

## Phenyx training

### Title

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### Description

The main objective of this training day is to encourage using Phenyx server by ProteoRed members. Pierre-Alain Binz from GeneBio is going to give a Phenyx training course showing the main capabilities of the last version of Phenyx server, including:

- Support of the major labelling technologies (isobaric iTRAQ, TMT, metabolic SILAC, chemical ICAT, ICPL...) and label-free approaches; first featured in 2.6 will be isobaric tags and spectral counting
- Analysis of simple to complex quantitation workflows: Multiple identification runs, replicates concept and multi-state analysis (time course experiments...)
- Support of international standards (MCP/MIAPe exports, mzML format...)
- Enhanced validation through an FDR estimation functionality and statistical report on the calibration status of the MS instrument
- A new in-house algorithm for extended PTM discovery: This feature (in the second-round search) looks for one modification per peptide in addition to all already pre-defined lists of modifications; it will ultimately look for mass shifts and intermolecular cross-links
- Expanded integration with third-party software (Scaffold, TPP, Progenesis LC-MS, ProteinCenter, Modiro®, ProteinScape...)
- An enhanced Database Manager to seamlessly install and update multiple public and proprietary sequence databases.

**Location:** Training Room, Prince Felipe Research Centre, Valencia, Spain

**Number of participants:** depends of room capacity, **Fee:** free course for ProteoRed members

**Date:** Oct 30th 2008

**Duration:** ~6 hours

**Organizer:** Bioinformatics working group (WG3) of ProteoRed and Prince Felipe Research Centre.

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### Contents

#### Thursday 30<sup>th</sup>, October 2008

11:00

Phenyx features and capabilities description

13:00

Lunch

14:30

Round table: discussion about specific features, problems in a practical session

~ 18:30

End of course

#### ***Teaching Staff***

**Pierre-Alain Binz**, GeneBio