

## Education

- 2005–2007 **Ph.D. in Molecular Medicine**, *University of Milano*, Milano, Italy.
- 1996–2002 **Master's degree in Pharmaceutical Biotechnology**, *University of Milano*, Milano, Italy, Evaluation: 103/110.
- 1995 **Maturità scientifica**, *Istituto Salesiano S.Ambrogio*, Milano, Italy, Final evaluation: 49/60.

## Ph.D. Thesis

- Title *Identifcation of disregulated metabolic pathways by transcriptomic analysis in renal cell carcinoma samples*
- Supervisor Dr.ssa Cristina Battaglia
- Description A bioinformatics approach based on pathway analysis is proposed in this work, in order to identify common deregulated pathways in samples from renal cell carcinoma samples.

## Master thesis

- Title *Study on the structure-function relationship of KAAT1, a Na<sup>+</sup>/K<sup>+</sup> dependent amino acid transporter*
- Supervisor Prof. Franca V. Sacchi
- Description A structure-function relationship study on the KAAT1 amino acid transporter from *Manduca sexta* using functional expression in *Xenopus laevis* oocytes.

## Attended courses

- March 2006 **6th Bioinformatics course**, *European School of Genetic Medicine*, Bertinoro di Romagna, Italy.
- June 2008 **NuGO Hands-on microarray data analysis course**, *University of Maastricht*, Maastricht, The Netherlands.

## Work experience

- March 2011–current **Bioinformatics work on microarray data for the Mario Negri Institute**, *Department of Oncology, Mario Negri Research Institute*, Milano, Italy.  
Research fellowship in Dr.Sergio Marchini's Translational Genomics unit to work on data analysis for microarray data and integration of heterogeneous data in the field of preclinical oncology.
- 2008–March 2011 **Bioinformatics work on microarray data for the University of Florence**, *Department of Pharmacology, University of Florence*, Florence, Italy.  
Research fellowship in Dr.Duccio Cavalieri's group to work on data analysis techniques for microarray data, especially regarding pathway analysis and database integration, on the fields of immunology and nutrigenomics.
- 2004–March 2009 **Bioinformatics work in the field of solid state tumors at Dr. Cristina Battaglia's laboratory**, *Centre of excellence CISI, University of Milano*, Milano, Italy.  
Data analysis of renal cell carcinoma data obtained through microarray experiments.
- 2003–2004 **Cellular and molecular biology research on mouse neuronal development at Dr. Vania Broccoli's laboratory**, *DIBIT, San Raffaele Scientific Park*, Segrate, Italy.  
Investigation of the expression of the ARX gene in primary cultured neurons.

2002-2003 **Work at Prof. Marco Parenti's laboratory on the function of caveolin-1 in neuronal development**, *DiMeSAB, University of Milano-Bicocca*, Monza, Italy.  
Analysis of the CAV-1 protein expression in cell cultures mimicking different neuronal development states.

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## Miscellaneous experience

April 2008 Participant and speaker at the **DC-THERA Annual Meeting** (Athens, Greece)  
June 2008 Teacher at the **NuGO hands-on microarray data analysis course** (Maastricht, The Netherlands) on the subject of pathway analysis  
November 2008 Speaker at the **I-ATLAS 2008: International Workshop on Gene Signalling Pathway Analysis and Representation for the Dendritic Cell** (Firenze, Italy) with the talk "Eu.Gene - a bioinformatic environment to query microarray databases with a pathway based logic"  
May 2009 Participant and speaker at the **DC-THERA Annual Meeting** (Marseille, France)

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## Computer skills

OS	Linux, UNIX, Windows		
programming	Python, R	scripting	Bash
GUI toolkits	Qt		
typography	L <sup>A</sup> T <sub>E</sub> X	image processing	GIMP
web design	XHTML, CSS	office suites	Openoffice.org, Microsoft Office
bioinformatics	functional annotation, pathway analysis, gene expression, data processing		

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## Skills

Writing Very good technical and non-technical writing skills

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## Languages

Italian	<b>Native</b>
English	<b>Very good</b>
Japanese	<b>Basic</b>

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## Interests

Pathway analysis Analysis of differentially regulated pathways in microarray data sets, as a viable alternative to traditional gene-based approaches.

Bioinformatics Bioinformatics and related topics in particular the aspects related to data integration, network topology reconstruction, and pathway analysis.

Open Source promotion Involved in the promotion of free and open source software, in particular KDE (<http://www.kde.org>)

Open Source contribution Contributed patches and code to the KDE Applications and Workspace and to the tablib project (<http://www.tablib.org>)

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## Publications

Luca Beltrame, Enrica Calura, Razvan Popovici, Lisa Rizzetto, Damariz Rivero Guedez, Michele Donato, Chiara Romualdi, Sorin Draghici, and Duccio Cavalieri. The Biological Connection Markup Language: a SBGN compliant format for visualization, filtering and analysis of biological pathways. *Bioinformatics*, May 2011. Accepted for publication.

Sergio Marchini, Duccio Cavalieri, Robert Fruscio, Enrica Calura, Daniela Garavaglia, Ilaria Fuso Nerini, Costantino Mangioni, Giorgio Cattoretti, Luca Clivio, Luca Beltrame, Dionyssios Katsaros, Luca Scarampi, Guido Menato, Patrizia Perego, Giovanna Chiorino, Alessandro Buda, Chiara Romualdi, and Maurizio D'Incalci. Association between miR-200c and the survival of patients with stage I epithelial ovarian cancer: a retrospective study of two independent tumour tissue collections. *Lancet Oncol*, Feb 2011.

Duccio Cavalieri, Damariz Rivero, Luca Beltrame, Sonja I Buschow, Enrica Calura, Lisa Rizzetto, Sandra Gessani, Maria C Gauzzi, Walter Reith, Andreas Baur, Roberto Bonaiuti, Marco Brandizi, Carlotta De Filippo, Ugo D'Oro, Sorin Draghici, Isabelle Dunand-Sauthier, Evelina Gatti, Francesca Granucci, Michaela Gündel, Matthijs Kramer, Mirela Kuka, Arpad Lanyi, Cornelis Jm Melief, Nadine van Montfoort, Renato Ostuni, Philippe Pierre, Razvan Popovici, Eva Rajnavolgyi, Stephan Schierer, Gerold Schuler, Vassili Soumelis, Andrea Splendiani, Irene Stefanini, Maria G Torcia, Ivan Zanoni, Raphael Zollinger, Carl G Figdor, and Jonathan M Austyn. DC-ATLAS: a systems biology resource to dissect receptor specific signal transduction in dendritic cells. *Immunome Res*, 6:10, Dec 2010.

Alessandra Aldinucci, Lisa Rizzetto, Laura Pieri, Daniele Nosi, Paolo Romagnoli, Tiziana Biagioli, Benedetta Mazzanti, Riccardo Saccardi, Luca Beltrame, Luca Massacesi, Duccio Cavalieri, and Clara Ballerini. Inhibition of immune synapse by altered dendritic cell actin distribution: a new pathway of mesenchymal stem cell immune regulation. *J Immunol*, 185(9):5102–5110, Nov 2010.

Sonja I Buschow, Edwin Lasonder, Hanneke W M van Deutekom, Machteld M Oud, Luca Beltrame, Martijn A Huynen, I. Jolanda M de Vries, Carl G Figdor, and Duccio Cavalieri. Dominant processes during human dendritic cell maturation revealed by integration of proteome and transcriptome at the pathway level. *J Proteome Res*, 9(4):1727–1737, Apr 2010.

Lisa Rizzetto, Mirela Kuka, Carlotta De Filippo, Alessandra Cambi, Mihai G Netea, Luca Beltrame, Giorgio Napolitani, Maria Gabriella Torcia, Ugo D'Oro, and Duccio Cavalieri. Differential IL-17 production and mannan recognition contribute to fungal pathogenicity and commensalism. *J Immunol*, 184(8):4258–4268, Apr 2010.

Silvio Bicciato, Roberta Spinelli, Mattia Zampieri, Eleonora Mangano, Francesco Ferrari, Luca Beltrame, Ingrid Cifola, Clelia Peano, Aldo Solari, and Cristina Battaglia. A computational procedure to identify significant overlap of differentially expressed and genomic imbalanced regions in cancer datasets. *Nucleic Acids Res*, 37(15):5057–5070, Aug 2009.

Luca Beltrame, Lisa Rizzetto, Raffaele Paola, Philippe Rocca-Serra, Luca Gambineri, Cristina Battaglia, and Duccio Cavalieri. Using pathway signatures as means of identifying similarities among microarray experiments. *PLoS One*, 4(1):e4128, 2009.

Ingrid Cifola, Roberta Spinelli, Luca Beltrame, Clelia Peano, Ester Fasoli, Stefano Ferrero, Silvano Bosari, Stefano Signorini, Francesco Rocco, Roberto Perego, Vanessa Proserpio, Francesca Raimondo, Paolo Mocarelli, and Cristina Battaglia. Genome-wide screening of copy number alterations and LOH events in renal cell carcinomas and integration with gene expression profile. *Mol Cancer*, 7:6, 2008.

F. Raimondo, M. Verga, S. Ferrero, I. Cifola, R. Spinelli, L. Beltrame, C. Peano, C. Bianchi, V. Angeloni, F. Rocco, F. Magni, A. Di Fonzo, V. Proserpio, M. Galli-Kienle, C. Battaglia, P. Mocarelli, and M. Pitto. Poster: Integration of genome wide molecular analysis and subcellular proteomics for renal cell carcinoma biomarker identification. In *2nd annual conference of the Italian Proteomic Association*, Acitrezza (Catania), Italy, 2007.

R. Spinelli, I. Cifola, S. Ferrero, L. Beltrame, P. Mocarelli, and C. Battaglia. Assessment of common regions and specific footprints of dna copy number aberrations across multiple affymetrix SNP mapping arrays. In *Fourth International Meeting on Computational Intelligence Methods for Bioinformatics and Biostatistics*, Portofino, Italy, 2007.

M. Zampieri, I. Cifola, D. Basso, R. Spinelli, L. Beltrame, C. Peano, C. Battaglia, and S. Bicciato. A computational procedure for the integrative analysis of genomic data at the single sample level. In *10th Symposium on Computer applications in biotechnology*, Cancún, Mexico, 2007.

Ingrid Cifola, Clelia Peano, Marco Severgnini, Roberta Spinelli, Luca Beltrame, Silvano Bosari, Ester Fasoli, Silvio Bicciato, and Cristina Battaglia. Poster: Integration of whole-genome SNP mapping and transcriptional data in the human metastatic renal carcinoma Caki-1 cell line. In *9th International Congress of the European Association for Cancer Research*, Budapest, Czech Republic, July 2006.

A. Callegaro, R. Spinelli, L. Beltrame, S. Bicciato, L. Caristina, S. Censuales, G. De Bellis, and C. Battaglia. Algorithm for automatic genotype calling of single nucleotide polymorphisms using the full course of TaqMan real-time data. *Nucleic Acids Res.*, 34(7):e56, 2006.