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CORRECTIONS

Structural stabilization of protein 4.1R FERM domain upon binding to apo-calmodulin: novel insights into the biological significance of the calcium-independent binding of calmodulin to protein 4.1R

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Volume 440 (2011), pp. 367–374

The published version of Figure 4(B) was incorrect; the corrected Figure and caption are shown here.

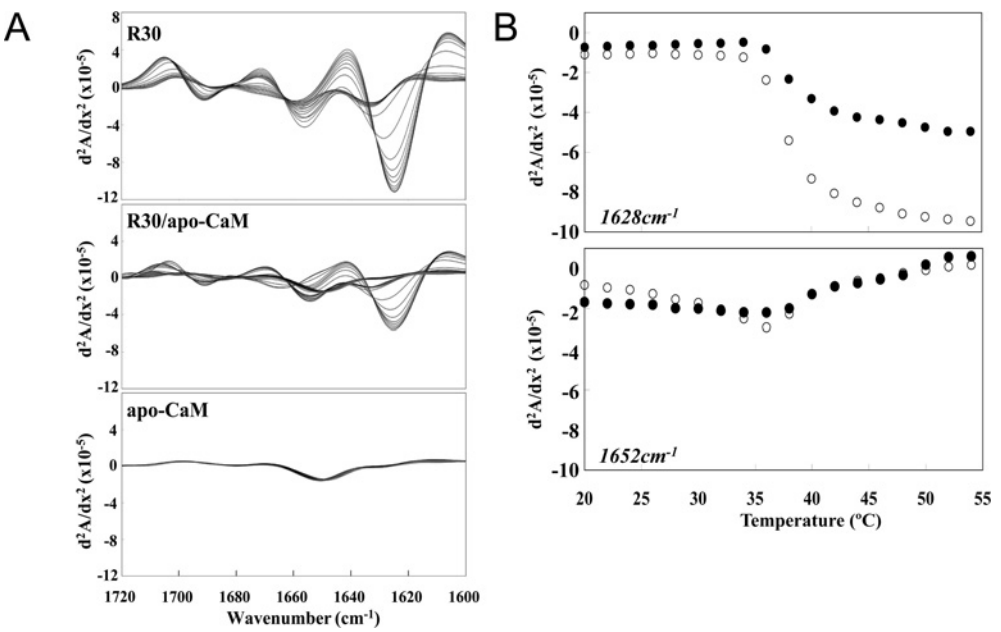

Figure 4 Changes in secondary structure of R30 in the presence and absence of apo-CaM as a function of temperature

(**A**) FTIR measurements enabled the visualization of the second derivative of change in the Amide I region (1720–1600 cm^{-1}). The second derivative of change in the Amide I region of R30 (top panel) and of R30 bound to apo-CaM (middle panel) as a function of temperature is shown. The derivative of apo-CaM alone is shown as control (bottom panel). (**B**) Changes in absorbance for specific regions of R30 (1628 cm^{-1} for α-helix and 1652 cm^{-1} for β-sheet structure) in the presence or absence of apo-CaM as a function of temperature are shown. ○, R30; ●, R30–apo-CaM complex. The same d^2A/dx^2 scale (y-axis) is used for both 1628 cm^{-1} and 1652 cm^{-1}.

Interfacial water molecules in SH3 interactions: a revised paradigm for polyproline recognition

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Volume 442 (2012), pp. 443–451

The wrong PDB code for the free Tsg101-UEV domain is given in the caption to Figure 1(D); the correct PDB code is 2F0R, not 2FOR.

Identification of autophosphorylation sites in eukaryotic elongation factor-2 kinase

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Volume 442 (2012), pp. 681–692

The published version of Figure 3(B) incorrectly featured an additional panel; the corrected figure is shown here.

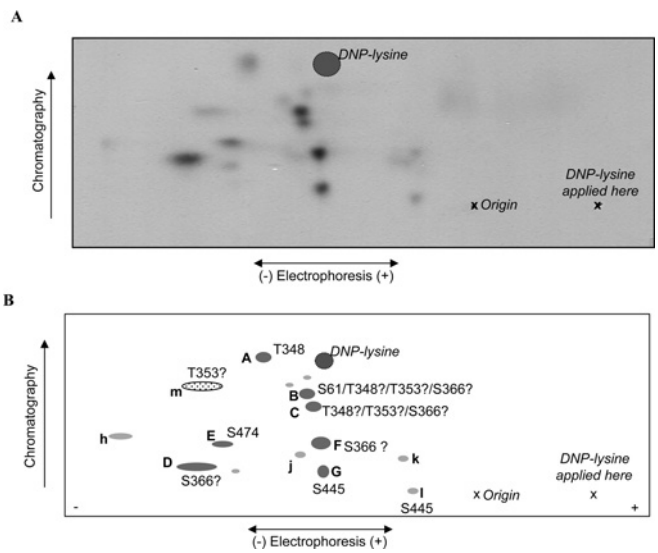

Figure 3 2D peptide maps from autophosphorylated wild-type eEF2K

Wild-type eEF2K was allowed to undergo autophosphorylation in the presence of Ca^{2+}/CaM and then subjected to tryptic digestion. Phosphopeptides were resolved by electrophoresis and chromatography (polarity and directions are indicated). Also shown are the position of the origin, where the peptide samples were applied, "X", and the final migration position of the DNP–lysine marker (cross-hatched circle). (**A**) Representative map of wild-type eEF2K; (**B**) schematic summary of peptides; lettering in capitals for major peptides (shown in dark grey) and in lower case for minor ones (light grey). The peptide shown by the dotted oval ('m') was only observed on maps from the eEF2K[T348A] mutant.