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Corrigendum

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Isolation and sequence analysis of *CDC43*, a gene involved in the control of cell polarity in *Saccharomyces cerevisiae*

(Recombinant DNA; yeast; cell-division cycle; bud emergence; helix-turn-helix; DNA-binding proteins)

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We have discovered errors in our published sequence of the *Saccharomyces cerevisiae CDC43* gene (Johnson et al., 1990). The correct nucleotide (nt) and amino acid (aa) sequences are shown in Fig. 1 below. The *CDC43* gene is identical in nt and aa sequence to the *S. cerevisiae CAL1* gene (Ohya et al., 1991), which is very similar in deduced aa sequence to the *S. cerevisiae DPR1* gene product (Goodman et al., 1988), a protein involved in the C-terminal modification of *RAS* proteins in *S. cerevisiae*. The synthetic lethality of a *cdc42 cdc43* double mutant (Adams et al., 1990) can now be rationalized if the *CDC43* gene product is involved in the post-translational modification of the *CDC42* gene product. Interestingly, the terminal morphologies of a *CDC43* temperature-sensitive mutant (Adams et al., 1990) and a Ca²⁺-dependent *CAL1* mutant (Ohya et al., 1984) grown under restrictive conditions are not identical; a *CDC43* mutant arrests as large, unbudded cells and a *CAL1* mutant arrests as cells with small buds. Clarification of this discrepancy must await molecular analysis of the nature of the conditional mutations.

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                                GA TCTTCTTTT TACCTGTTT ATTCACTTT TTTTTTTTT -211
CTGAGTTGTT GCGCCTTGA AGAATGGAAA AGCAATAGTT TCAGTGACTA TAGTATACAA TCAAACACCC -141
CGCCAGTTCA AAACCTATTAC TTGCTGACTA ACCCCCAAGT CAICTCTAGC AATTTAAATT TCAATTTTAA -71
GAAAACCTTT ATTTATCCAA CGTGAACAAG TACTTTC AAG CACTTCTGCC CACCCGTATA TCGTGGAAAA -1

ATG TGT CAA GCT ACC AAT GGC CCG AGT AGA GTT GTG ACT AAA AAG CAT AGG AAA TTT TTC GAA 63
Met Cys Gln Ala Thr Asn Gly Pro Ser Arg Val Val Thr Lys Lys His Arg Lys Phe Phe Glu

AGA CAT CTA CAG TTG CTT CCC TCT TCA CAT CAG GGA CAT GAC GTG AAC AGA ATC GCC ATA ATA 126
Arg His Leu Gln Leu Leu Pro Ser Ser His Gln Gly His Asp Val Asn Arg Met Ala Ile Ile

TTC TAC TCA ATC TCA GGA CTC TCT ATA TTT GAT GTT AAC GTT TCT GCC AAG TAC GGC GAT CAT 189
Phe Tyr Ser Ile Ser Gly Leu Ser Ile Phe Asp Val Asn Val Ser Ala Lys Tyr Gly Asp His

CTT GGC TGG ATG GGC AAA CAT TAT ATC AAA ACA GTG CTG GAT GAT ACA GAA AAT ACT GTG ATA 252
Leu Gly Trp Met Arg Lys His Tyr Ile Lys Thr Val Leu Asp Asp Thr Glu Asn Thr Val Ile

TGT GGA TTT GTT GGA AGC TTA GTC ATG AAT ATC CCT CAC GCA ACA ACC ATT AAT CTA CCA AAT 315
Ser Gly Phe Val Gly Ser Leu Val Met Asn Ile Pro His Ala Thr Thr Ile Asn Leu Pro Asn

ACT CTC TTT CCA TTC TTC TCC ATC ATT ATG CTG AGA GAT TAC GAG TAT TTT GAG ACT ATA CTA 378
Thr Leu Phe Ala Leu Leu Ser Met Ile Met Leu Arg Asp Tyr Glu Tyr Phe Glu Thr Ile Leu

GAC AAA AGA AGC CTG CCG AGA TTT GTT TCT AAG TGC CAA CGA CCT GAC CGT GGC TCG TTT GTA 441
Asp Lys Arg Ser Leu Ala Arg Phe Val Ser Lys Cys Gln Arg Pro Asp Arg Gly Ser Phe Val

TCT TGT TTA CAC TAT AAG ACA AAT TGT GGA TCT TCG GTT GAT TCA GAC GAT TTA AGG TTT TCG 504
Ser Cys Leu Asp Tyr Lys Thr Asn Cys Gly Ser Ser Val Asp Ser Asp Asp Leu Arg Phe Cys

TAC ATC GCA GTT GCC ATT CTG TAC ATA TGC GGA TGC CGA TCC AAA GAA GAC TTT GAT GAA TAC 567
Tyr Ile Ala Val Ala Ile Leu Tyr Ile Cys Gly Cys Arg Ser Lys Glu Asp Phe Asp Glu Tyr

ATT GAT ACT GAG AAG TTG CTT GGC TAT ATA ATG TCG CAA CAA TGG TAC AAC GGA GGT TTC GGT 630
Ile Asp Thr Glu Lys Leu Leu Gly Tyr Ile Met Ser Gln Gln Cys Tyr Asn Gly Ala Phe Gly

GCC CAC AAT GAA CCA CAC TCA GGG TAC ACA TCT TGT GCG CTG TCT ACC TTA GCT TTA CTC TCT 692
Ala His Asn Glu Pro His Ser Gly Tyr Thr Ser Cys Ala Leu Ser Thr Leu Ala Leu Leu Ser

AGT TTG GAA AAG CTA TCA GAC AAG TTT AAA GAA CAC ACC ATA ACC TGG CTA TTA CAT AGG CAA 756
Ser Leu Glu Lys Leu Ser Asp Lys Phe Lys Glu Asp Thr Ile Thr Trp Leu Leu His Arg Gln

GTA TCA AGC CAT GGA TGT ATG AAA TTT GAA AGC GAA TTG AAT GCC AGC TAT GAT CAA TCT GAT 814
Val Ser Ser His Gly Cys Met Lys Phe Glu Ser Glu Leu Asn Ala Ser Tyr Asp Gln Ser Asp

CAT GCC CGT TTC CAG CGA AGG CAG AAC AAC TTC GGT GAT ACG TGT TAC GCA TTT TGG TGC TTA 882
Asp Gly Gly Phe Gln Gly Arg Glu Asn Lys Phe Ala Asp Thr Cys Tyr Ala Phe Trp Cys Leu

AAT TCA CTA CAG TTA CTA ACA AAG GAT TGG AAA ATG CTA TGC CAA ACT GAA CTA GTC ACA AAT 945
Asn Ser Leu His Leu Leu Thr Lys Asp Trp Lys Met Leu Cys Gln Thr Glu Leu Val Thr Asn

TAT TTG CTT GAT CGA ACG CAA AAA ACA TTA ACT GGA GGC TTT ACT AAA AAT GAC GAA GAA GAT 1008
Tyr Leu Leu Asp Arg Thr Gln Lys Thr Leu Thr Gly Gly Phe Ser Lys Asn Asp Glu Glu Asp

GCT GAT TTA TAT CAC AGC TGT CTA GGG AGC GCT GCG TTA GCA TTA ATT GAG CGG AAA TTT AAT 1071
Ala Asp Leu Tyr His Ser Cys Leu Gly Ser Ala Ala Leu Ala Leu Ile Glu Gly Lys Phe Asn

GGA GAA TTA TGC ATA CCT CAA GAA ATA TTT AAT GAT TTT ACT AAA AGG TGC TGT TTT TGA 1131
Gly Glu Leu Cys Ile Pro Gln Glu Ile Phe Asn Asp Phe Ser Lys Arg Cys Cys Phe

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Fig. 1. Nucleotide sequence of the *CDC43* gene and predicted aa sequence of the *CDC43* product. The *CDC43* gene is predicted to encode a polypeptide of 376 aa, which is 163 aa longer than our published version (Johnson et al., 1990). The nt sequence is numbered relative to the A of the putative start codon. The GenBank accession number is M31114. The corrected nt sequence was generated by removing a 'C' at nt 637 and a 'T' at nt 691, and by adding an 'A' at nt 724 and 191 additional nt at the end of the published sequence. The remainder of the published sequence is unchanged.