

Sequence of the *Candida albicans* gene encoding actin

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Using the *S. cerevisiae* ACT gene (1,2) as a probe, we isolated the ACT gene of *C. albicans* from a genomic bank of strain ATCC 10231 (3). The sequence of a 3.206 kb *Clal-Sall* fragment contains the potential coding region for *C. albicans* actin, which appears to have 94.4, 88.5 and 86.1% homology to actins of *S. cerevisiae* (1,2), *A. nidulans* (4) and *S. pombe* (5), respectively. The position of the single intron is deduced from the consensus sequences at the 5' end (GTATGT), the branch point (TACTAAC) and the 3' end (TAG) of the intron (6,7)(underlines). This gene appears expressed, because (1) it is unique in the *C. albicans* genome, as revealed by Southern blotting experiments and (2) it encodes a single mRNA species of about 1.5 kb.

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1 ATCGATAGAGCTATTAAGATCACCAGCCCTGCTTTATAATAAACTTAGTCTAATATTTCTTTTGGACGAGATAGAAACTGTTCTCAGGTG
91 GCAAAACACAGCTTAAAGCTCTGTGTTAAAABAAAGATCTCCGGCTATGCCAACAAAAGGAGTGACATTATATGTAAGAAAGAAATGTT
181 GTAATTCGCGAABACAACTTTAATGCTACTGTGCGCCACCAATATCTATGGCCAAGGGCCCTTAAACATGCCCGGAAATATA
271 CACTCAAGGTAAACCTACTATGCTTTAGAGCCCTCAGGATCAATTTGTTTAAATGAATGACTGCCAAAACTAGAAAAGTAGCCCTTAC
361 ATAAAGCAAGCTAATGTTTACAGAGAGTTTAGTAAACCAATGAAGCAAGTATATCTGGCAAACTTGAAACTTATCTGTGAATATAGAGCT
451 CATAGTAAAAGTGTAAGAAAGAGTAAAGGCAGACCAAAATCAAAATTTGCAACAGTACAAAGAAATTTTCAGCCGTCAAACTAGAGAA
541 TAATAAGAAAACGGCCCTTCAAABAAAGAAAATTTTAGTTTTCCTTTGTTGTGGGTGTGGCTATTATATATATAGTTTT
631 ACTCGTAATACCAATAAAATTTCCGGTTGATAGGTTTATTTAATAAGCTAATTTGTTTCTAATCGTGAATTTATGCTGTGTATATA
721 AGTAGTGTGGTGCACCTCCCAAAAATTTTGTGTATATAGTCCGTTAAAGAGAAAAGAAAAGATCCATACACACAGCTTAAT
811 AGTGTTCACAGTAAATACCTATATTTTGTCTAATTTGCTTTTCAGCCAGGATTTATGCAACGAACTAATTTT
901 TTTATATATTTTCAGATTTCTTTTTCTTCTTCTTCAATTTTCACTCTGTTCTTCTCTTAGAAACATTTATCT

991 CGATATAAATATAAAAAATAATCATTCAA ATG GAC GGT G GTATGTTTTAAATTTAGCTTCAATTTCAATTGATTGATTAAT

1076 CAGTGTATTGGTTTCAATATGACAAATGGGTAGGGTGGGAAACCTTCATTTTCAATTCAGATCAAACTTTTTTGTGTGCACATAATTT
1166 TCRCGTTTGGGATGTTACTGTACATTAAATATACACACATCAGCTTATAATTTTGAAGTAAATTTATCAGATATGTTGTGACAGATC
1256 ATGGAAATGGCTAACTTCAATGTAATCTGTTCTCCCTTTTCAAAGTTTCAGCTTTTTTTGATTGATTGATTGATTCGTCCGCGAGT
1346 TTTCAAACCAATTCGGTAGTAACTCTATCAATCAATGTACGACAAAGGCTCAATATTCAAAATTTGCAATGTTTTATGTTTCTCAG
1436 GTGACTTTGTCAAGCAATTTGATTCAACATTTGCTTTTGGTGTGTTGACGAGTTCCTAGTITGGACTTGTGTTTATCTGGACTATACAG
1526 ATTTCCCGGCTCACTAATGTTTTTTTTTTCGACGCTCAGTGCACACAATAAACAACACAAACACAAACACAGCAAGAAAATAA
1616 ACGAACAATTGAATGAAACCAAGCCAACCTGAAAATTCCTTATTTAAATGACTGCATACCTAACCCATTTTTATAG AA GAA GTT
1700 GCT GCT TTA ATT ATC GAT AAC GGT TCT GGT ATG TGT AAA GCC GGT TTT GCC GGT GAC GAC GCT CCA AGA
1769 GCT GTT TCC CCA TCT CTT TTT GGT AGA CCA AGA CAT CAA GGT ATC ATG TGT GGT CCA AAA GAT
1838 TCT TAT GTT GGT GAT GAA GCC CAA TCC AAA AGA GGT ATT TTG ACC TTG AGA TAC CCA ATT GAA CAC GGT
1907 ATT GTT TCC AAC TGG GAC ATT GAA AAA ATC TGG CAT CAC ACT TTT TAC AAT GAA TTG AGA GTT GCT
1976 CCA GAA GAA CAT CCA GTT TTG TTG ACC GAA GCT CCA ATG AAT CCA AAA TCC AAC AGA GAA AAG ATT ACT
2045 CAA ATT ATG TTT GAA ACT TTT AAT TCT CCA GCT TTC TAC TTT CCA GCT GAT GCT GTT TCT TTG TAC
2114 TCT TCT GGT AGA ACT ACG GGT ATT GTT TTG GAT TCT GGT GAT GGT GTT ACT CAC GTT GTT CCA ATT TAC
2183 GCT GGT TTC TTA CCA CAT GGT ATT TTA AGA ATT GAT TTG GCT GGT AGA GAC TTT ACC AAC CAT TTG
2252 TCC AAG ATT TTG TCT GAA CGT GGT TAC GAT TTC ACT ACT AGT GCT CAA AGA GAA ATT GTC AGA GAC GTT
2321 AAA GAA AGA TTG TGT TAC GCT TGT GAT TTT CCA CAA GAA ACT GCT TCT TCT CAA TCT TCT GCT
2390 ATT GAA AAA TCT TAT GAA TTA CCA GAT GGT CAA GTT ACT ACT ATT GGT AAC GAA AGA TCT AGA GCT CCA
2459 GAA GCT TTG TTC AGA CCA GCT GAT TTA GGT TTG GAA GCT GCT GGT ATT GAC CAA ACC ACT TTC AAC TCC
2528 ATC ATG AAG TGT GAC ATT GAT GGT AGA AAA GAA TTA TAC GGT AAC ATT GGT ATT GGT GGT ATT ACC
2597 ATG TTC CCA GGT ATT GCT GAA CGT ATG CAA AAG GAA ATT ACT GCT TTG GCT CCA TCT TCT ATT AAA GTT
2666 AAG ATT ATT GCT CCA CCA GAA AGA AAA TAC TCT GTC TGG ATT GGT GGT TCT ATT TTG GCT TCA TTG TCT
2735 ACT TTC CAA CAA ATG TGG ATT TCA AAA CAA GAA TAC GAC GAA TCT GGT CCA TCC ATT GTT CAC CAC AAA
2804 TGT TTC TAA GAGTAAATCTGGAAATCTGGAAATCTGGTTTTGTATCTTGTTATTCTCTTTTTGTTATTACATATAACTTGT

2891 TACTTTTTTAAAAAATCTTTGTTATTTTATAAATATATAAACTAAATTTAAGAAAAAGAAAAATGTTTTATTGAGAGATTGATA
2981 TTTTCTTGAAATTTAGCTTTTATAAAGTATTATTATGTAAAAAACAAAATATAACATATAAAAGTAAAGACTATAAAAAATG
3071 CCACCAAGGCAATTTCTAATCTTTGTGTTGTTTTCATCTTCTGTCTAGAGGAACATTATTTATTATTTTCGTCCAGGGTATTTTC
3161 TCTTTGTTGATTCATCCCATTCATCATATAAATGTGCGA
    
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