blood® Errata

De Bruyne E, Bos TJ, Schuit F, et al. IGF-1 suppresses Bim expression in multiple myeloma via epigenetic and posttranslational mechanisms. *Blood*. 2010;115(12):2430-2440.

On page 2435, in Figure 2C, the blot for total FOXO3a is the wrong image due to an error in figure preparation. The corrected Figure 2C is shown below. The authors apologize for the error.

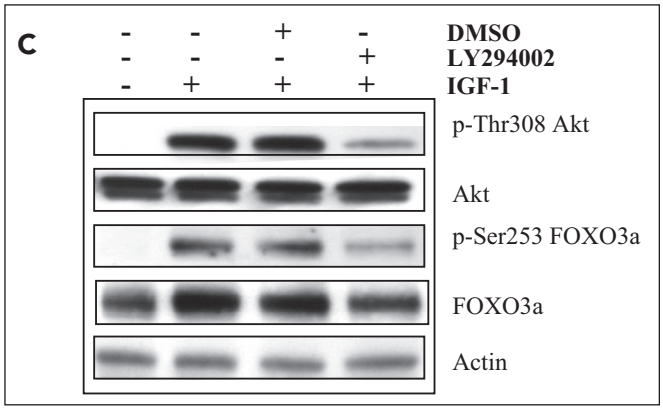

Figure 2. IGF-1 down-regulates Bim expression in the human Karpas707 cells through the PI-3K and p42/44 MAPK pathways. (C) Cells were starved 24 hours, pretreated with LY294002 (1 hour of preincubation; 10 μM) and stimulated with IGF-1 for 10 minutes. Next, the levels of p-Akt, tot-Akt, p-FoxO3a, and tot-FoxO3a were analyzed by Western blot. To confirm equal loading levels of actin were determined.

https://doi.org/10.1182/blood.2023022049

Hu J, Dang N, Menu E, et al. Activation of ATF4 mediates unwanted Mcl-1 accumulation by proteasome inhibition. *Blood*. 2012;119(3):826-837.

On page 834, Figure 6F has an error that occurred during preparation of the figure. The 2 images that show the XBP-1U and XBP-1s bands in LP1 cells after treatment with bortezomib (Btz) and tunicamycin (Tun) are actually the same one, namely, the image of Btz-treated cells. The corrected Figure 6F is shown below. The authors apologize for the error.

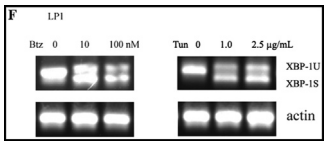

Figure 6. The role of XBP1 in UPR-mediated Mcl-1 expression. (A-F) RT-PCR analysis of XBP1 splicing in different MM cell lines. The MM cell lines OPM2, MMS1, U266, 5T33vt, RPMI-8226, and LP1 were treated with bortezomib and tunicamycin for 24 hours at varying doses. RNA isolation and RT-PCR were performed as described in "Methods." In the human MM cell lines OPM2, MMS1, U266, RPMI-8226, and LP1, the 210- and 184-bp DNA fragments correspond to unspliced and spliced human *XBP1* mRNAs, respectively. In 5T33vt cells, the 343- and 327-bp DNA fragments correspond to unspliced and spliced mouse *Xbp1* mRNAs, respectively.

https://doi.org/10.1182/blood.2023022044