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APPOINTMENTS	<i>Senior Research Associate</i> Cambridge, UK Group Leader – Computational Proteomics Unit	University of Cambridge October 2013 –
	<i>Visiting Scientist</i> 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.	
PREVIOUS APPOINTMENTS	<i>Post-Doctoral Research Associate</i> University of Cambridge, Cambridge, UK	Jan 2010 – Sept 2013
	<i>Bioinformatician, Project Leader</i> DNAVision, Gosselies, Belgium	Aug 2006 – Dec 2009
EDUCATION	2000 – 2006 (viva 2006-07-27) <i>PhD</i> in Science (Molecular Biology Department) Free University of Brussels (ULB), Belgium 2000 – 2001 Master of Advanced Studies (DEA) in Sciences Free University of Brussels (ULB), Belgium 1997 – 2000 Masters in Biology (highest honors) Free University of Brussels (ULB), Belgium	
SELECTED PUBLICATIONS (OUT OF 26)	Huber W. <i>et al.</i> , Orchestrating high-throughput genomic analysis with Bioconductor , Nat Methods 2015 Jan 29;12(2):115-21. Gatto L. , Breckels LM, Burger T, Wiczorek 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. <i>Using R and Bioconductor for proteomics data analysis</i> . Biochim Biophys Acta 2014 Jan;1844(1 Pt A):42-51. Chambers M. <i>et al.</i> <i>A Cross-platform Toolkit for Mass Spectrometry and Proteomics</i> , Nature Biotechnology , 30, 918 – 920, 2012.	

	<p>Gatto L. and Lilley K.S. <i>MSnbase – an R/Bioconductor package for isobaric tagged mass spectrometry data visualisation, processing and quantitation</i>, Bioinformatics, 28(2), 288-289, 2012.</p>
SELECTED SOFTWARE DEVELOPMENT	<p>Manipulating and exploring protein and proteomics data, 2014.</p> <p>pRolocGUI: Interactive visualisation of organelle (spatial) proteomics data, 2014.</p> <p>rpx: An R interface to the ProteomeXchange repository, 2014.</p> <p>pRoloc: A unifying bioinformatics framework for organelle proteomics, 2012.</p> <p>hpar: A simple interface to and data from the Human Protein Atlas project, 2012.</p> <p>rols: An R interface to the Ontology Lookup Service, 2012.</p> <p>MSnbase: Base Functions and Classes for MS-based Proteomics, 2011.</p> <p>mzR: Raw mass-spectrometry data parsig library.</p>
SELECTED ORAL COMMUNICATIONS (INVITED TALKS)	<p>Gatto L. <i>Spatial proteomics: Combining experimental and annotation data to predict protein sub-cellular localisation</i>. 13 Jan 2015, European Bioconductor Developer meeting, EMBL, Heidelberg.</p> <p>Gatto L. <i>An overview of the (growing) R/Bioc ecosystem for mass spectrometry and proteomics</i>, MRC Clinical Sciences Centre, Imperial College London, 5 December 2014, London.</p> <p>Gatto L. <i>Computational Challenges in Mass Spectrometry-Based Spatial Proteomics</i>, HUPO meeting, Computational Mass Spectrometry Initiative, 8 Oct 2014, Madrid.</p>
CURRENT GRANTS	<p>May 2014 – Oct. 2015 BBSRC Tools and Resources Development Fund (£144,112). <i>Automated identification of optimal data-specific organelle clusters using freely available protein annotations</i>. PI Laurent Gatto, University of Cambridge.</p> <p>March 2014 – February 2018 BBSRC Strategic Longer and Larger grant. <i>A spatio-temporal map of the developmental fly interactome</i>. Research co-investigator, with PI Professor Simon Hubbard, University of Manchester.</p> <p>March 2013 – November 2015 Addenbrookes Charitable Trust. <i>Protein biomarkers for vascular calcification in end-stage renal disease</i>. Co-applicant, with PI Dr Thomas Hiemstra, University of Cambridge.</p>
TEACHING	<p>I am regularly teaching at national and international workshops and University courses (i.e. MPhil in Computation Biology, Cambridge in 2012-2014) on computational biology, scientific programming and Software Carpentry Bootcamps. These teaching activities are on a voluntary basis.</p>
REVIEWING ACTIVITIES	<p>Journals: Proteomics, Bioinformatics, BMC Genomics, BMC Research Notes, Expert Reviews in Proteomics, Journal of Proteomics, F1000Research, PeerJ, Journal of Open Research Software.</p> <p>Conferences: ISMB/ECCB. Funding agencies: Medical Research Council.</p>