TABLES.CHR2_ARS.TXT
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The content of this file is part of the data unraveled by a consortium of
European laboratories supported by the Commission of the European Union
in the framework of sequencing yeast chromosome II.

H. Feldmann et al. (1994) ' Complete sequence of yeast chromosome II', submitted

The dataset was developed in collaboration of
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>>>> The data may be used for scientific purposes under the
condition that the proper references are given. <<<<<

We have made every effort to ensure liability of the data and
cannot be responsible for the consequences to users of any
errors resulting from its use.

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Table 10. Yeast chromosome II: List of ARS consensus sequences, putative ABF1 and OBF1 binding sites

(A) ARS consensus sequences

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1                    WTTTATRTTTW
       116,603: TTTTT TTTTATATTTT TTTTC
       189,772: TATGA TTTTATGTTTA TAAAG
       232,297: AATTA TTTTATGTTTT TGTTT
       320,083: GAGAG TTTTATGTTTA CAGTA
       362,748: CTAAG TTTTATATTTT CTGCA
       375,152: CATTT TTTTATGTTTT TTCTA
       414,241: CCCCT TTTTATGTTTT GGTTT
       537,400: GGACA TTTTATATTTT TGAGC
       562,826: GATTT TTTTATATTTT AATCA
       597,195: GCATC ATTTATGTTTT CCCCA
       616,765: TTTTT ATTTATATTTT TCTTC
       626,058: TATTT ATTTATATTTA TTTTT
       659,044: ATATT ATTTATGTTTT TCTCA
       749,039: ATGCT TTTTATATTTT CTTTC
       786,471: TATCG ATTTATATTTT CCAAC
       806,421: AATAT TTTTATGTTTA GGTGA

1 /Rev               WAAAYATAAAW
           606: TCACC TAAACATAAAA ATTAT
        78,493: AAGGT TAAACATAAAA AGTAG
        95,810: AACGA TAAACATAAAA TAAAC
       160,181: AAATG AAAATATAAAT TACAA
       164,252: TTCAC TAAATATAAAA CTGAT
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        235,361: AAGGG AAAATATAAAT AAATA
        239,287: GTTAG AAAATATAAAA CAATA
        249,070: AATAC AAAACATAAAA ATAAA
        250,788: ACAAT AAAATATAAAT CAATA
        282,745: GAGGG AAAATATAAAT GTTTT
        327,080: CGAGT AAAATATAAAT TATTT
        367,704: TAAAA AAAATATAAAA TTACA
        389,074: GAAAT AAAATATAAAA AAATT
        402,040: AGAAC AAAATATAAAT AAATA
        452,542: ACACG AAAATATAAAT ACATC
        498,501: TCAAA AAAATATAAAA ACACT
        565,473: CATAT TAAACATAAAT ACGCA
        613,671: CTATC TAAATATAAAT ATGTG
        768,035: TTTCA TAAACATAAAA TCCTT
        786,778: AATTA TAAATATAAAA GCAAG

     Total finds:         36

(B) ARS-binding factor 1, consensus sequences

1                    RTCRYNNNNNACG
           385: CCCAC ATCATTATGCACG GCACT
        31,992: CTTTG ATCGTCTATGACG ATTTG
        34,678: TGTTG ATCACGCGAAACG GTAAA
        41,300: AATGC ATCATTCTAAACG GGCGG
        61,354: GTGGC ATCATCAGGAACG AGTTT
        69,105: TCTAT ATCGTGTTGCACG AAGGA
        95,371: CGTTG GTCGCTATTCACG GAATG
       109,599: TACAG GTCGTCTTCCACG TGGTA
       114,178: AGTTT GTCATATTTGACG CGAGG
       122,973: TCAAC ATCATCTCTTACG GATTG
       130,207: ATTGG ATCACGGGCGACG GACAA
       139,544: CCACC GTCGTCAAGCACG AAACA
       139,941: TTGTT ATCACCAATAACG AGAAA
       140,015: GTTGA ATCACTAATTACG AAAGA
       187,682: CCGTG ATCGCGCGCCACG GGCCG
       191,757: AATAC GTCATCCTGAACG TTCAT
       195,366: ATAGA ATCATTACCAACG TCAAC
       210,545: GTATA GTCACTTTCTACG AAGCA
       221,065: ATGAT ATCATGTAAAACG AGGCA
       264,061: GGCTG GTCGCGCCCGACG GGTTC
       274,673: TTAGC ATCACAAAATACG CAATA
       279,792: CGTCC ATCATTCCTAACG CTATC
       285,453: TCAAC GTCACCCTCAACG TGGAT
       286,148: GCGTG GTCATTCAATACG GAGAA
       291,526: CACTG ATCATAACAAACG TCCAA
       293,985: TTAAT ATCACGTCACACG ACGCA
       303,967: TGAGG ATCATCCAACACG TGCGA
       330,379: TCGTC GTCGTCATCCACG ACTAT
       331,505: ATTGC GTCACTCGCGACG TAAAC
       336,135: TTCAT ATCACGGCATACG TTAAC
       345,493: CTTGT ATCATCATGAACG CTTTT
       350,717: TAAAC GTCATCTCGCACG ATATG
       369,261: CTTGG ATCATGAAGTACG TCTCG
       381,462: TGGCT ATCGTGGACCACG CTTTC
       386,473: TTCAT ATCATTATCAACG TAAAA
       386,537: GCAGT ATCATCCTTCACG ACCCG
       388,216: GTCTC ATCGTCTCCAACG CATGA
       403,527: GAAAC GTCGTCAACAACG GAATC
       421,906: ACAGC ATCGTTAATGACG TATCT
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        423,756: ACAGC ATCGTTAATGACG TATCT
        438,885: GGTAT ATCATTTCAAACG AATAA
        446,371: TAGAT ATCGTTCTGAACG GCTGA
        446,409: AGAAC ATCACTTTACACG GATCG
        452,529: GTCAT ATCACAGTACACG AAAAT
        452,735: CAGTG ATCATCTTGCACG TTGCT
        478,638: AGATA ATCGCTCTTTACG GTTTG
        555,109: TATTC ATCGTCATATACG GAACA
        570,367: GAAGG ATCATGACTAACG TTTGC
        589,283: CCACT ATCATCGGGAACG GTACA
        639,411: ATATT GTCGTGGGCCACG AATGA
        667,817: GGGCA ATCATAATTAACG TTTAG
        676,094: GCAGC ATCGTTATACACG TAGTG
        688,224: GGTCG ATCATCTTTTACG CCAAG
        741,603: AATGA ATCATAGGATACG TTAGA
        755,096: TAATA ATCACATTACACG AATAA
        762,107: TTATT ATCACGTTTCACG GATTA
        776,456: TTATC ATCGTGTTATACG ATGCG

1 /Rev                  CGTNNNNNRYGAY
         15,429: ATCGC CGTAAAGTATGAT GTGTA
         31,994: TTGAT CGTCTATGACGAT TTGTC
         55,409: GTGCT CGTGACATATGAC TCCAA
         81,932: GTGTT CGTGCGTCGCGAT TTTTT
         95,411: CTGCT CGTCCTGGGTGAC CTTTT
        107,545: ATTTT CGTCAGGCGTGAT ATCAG
        118,931: GCATC CGTGTTTCGTGAC ATCAT
        135,105: GTGTT CGTACGGAGCGAT AATTG
        147,857: CTATT CGTTTGAGGCGAT GAACA
        158,361: GTGCT CGTGCATCGTGAT GTTAT
        166,359: ACTTA CGTATTAAATGAC GTACT
        174,352: GTTAG CGTCTTCAACGAC GGTCG
        180,593: TATGA CGTTCTCGATGAT CTTCA
        180,629: TTTCC CGTAACATATGAT ATATC
        196,445: TGCTC CGTTCAACGCGAT CATTG
        226,777: TACCT CGTCCAGTATGAT TGTTA
        232,398: CCTTA CGTCGGTGACGAC GATAT
        232,678: CAAAG CGTAAGTTATGAT CTTAT
        252,148: ACTAT CGTATCTAATGAC TGTGG
        252,185: CTTAG CGTCTGCGATGAC GATAT
        281,182: CTTAC CGTTAATTACGAC AAATT
        284,723: ATCAC CGTCTTCAACGAC ATAGT
        291,113: GAGCA CGTTTTTGATGAT CAAAT
        291,940: GTATC CGTTGATAATGAC TGTCA
        303,702: GACCG CGTTCATCATGAT GAGGA
        304,636: CTTAA CGTGTTCCACGAT CTTGT
        330,381: GTCGT CGTCATCCACGAC TATGT
        331,504: AATTG CGTCACTCGCGAC GTAAA
        358,693: TATAT CGTTTTTAATGAT TGCAA
        395,017: CCTAA CGTATAGTGTGAT ACCGA
        420,547: CTTGT CGTGCGCTATGAT AAACA
        460,568: CCCTT CGTCCTCAGTGAC CTCTC
        472,640: GGTAA CGTCTGTGGTGAC GCTAA
        477,641: CGAGG CGTAGAAAATGAT CACTA
        489,473: AAAAC CGTTGTGAGTGAC CGAAA
        529,087: CTTTA CGTATAAAATGAT ATATT
        555,180: CTGGG CGTGTTCCATGAC GTATT
        559,079: GATCT CGTGGTATGTGAT ATCGT
        559,094: GATAT CGTGTCTAATGAC TTGAC
        561,196: AATCT CGTTTCGAATGAT TTAAT
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       562,660: TTACC CGTCCTGTACGAT GCAGT
       570,201: CTCCT CGTATGATGTGAT TTTTG
       584,460: CATAG CGTATTTCATGAT GGGTC
       587,789: ACATC CGTTTTCGGTGAT GCGGT
       609,263: CTCAC CGTCAAGTGCGAT TTCCG
       609,464: GAACC CGTCGTTGACGAT AGGTT
       612,687: GAACC CGTAAAAGATGAT ATTTA
       631,956: ATAGG CGTTTCGAATGAT GGTAA
       641,330: TTCTC CGTACAACACGAT AAAAT
       645,190: CTGCT CGTCTTGAGCGAC AGGGC
       656,735: GGACA CGTCGTTAGTGAC AATCG
       662,718: TAAGT CGTATGGTATGAC TGGCA
       696,995: CCCGA CGTGGTCGATGAT CGCAG
       734,688: GAAGA CGTGGGCAGCGAC GAAGC
       764,742: GAAAG CGTGTAAAGTGAT ACAGA
       764,766: CCTAC CGTGTCTAATGAT ATCGT
       765,275: TTTTT CGTTGAATGCGAC TCTTA
       776,458: ATCAT CGTGTTATACGAT GCGGA
       780,979: TTCGA CGTACCAAACGAT TGGTA
       801,275: ATCCT CGTTCATTATGAT ATTTA
       806,640: AGTGC CGTGAATAATGAT GTGAG

     Total finds:         118
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(C) Origin of replication-binding factor 1, consensus sequences

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1                    CAAGTGCCGTGCATAATGATGTGGGT
       806,633: TGAGG caagtgccgtgaataatgatgtgagt GCATT mis=2

1 /Rev               ACCCACATCATTATGCACGGCACTTG
           379: AATGC ACCCACATCATTATGCACGGCACTTG CCTCA

     Total finds:          2
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