----+-----+-----+-----+-----+
TTTCCTAGAAGTGGATCTAGGAAAAGGCCTTAAGGTTTAGTTAGATTTTATATATACTCA

6961 AAACCTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTC 7020
-----+-----+-----+-----+-----+-----+
TTTGAACCAGACTGTCAATGGTTACGAATTAGTCACTCCGTGGATAGAGTCGCTAGACAG

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7021 TATTTTCGTTTCATCCATAGTTGCCTGACTCCCCGTCGTGTAGATAACTACGATACGGGAGG 7080
-----+-----+-----+-----+-----+-----+
ATAAAGCAAGTAGGTATCAACGGACTGAGGGGCAGCACATCTATTGATGCTATGCCCTCC

7081 GCTTACCATCTGGCCCCAGTGCTGCAATGATAACCGCGAGACCCACGCTCACCGGCTCCAG 7140
-----+-----+-----+-----+-----+-----+
CGAATGGTAGACCGGGGTCACGACGTTACTATGGCGCTCTGGGTGCGAGTGGCCGAGGTC

7141 ATTTATCAGCAATAAACAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGGTCTTGCAACTT 7200
-----+-----+-----+-----+-----+-----+
TAAATAGTCGTTATTTGGTCGGTCGGCCTTCCCGGCTCGCGTCTTACCAGGACGTTGAA

7201 TATCCGCTCCATCCAGTCTATTAATTGTTGCCGGAAGCTAGAGTAAGTAGTTCCGCCAG 7260
-----+-----+-----+-----+-----+-----+
ATAGGCGGAGGTAGGTCAGATAATTAACAACGGCCCTTCGATCTCATTTCATCAAGCGGTC

TTAATAGTTTGCGCAACGTTGTTGCCATTGCTGCAGGCATCGTGGTGTACGCTCGTCGT

7261 -----+-----+-----+-----+-----+-----+ 7320
AATTATCAAACGCGTTGCAACAACGGTAACGACGTCCGTAGCACCACAGTGCGAGCAGCA
TTGGTATGGCTTCATTTCAGCTCCGGTTCCCAACGATCAAGGCGAGTTACATGATCCCCCA
7321 -----+-----+-----+-----+-----+-----+ 7380
AACCATACCGAAGTAAGTCGAGGCCAAGGGTTGCTAGTTCGCTCAATGTACTAGGGGGT
TGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCTCCGATCGTTGTCAGAAGTAAGTTGG
7381 -----+-----+-----+-----+-----+-----+ 7440
ACAACACGTTTTTTTCGCCAATCGAGGAAGCCAGGAGGCTAGCAACAGTCTTCATTCAACC
CCGCAGTGTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACTGTCATGCCAT
7441 -----+-----+-----+-----+-----+-----+ 7500
GGCGTCACAATAGTGAGTACCAATACCGTCGTGACGTATTAAGAGAATGACAGTACGGTA

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CCGTAAGATGCTTTTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAATAGTGTA
7501 -----+-----+-----+-----+-----+-----+ 7560
GGCATTCTACGAAAAGACACTGACCACTCATGAGTTGGTTCAGTAAGACTCTTATCACAT
TGCGGCGACCGAGTTGCTCTTGCCCGGCGTCAACACGGGATAATACCGCGCCACATAGCA
7561 -----+-----+-----+-----+-----+-----+ 7620
ACGCCGCTGGCTCAACGAGAACGGGCCGAGTTGTGCCCTATTATGGCGCGGTGTATCGT

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GAACTTTAAAAGTGCTCATCATTGGAAAACGTTCTTCGGGGCGAAAACCTCTCAAGGATCT
7621 -----+-----+-----+-----+-----+-----+ 7680
CTTGAAATTTTACGAGTAGTAACCTTTTGCAAGAAGCCCCGCTTTTGAGAGTTCCTAGA
TACCGCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACTGATCTTCAGCAT
7681 -----+-----+-----+-----+-----+-----+ 7740
ATGGCGACAACCTCTAGGTCAAGCTACATTGGGTGAGCACGTGGGTTGACTAGAAGTCGTA
CTTTTACTTTACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAA
7741 -----+-----+-----+-----+-----+-----+ 7800
GAAAATGAAAGTGGTCGCAAAGACCCACTCGTTTTTTGTCCTTCCGTTTTTACGGCGTTTTT
AGGGAATAAGGGCGACACGGAAATGTTGAATACTCATACTCTTCCTTTTTTCAATATTATT
7801 -----+-----+-----+-----+-----+-----+ 7860
TCCCTTATTCCCCTGTGCCTTTACAACCTTATGAGTATGAGAAGGAAAAAGTTATAATAA
GAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAA
7861 -----+-----+-----+-----+-----+-----+ 7920
CTTCGTAAATAGTCCCAATAACAGAGTACTCGCCTATGTATAAACTTACATAAATCTTTT

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ATAAACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTCTAAGAAA
 7921 -----+-----+-----+-----+-----+-----+-----+ 7980
 TATTTGTTTATCCCCAAGGCGCGTGTAAGGGGCTTTTTCACGGTGGACTGCAGATTCTTT

 CCATTATTATCATGACATTAACCTATAAAAATAGGCGTATCACGAGGCCCTTTTCGTCTTC
 7981 -----+-----+-----+-----+-----+-----+-----+ 8040
 GGTAATAATAGTACTGTAATTGGATATTTTTTATCCGCATAGTGCTCCGGGAAAGCAGAAG

 AAGA
 8041 ---- 8044
 TTCT

Enzymes that do cut and were not excluded:

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

Enzymes that do not cut:

AccI	AflII	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	SunI	SwaI		

Enzymes excluded; MinCuts: 1 MaxCuts: 2

AceIII	AcI	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	Bsp1286I	BspGI	BspMI	BsrI	BsrBI	BsrDI	BsrFI
BssSI	BstXI	BstYI	Cac8I	CjeI	CjeI	CjePI	CjePI
ClaI	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	MspAlI	MwoI	NarI	NciI
NgoAIV	NlaIII	NlaIV	NspI	Pfl1108I	PflMI	PleI	Psp1406I
PstI	PvuI	PvuII	RcaI	RsaI	SapI	Sau96I	Sau3AI
ScrFI	SfaNI	SfcI	SimI	SspI	StyI	TaiI	TaqI
TaqII	TaqII	TauI	TfiI	ThaI	TseI	Tsp45I	Tsp4CI
Tsp509I	TspRI	Tth111III	VspI	XbaI	XcmI		