

NEWS:

Quantitative phosphoproteomics to characterize cell lines and drug resistance in cancer

LC-MS/MS label-free phosphoproteomics is a mature workflow (Piersma and all.(1)) which can be used for global quantitative profiling of biological cell lines and tissues to map signaling networks in comparative analyses. Then, by data treatment, it gives access to involved kinases.

The same approach was used by Nagata and all. (2) to study tumor drug resistance on cell lines. The results indicate that the effects of even so-called 'molecularly targeted' drugs, are broad rather than convergent, and that the mechanisms of action of such drugs during continuous administration are extremely complex.

(1) Feasibility of label-free phosphoproteomics and application to base-line signaling of colorectal cancer cell lines. Piersma SR, and all.2015

<http://www.ncbi.nlm.nih.gov/pubmed/25841592>

(2) Augmentation of multiple protein kinase activities associated with secondary imatinib resistance in gastrointestinal stromal tumors as revealed by quantitative phosphoproteome analysis. Nagata K, and all. 2015

<http://www.ncbi.nlm.nih.gov/pubmed/25554490>

High-resolution nano LC-MS/MS quantitative proteomics and CORAVALID™ data processing: The efficient tool

- ***Tumor kinome profiling***
 - In untargeted mode, which kinase is under or over expressed in the tumor
- ***Kinome inhibition profiling***
 - Comparison of conditions with and without inhibitor in an untargeted mode
- ***Drug inhibition measurement***
 - IC50 of all identifiable kinases in an untargeted mode
- ***Phosphoproteomics***
 - Serine/threonine mono- and polyphosphorylated phosphoproteins
 - PTMs modifications after phosphoproteins enrichment

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