



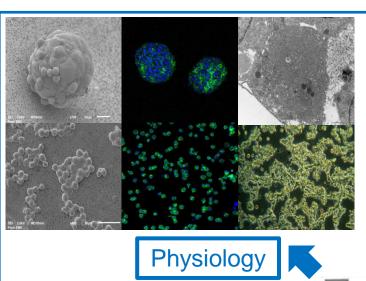
# Applications of Proteomics in Fish Liver Studies

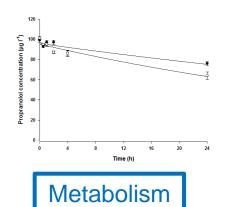
Vikram Sharma, PhD
Systems Biology Centre, Plymouth University

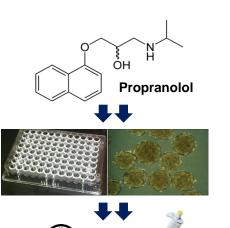


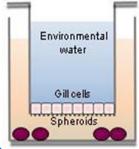


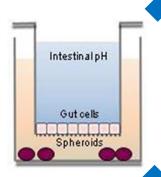


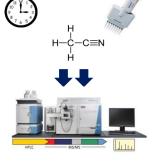




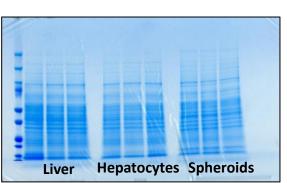








Proteomics

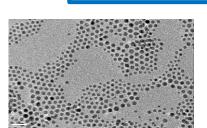


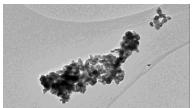


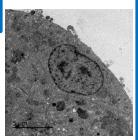


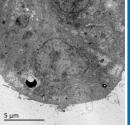


## Toxicology









## **Workflow: Proteomics with Plymouth University**





#### CELL CULTURE OR TISSUE

Proteins for bottom-up analyses come from a variety of sources.



#### EXTRACTION OF PROTEINS

Proteins are extracted and, in some cases, fractionated to reduce complexity.

#### GENERATION OF PEPTIDES

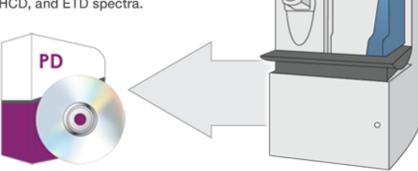
Proteins are denatured, reduced, alkylated, and digested into peptides.

Peptides are, in some cases, fractionated to reduce complexity.



#### AUTOMATED DATA ANALYSIS

Peptides are identified using Proteome Discoverer software, an automated program capable of analyzing CID, HCD, and ETD spectra.



#### ANALYSIS BY LC-MS/MS

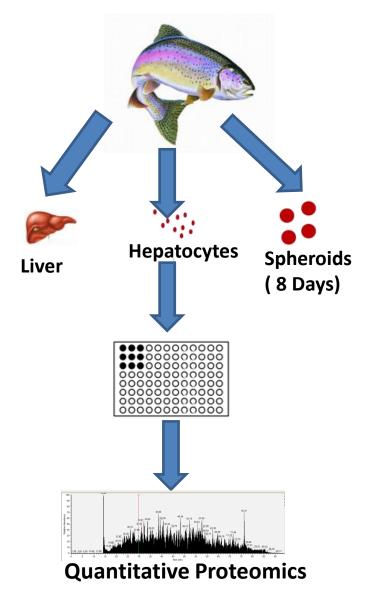
Peptides are analyzed by LC-MS/MS on Orbitrap-based mass spectrometers.

6/16/2017 Source: www.planetorbitrap.com

# Proteomic Characterisation of *in vivo* and *in vitro* liver models

(Liver Tissue, Primary Cells & Spheroids)

## **Experimental Design**



## 3 Biological Replicates (Number of Samples:9)

Author's nersonal con

Ecotoxicology (2012) 21:2419-2429 DOI 10.1007/s10646-012-0965-5

TECHNICAL NOTI

Towards a more representative in vitro method for fish ecotoxicology: morphological and biochemical characterisation of three-dimensional spheroidal hepatocytes

Matthew G. Baron · Wendy M. Purcell · Simon K. Jackson · Stewart F. Owen · Awadhesh N. Jha

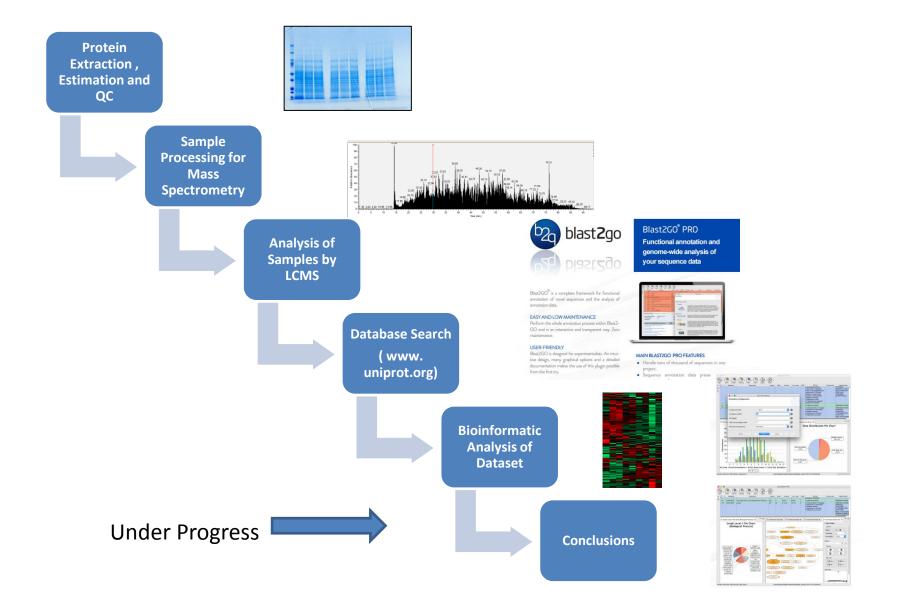
Accepted: 8 June 2012/ Published online: 26 June 2012

Abstract The use of fish primary cells and cell lines offer an invitro abstractive for assessment of themsical society and the evaluation of environmental samples in econoxicology. However, their uses are not without lineations such as short culture periods, and loss of fractionality, particularly with primary finare. White three-dimensional ophersidy is consistent of the primary finare. White three-dimensional ophersidy as to the primary finare, white three-dimensional opherside positions are also as the production of the produ

lower than 2D cultures (P < 0.01), It is therefore suggested that matter aphreviols can maintain a high degree of functional, hischemical and mosphological status over-time in culture that is supported to conventional 2D models and can provide realistic organospic responses in vitos. Troot aphreviols that take "6-6 days to need maturity would be saintable for use in scate notscological tests and since it is possible to culture individual aphreviols for over a mentity, there is potential for this work to lead towards in vitro bio-accumulation alternatives and to conduct high freezighus screens of chronic exposure. This is an important step forward for develocious alternative in vitro tools in future with

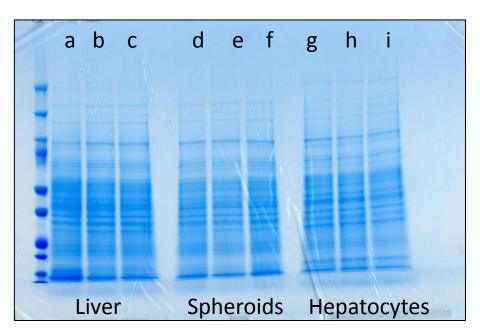
Baron et al, 2012

## **Workflow: Rainbow Trout Proteomics**

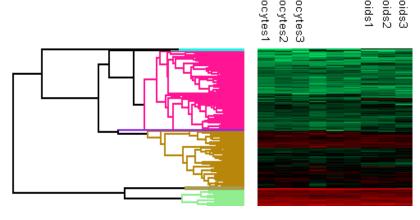


# **Preliminary Data**

## SDS GEL & MS Analysis



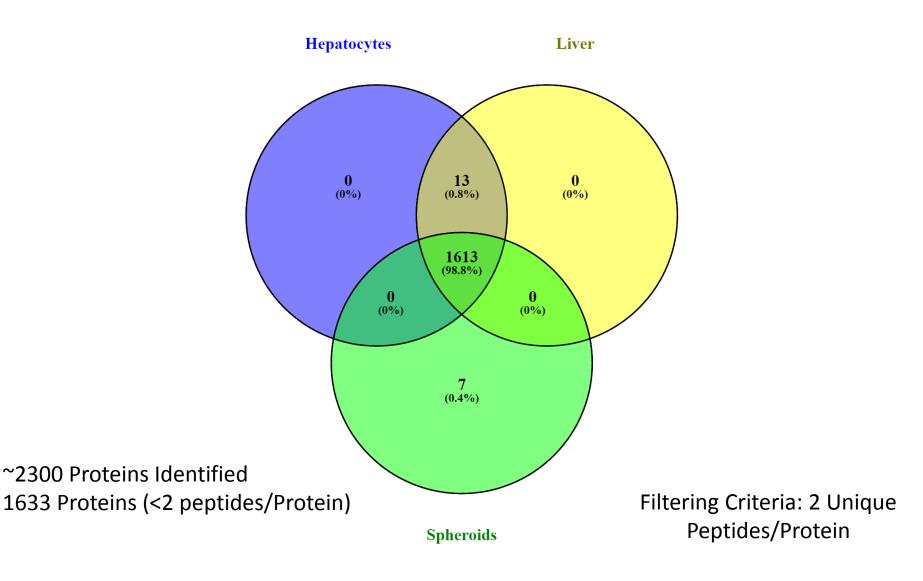
Quality Check on 4-12% Gradient Gel



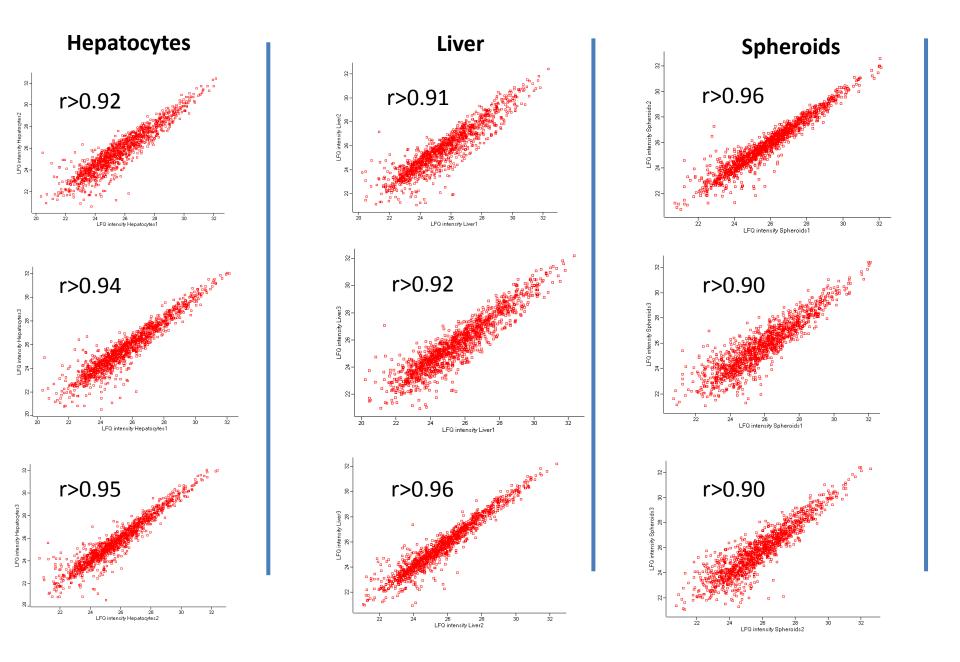
Hierarchical Clustering on LFQs

LFQ: Label Free Quantification

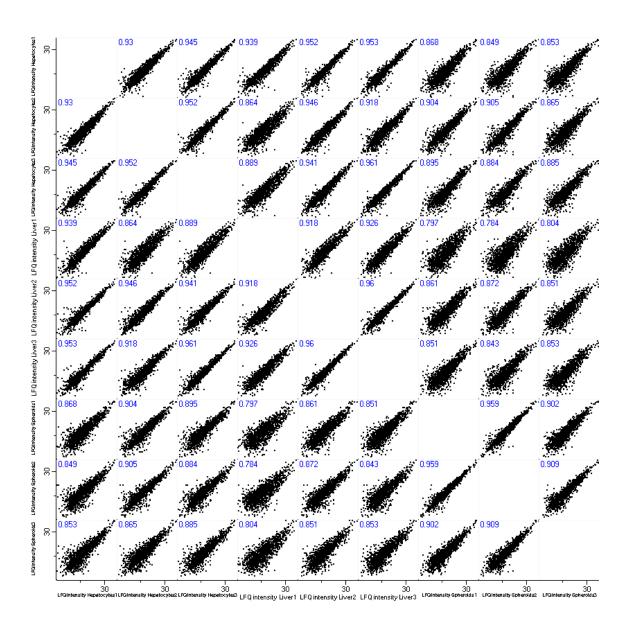
## Identified Proteins among models



## **Correlation in Replicates**

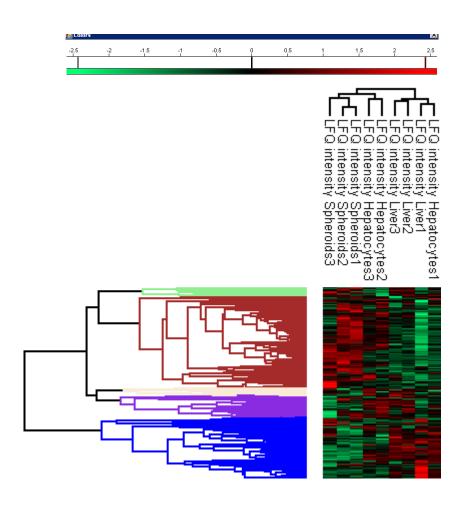


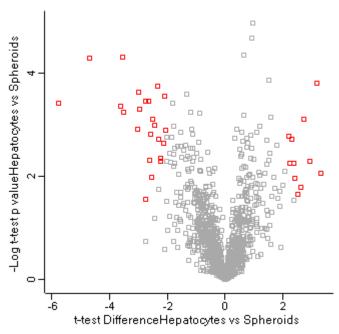
## Correlation: Experimental Groups



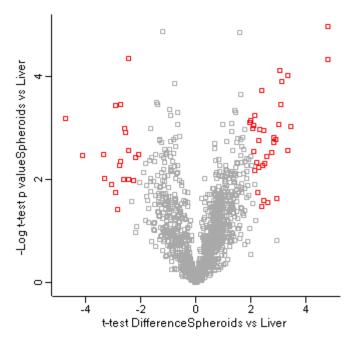
r=0.78 to 0.96

# Hierarchical Clustering Analysis (z normalised LFQs)



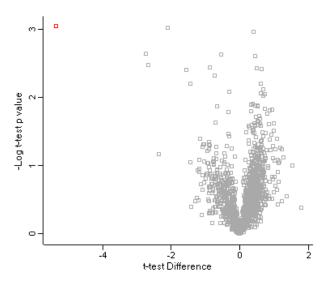


**Spheroids vs Hepatocytes** 



**Spheroids vs Liver** 





**Liver vs Hepatocytes** 

## Annotation Extraction by Blast2go



Blast2GO<sup>®</sup> is a complete framework for functional annotation of novel sequences and the analysis of annotation data.

#### EASY AND LOW MAINTENANCE

Perform the whole annotation process within Blast2-GO and in an interactive and transparent way. Zero maintenance.

#### USER-FRIENDLY

Blast2GO is designed for experimentalists. An intuitive design, many graphical options and a detailed documentation makes the use of this plugin possible from the first try.

### Blast2G0° PRO

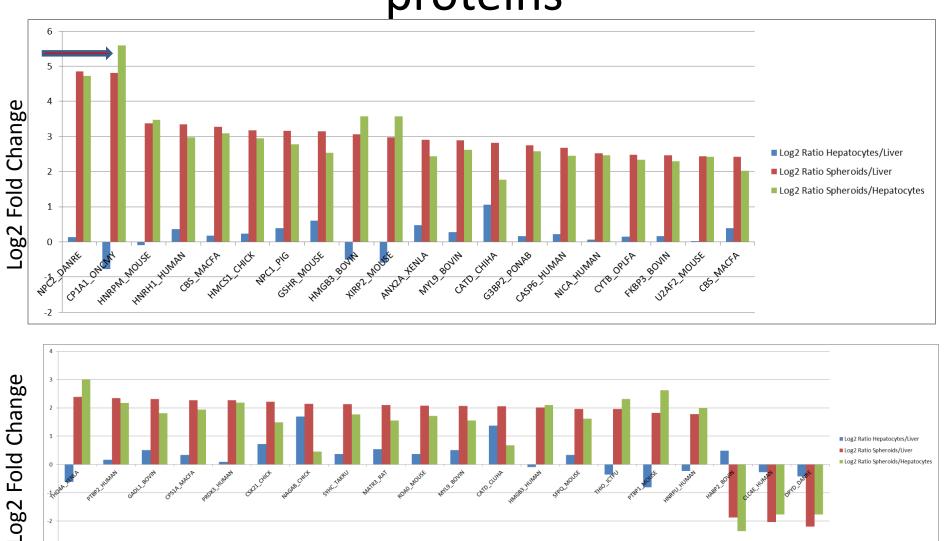
Functional annotation and genome-wide analysis of your sequence data

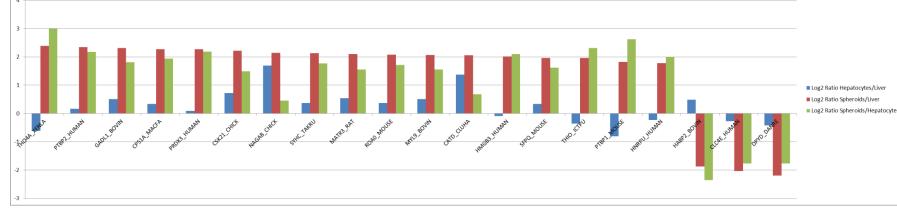


#### MAIN BLAST2GO PRO FEATURES

- Handle tens of thousand of sequences in one project.
- Sequence annotation data presented in

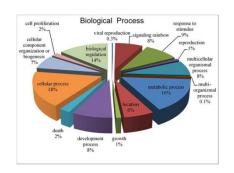
Proteomic Profile: Significantly altered proteins

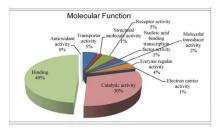


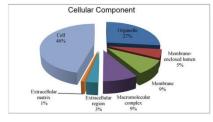


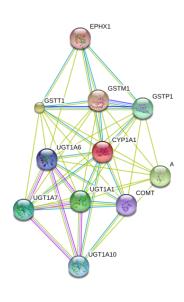
## **Ongoing Analysis**

- Functional Significance of Altered Proteins
- Annotation Enrichment Analysis
- Comparative Proteomics









PLOS ONE | DOI:10.1371/journal.pone.0121778 March 20, 2015

STRING DB-CYP1A1





### RESEARCH WITH PLYMOUTH UNIVERSITY



#### Our current team

The Genetic Toxicology & Ecotoxicology Research Group has a varied resource of researchers.

Meet our team





