

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.

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A

MRSSSTLSILLLCILGASIAQN_L | NDANQDILQQVINGFYEQNK_LADPSTIVPCIDSTTAANIVALVPQVLK_KASSIL_TIAQVPALVENFV_K 90

TLNPAVGECLKDNKEVAELATVFDVSKITQQA_IINWATGHASTVTG_EASTLNKLWSGAQYNQFGNNASSFAHTVIDQISGKSV_SES | NDA 179

NQDIIQQVINGFYEQNK_LADPTTIVPCIDTTAANIVALVPQVLK_KASSIL_TIAQVATLVENFVK_TLNPAVGECLKDNKEVAELATVFDV_S 270

KITQQA_IINWATGHASTVTG_EATTLNKLWSSAQYNQLGNNASSFAHTVINQISGNSV_SES | NDANQDIIQQVINGFYEQNK_LADPTTIVP 359

CIDTTTAA_NIVALVPQVLK_KASSIL_TIAQVATLVENFVK_TLNPAVGECLKDNKEVAELATVFDVSKITQQA_IINWATGHASTVTG_EATTLN 450

KLWSSAQYNQLGNNASSFAHTVINQISG_N | ANDI | NATNQQILQDFYNGLYQQQGLPNPTFTVCYPDAAAADFVNFA_PGPLKKGSSIL_T 537

INAAFTDLQKFTEDQAAKYPQIGEC_SSKNYASELQALS_DALGVKNPATVQD_TIKNYITANLSSTTKAFGDANNSWKGSNYVQSGKQVSAWV_K 628

LALAK_N | QMTEEEV | NATNQQILQDFYNGLYQQQGLPNPTFTVCYPDAAAADFVNFA_PGPLKKGSSIL_TINAAFTDLQKFTEDQAAKYP 715

PQIGEC_SSKNYASELQALS_DALGVKNPATVQD_TIKNYITANLSSTTKAFGDANNSWKGSNYVQSGKQVSAWV_KLALAK_N | AFS_EDQQIMF 803

B

Repeat I Repeat II Repeat III Repeat A Repeat B

$\frac{1}{2}$ $\frac{1}{2}$ $\frac{1}{2}$ 3 3 100 a.a.

C

CaM-Binding Site

I: 318 NILPDVKKGFSLRKKLRDAIEIVKLNNR 345
* * * * *

II: 28 DILQQVINGFYEQNK_LADPSTIVPCIDS 55
* * * * *

III: 182 DIIQQVINGFYEQNK_LADPTTIVPCIDT 209
* * * * *

III: 336 DIIQQVINGFYEQNK_LADPTTIVPCIDT 363
* * * * *

2: 288 DVRKDLN_NIVLSGGTTMFP_GIAERLSKEVSALAPSSMK 327
* * * * *

I: 32 QVINGFYEQNK_LADPSTIVPCIDSTTAANIVALVPQVLK 70
* * * * *

II: 186 QVINGFYEQNK_LADPTTIVPCIDTTAANIVALVPQVLK 224
* * * * *

III: 340 QVINGFYEQNK_LADPTTIVPCIDTTAANIVALVPQVLK 378
* * * * *

3: 390 LSNEEFKTYNYPKYRAEALLSHAPRLSDGADLLTKLLQFEGRN_RISAEDAMKHP 444
* * * * *

A: 504 LPNPTF-TVCYPDAAAADFVNFA_PGPLKKGSSIL_TINAAFTDLQKFTEDQAAKYP 557
* * * * *

B: 632 LPNPTFVTVCPDAAAADFVNFA_PGPLKKGSSIL_TINAAFTDLQKFTEDQAAKYP 685
* * * * *

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/DBJ 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/DBJ 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.