NEWS:

Untargeted LC-MS/MS proteomics to characterize and understand toxicity

A recent study (1) **showed how quantitative LC-MS/MS proteomics allowed to find 173 proteins altered by toxic conditions. Then by further data treatment, major pathways involved in arsenic toxicity response could be determined. This gives an interesting contribution for toxicity understanding.**

(1) Proteomics-Based Identification of Differentially Abundant Proteins from Human Keratinocytes Exposed to Arsenic Trioxide. Udensi UK and all. 2014
http://www.ncbi.nlm.nih.gov/pubmed/25419056

This way, you can also easily check the positive and toxic effects of your compounds:

High-resolution nano LC-MS/MS quantitative proteomics and CORAVALID™ data processing: The efficient discovery tool
High-resolution SRM LC-MS/MS quantitative proteomics: The efficient multiplex confirmatory method

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