The EMBO Journal (2005) 24, 1092–1093 | © 2005 European Molecular Biology Organization | All Rights Reserved 0261-4189/05
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Corrigenda

Cullin-based ubiquitin ligases: Cul3–BTB complexes join the family

Lionel Pintard, Andrew Willems and Matthias Peter

The EMBO Journal (2005) **24,** 1092. doi:10.1038/sj.emboj.7600623

Correction to: *The EMBO Journal* (2004) **23**, 1681–1687. doi:10.1038/sj.emboj.7600186

Due to redundant and confusing nomenclature, the authors have introduced a mistake in the above review. In this review, they list Smac3/Diablo proteins, involved in apoptosis, as BTB/Kelch proteins. Partly based on this point, they speculate that these proteins might act as substrate-specific adaptors of Cul-3 based E3-ligases. It appears that this protein is distinct from another BTB/Kelch-containing protein also called Diablo. Therefore, the authors' speculation that Cul-3 based ligases could play a role in apoptosis is not correct and misleading.

The authors apologize for this error.

Human Orc2 localizes to centrosomes, centromeres and heterochromatin during chromosome inheritance

Supriya G Prasanth, Kannanganattu V Prasanth, Khalid Siddiqui, David L Spector and Bruce Stillman

The EMBO Journal (2005) **24,** 1092–1093. doi:10.1038/sj.emboj.7600624

Correction to: *The EMBO Journal* (2004) **23,** 2651–2663. doi:10.1038/sj.emboj.7600255

Due to an author error, the X-axis in Figure 3D was mislabelled as INA instead of DNA. The correct figure is reproduced below.

The authors apologize for this error.

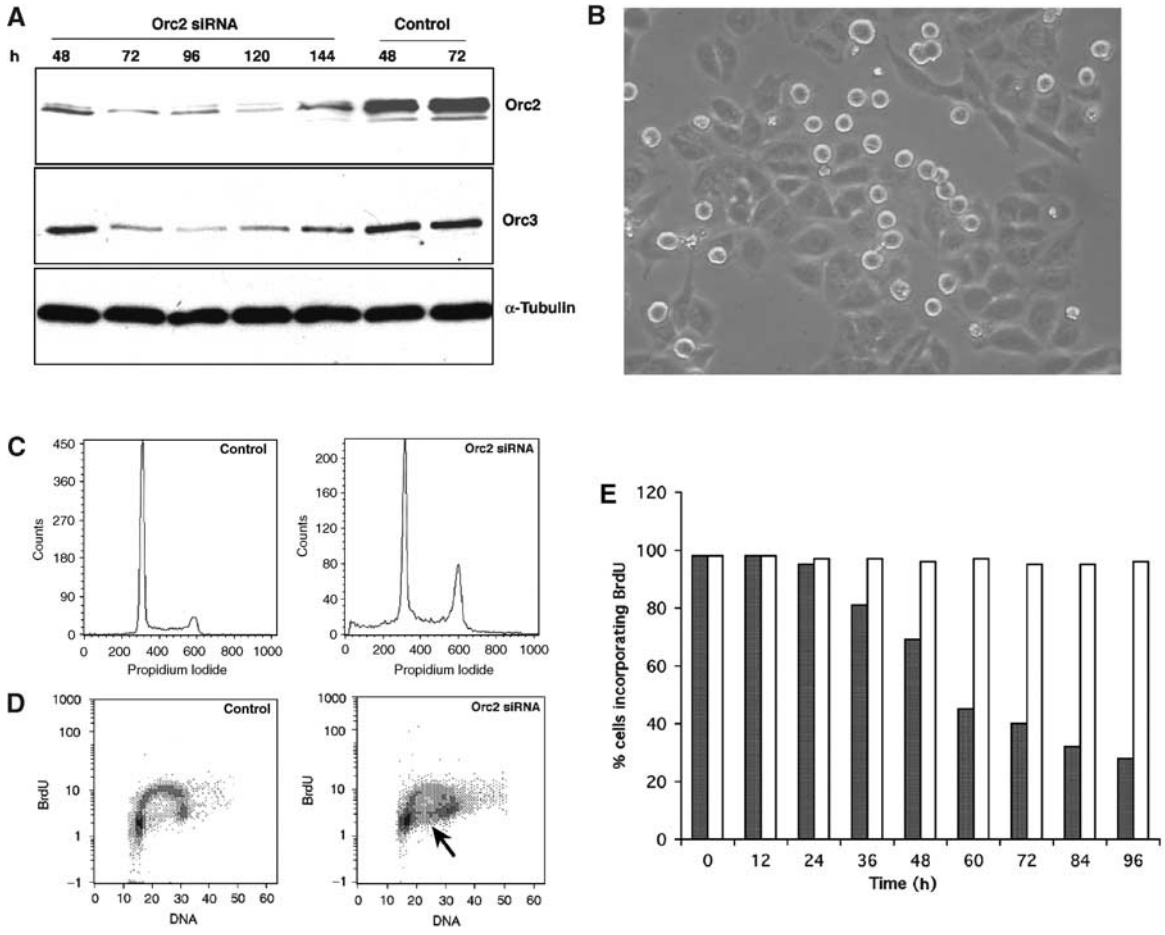

Figure 3 Orc2 depletion has dual execution points. (**A**) Immunoblot of whole-cell extract from cells transfected with Orc2 siRNA duplex or control luciferase siRNA and harvested at different time points. Cells were transfected at 0, 24 and 48 h at about 20% starting confluence. Efficacy of RNAi was assessed by immunoblotting to detect Orc2. α-Tubulin levels were used as loading controls. Orc3 levels were also modulated and, with the reappearance of Orc2 in the cells at 144 h, the levels of Orc3 also increased. (**B**) Orc2 depletion at 72 h post siRNA shows morphologically two distinct populations of cells: the flat adherent cells and the rounded mitotic cells. (**C**) DNA content of control and Orc2 siRNA-treated cells at 48 h was determined by flow cytometry. Note a broader S phase and an increase in G2/M in Orc2 siRNA-treated cells. (**D**) Two-dimensional FACS to assess BrdU incorporation (10 min pulse) and DNA content by propidium iodide (PI) was assessed by flow cytometry in control and Orc2-depleted cells at 72 h. Note an increase in G2/M and accumulation of cells in S phase without incorporation of BrdU (see arrow) in Orc2-depleted cells. (**E**) Histogram showing the percentage of cells incorporating BrdU during a 24 h label at different time points after transfection, with Orc2 (gray bars) or luciferase control (white bars) siRNA duplexes. BrdU incorporation was allowed for 24 h to ensure that all cells had a chance to pass through at least one S phase.