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On the cover: Subcellular quantitative proteomics identified rapidly depleted proteins, which were enriched for a number of biological processes. These proteins can be depleted by a number of mechanisms. This analysis also showed that proteasome inhibition induced a negative feedback loop that inhibits translation. In the background is a cell stained for the PRR11 protein, a novel cell cycle regulated protein that is rapidly degraded. For details, see article by Mark Larance *et. al.*, pages 638–650.

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Refined Preparation and Use of Anti-diglycine Remnant (K- ϵ -GG) Antibody Enables Routine Quantification of 10,000s of Ubiquitination Sites in Single Proteomics Experiments

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