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Research

On the cover: The workflow for "Proteomic Phenotyping". Using SILAC we obtained relative expression map of more than 4000 proteins between primary hepatocytes and Hepa1–6 cell line, which was in turn mined by a novel bioinformatics approach. Our analysis revealed that Hepa1–6 cells were deficient in mitochondria, reflecting re-arrangement of metabolic pathways, drastically up-regulate cell cycle-associated functions, and largely shut down drug metabolizing enzymes characteristic for the liver. For details, see the article by Pan *et al.*, pages 443–450.

[S] Online version of this article contains supplemental material. ⌘ Author's Choice

Additions & Corrections