

# NEWS:

## Clinically relevant post-translational modifications

**Mass spectrometry-based proteomics** has considerably extended our knowledge about the occurrence and dynamics of **protein post-translational modifications (PTM)**. So far, **quantitative proteomics** has been mainly used to study PTM regulation in cell culture models, providing new insights into the role of aberrant PTM patterns in human disease.

A nice review of Pagel and all (\*), explains how quantitative proteomics holds a great potential to discover, validate and accurately quantify biomarkers in body fluids and primary tissues.

(\*) Pagel O. and all. Current strategies and findings in clinically relevant post-translational modification-specific proteomics. *Expert Rev Proteomics*. 2015 May 4; 12(3): 235–253.

doi: [10.1586/14789450.2015.1042867](https://doi.org/10.1586/14789450.2015.1042867) <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC4487610/>

**With MS-Phylogene, you can also characterize the PTMs and understand the effects.**

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

***High-resolution MRM nano LC-MS/MS quantitative proteomics: The efficient tool for follow-up***

### **PHYLOGENE**

62, Route Nationale 113

30620 BERNIS

Tel : +33 4 66 04 77 99

Fax : +33 4 66 04 77 97

e-mail : [gskorski@phylogene.com](mailto:gskorski@phylogene.com)

web : [www.phylogene.com](http://www.phylogene.com)

<http://ms.phylogene.com>