

# Laurent Gatto, PhD

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## Senior Research Associate

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## RESEARCH STATEMENT

My research interests centre around three main areas: (1) Development of computational analyses methods for quantitative proteomics data, with a special emphasis on organelle proteomics experiments; (2) Implementation of state-of-the-art analysis strategies into robust high-quality toolkits leading to robust data analysis and reproducible results. (3) Utilisation and combination of various sources of data to infer relevant biological interpretation.

## APPOINTMENTS

*Senior Research Associate*  
Cambridge, UK  
Group Leader – Computational Proteomics Unit

University of Cambridge  
**October 2013 –**

*Visiting Scientist*  
Cambridge, UK  
Member of the Proteomics identifications database (PRIDE) team.

EMBL/EBI  
**January 2010 –**

[Software Sustainability Institute Fellow](#) 2014.

[Software Carpentry](#) Instructor.

[Bioconductor](#) project, associated member.

## SELECTED PUBLICATIONS (OUT OF 26)

Huber W. *et al.*, [Orchestrating high-throughput genomic analysis with Bioconductor](#), **Nat Methods** 2015 Jan 29;12(2):115-21.

**Gatto L.**, Breckels LM, Burger T, Wieczorek S and Lilley KS [Mass-spectrometry based spatial proteomics data analysis using pRoloc](#), **Bioinformatics**, 2014 May 1;30(9):1322-4.

**Gatto L.**, Christoforou A. *Using R and Bioconductor for proteomics data analysis*. **Biochim Biophys Acta** 2014 Jan;1844(1 Pt A):42-51.

Chambers M. *et al.* *A Cross-platform Toolkit for Mass Spectrometry and Proteomics*, **Nature Biotechnology**, **30**, 918 – 920, 2012.

**Gatto L.** and Lilley K.S. *MSnbase – an R/Bioconductor package for isobaric tagged mass spectrometry data visualisation, processing and quantitation*, **Bioinformatics**, **28**(2), 288-289, 2012.

## SELECTED SOFTWARE DEVELOPMENT

[Pbase](#): Manipulating and exploring protein and proteomics data, 2014.

[pRolocGUI](#): Interactive visualisation of organelle (spatial) proteomics data, 2014.

[rpx](#): An R interface to the ProteomeXchange repository, 2014.

**pRoloc**: A unifying bioinformatics framework for organelle proteomics, 2012.

**synapter**: Label-free data analysis pipeline for optimal identification and quantitation, 2012.

**hpar**: A simple interface to and data from the Human Protein Atlas project, 2012.

**rols**: An R interface to the Ontology Lookup Service, 2012.

**MSnbase**: Base Functions and Classes for MS-based Proteomics, 2011.

**mzR**: Raw mass-spectrometry data parsig library.

SELECTED ORAL  
COMMUNICATIONS  
(INVITED TALKS)

Gatto L. *Spatial proteomics: Combining experimental and annotation data to predict protein sub-cellular localisation*. 13 Jan 2015, European Bioconductor Developer meeting, EMBL, Heidelberg.

Gatto L. *An overview of the (growing) R/Bioc ecosystem for mass spectrometry and proteomics*, MRC Clinical Sciences Centre, Imperial College London, 5 December 2014, London.

Gatto L. *Computational Challenges in Mass Spectrometry-Based Spatial Proteomics*, HUPO meeting, Computational Mass Spectrometry Initiative, 8 Oct 2014, Madrid.

Gatto L. and Lilley K.S., *Unified omics data containers for robust, transparent and flexible computational biology*, PROSPECTOM Workshop 29 – 30 November 2012, Grenoble, France.

CURRENT  
GRANTS

May 2014 – Oct. 2015 BBSRC Tools and Resources Development Fund (£144,112). *Automated identification of optimal data-specific organelle clusters using freely available protein annotations*. **PI Laurent Gatto**, University of Cambridge.

March 2014 – February 2018 BBSRC Strategic Longer and Larger grant. *A spatio-temporal map of the developmental fly interactome*. **Research co-investigator**, with PI Professor Simon Hubbard, University of Manchester.

March 2013 – November 2015 Addenbrookes Charitable Trust. *Protein biomarkers for vascular calcification in end-stage renal disease*. **Co-applicant**, with PI Dr Thomas Hiemstra, University of Cambridge.

REVIEWING  
ACTIVITIES.

**Journals**: Proteomics, Bioinformatics, BMC Genomics, BMC Research Notes, Expert Reviews in Proteomics, Journal of Proteomics, F1000Research, PeerJ, Journal of Open Research Software.

**Conferences**: ISMB/ECCB.

**Funding agencies**: Medical Research Council.