# Review of: "The C-terminal domain of Hsp70 is responsible for paralog-specific regulation of ribonucleotide reductase"

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This is an interesting functional analysis of the roles of C terminal domains of the molecular chaperone Hsp70 isoforms. The authors used domain swap mutant forms of model Hsp70 proteins from yeast to demonstrate functional capabilities of the Hsp70 SBD. I have the following minor comments:

1. line 128-129: Is there any reason MMS would have resulted in a different response in the cells? Does it have a unique mode of action that brought about the reported observations?
2. line 137-138: The authors refer to previous studies in line with their current findings. However, a reference is missing for this.
3. Fig2: How was the quantification done (referring to the numbers below the blots)? Taking the PGK1 gene as the loading control, it seems there is some variation in this. Was there any standardization to the PGK1 gene?
4. Figure 3: Loading control (PGK1) seemed inconsistent