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ERRATUM

Volume **264,** Number 1 (1999), in Article ID bbrc.1999.1354, "Molecular Cloning of the Gene for p85 That Regulates the Initiation of Cytokinesis in *Tetrahymena,*" by Kohsuke Gonda, Kimiko Nishibori, Hiroyoshi Ohba, Atsushi Watanabe, and Osamu Numata, pages 112–118: On page 115, in Fig. 3A it was reported that Repeat I was from amino acid residues 1 to 176, as indicated with a solid line. However, this was incorrect. Repeat I should be from amino acid residues 23 to 176. In Fig. 3B the homologous regions between p85 and parts of the other proteins as indicated by numbers and lines differed slightly from what was depicted. In Fig. 3C, the CaM-binding site of yeast CaM II kinase should be from amino acid residues 324 to 345 instead of residues 331 to 345. The legend was correct as printed. For the reader's convenience, the corrected figure and legend are printed below.

This erratum is Article ID doi:10.1006/bbrc.1999.1839.

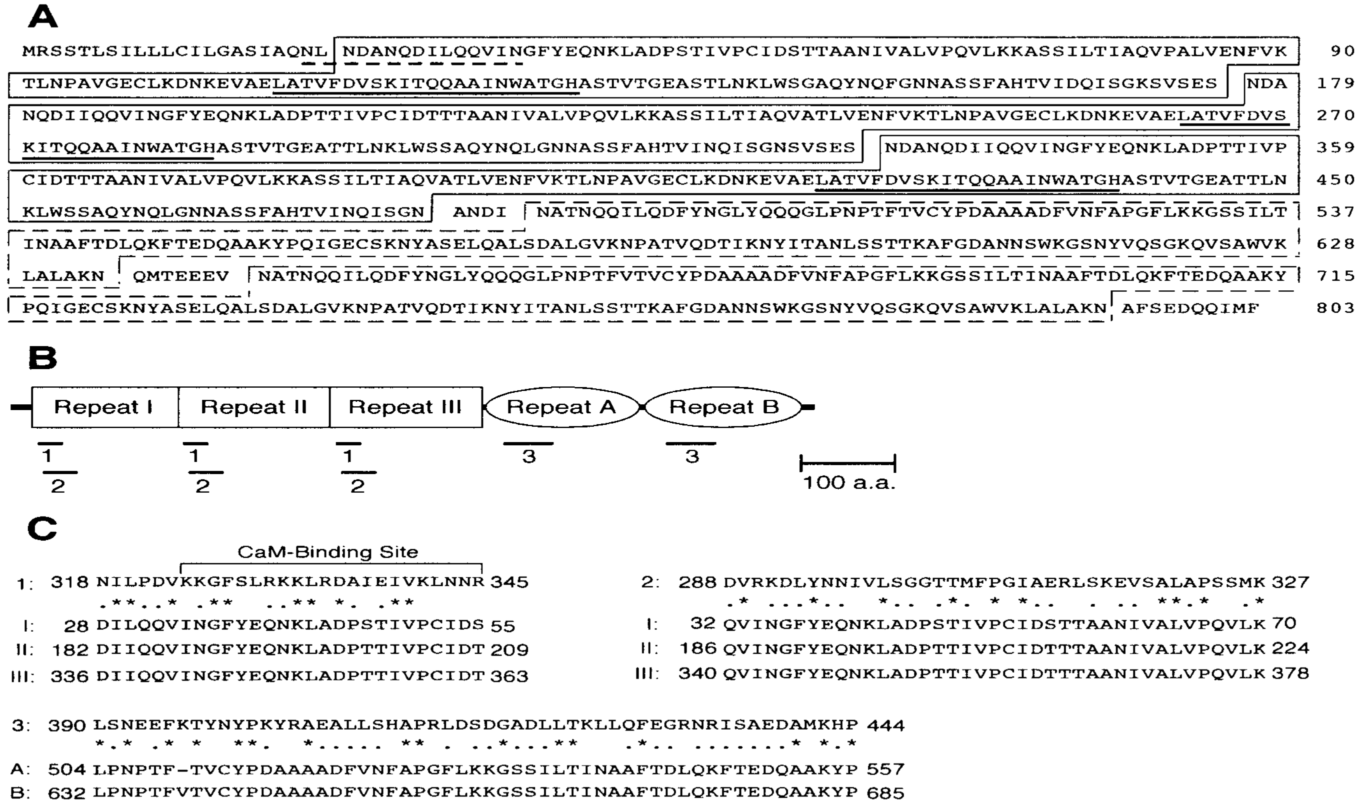

FIG. 3. Amino acid sequence of wild type p85 and comparison with other proteins. (A) A predicted amino acid sequence of wild type p85. The one letter amino acid code is used throughout. The 803-amino-acid protein contains two kinds of repeat sequences that are enclosed with solid and broken lines, respectively. A broken underline indicates the N-terminal amino acid sequence of purified p85, and underlines indicate that of its fragment digested by V8 protease. These data are available from GenBank/EMBL/DDBJ under Accession No. D84491. (B) A schematic drawing of the predicted primary structure of p85. The two kinds of repeat sequences are designated as Repeats I, II, and III and Repeats A and B. Regions homologous to parts of other proteins are underlined with numbers, 1: CaM II kinase in *S. cerevisiae;* 2: actin in *T. thermophila;* and 3: PCTAIRE-1 kinase in human. GenBank/EMBL/DDBJ accession numbers: CaM II kinase, X56961; actin, M13939; PCTAIRE-1, X66363. (C) Sequence alignments between the wild type p85 and parts of other proteins. 1, 2, and 3 are equivalent to those shown in (B). I, II, and III and A and B show the Repeats I, II, and III and the Repeats A and B, respectively. Asterisks indicate identity, and dots indicate similarity.