Lorenzo Calviello

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Current address:
513 Parnassus Avenue, HSW 715
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Nationality: Italian

Education

Feb 2013 – Dec 2017	**PhD in Molecular Biology, summa cum laude**, MDC/BIMSB (with Humboldt University) Berlin, Germany.
Dec 2009 – Jul 2012	**Master's degree in Cell and Molecular Biosciences, cum laude**, University of Pisa, Italy.
Sep 2006 – Dec 2009	**Bachelor degree in Biomolecular Sciences, cum laude**, University of Pisa, Italy.

Research Experience

Jul 2018 – Present	**Postdoc**, Human RNA Biology, University of California San Francisco, USA. *References:* Prof. Dr. Stephen Floor. Stephen.Floor@ucsf.edu
Dec 2017 – Jul 2018	**Postdoc**, Computational Regulatory Genomics, Max Delbrück Center for Molecular Medicine, Berlin, Germany. *References:* Prof. Dr. Uwe Ohler; Dr. Altuna Akalin. Uwe.Ohler@mdc-berlin.de, Altuna.Akalin@mdc-berlin.de
Feb 2013 – Dec 2017	**PhD Thesis**, "Detecting and quantifying the translated transcriptome with Ribo-seq data". Computational Regulatory Genomics, Max Delbrück Center for Molecular Medicine, Berlin, Germany. Selected for a 3-year centrally funded position. *References:* Prof. Dr. Uwe Ohler - Uwe.Ohler@mdc-berlin.de
Jul 2011 – Jul 2012	**Master Thesis**, "Quasi-Cellular Systems: Stochastic Simulation Analysis at Nanoscale Range". Department of Computer Science, University of Pisa, Italy *References:* Dr. Roberto Marangoni - roberto.marangoni@unipi.it
Apr 2009 – Dec 2009	**Bachelor Thesis**, "Survey of killing abilities of Caedibacter-infected hosts and description of other Paramecium symbionts" Department of Biology, University of Pisa, Italy *References:* Prof. Dr. Giulio Petroni - giulio.petroni@unipi.it

Selected Oral Presentations

Nov 2017	**UCSF and Stanford University, USA**: internal seminar valid for postdoctoral interview - UCSF (with Stephen Floor) and Stanford University (with Maria Barna): "Detecting and quantifying the translated transcriptome with Ribo-seq data"
Dec 2016	**Bioinformatics Workshop MDC Berlin, Germany**: seminar for researchers attending the TRR175 Galaxy forum. title: "Monitoring translation one codon at a time"
Oct 2016	**Computational RNA Biology Conference (Wellcome Genome Campus, Hinxton, England)**: "Detecting and quantifying translation on multiple RNA isoforms"
Sep 2015	**EMBO Conference: Protein synthesis and translational control (EMBL, Heidelberg, Germany)**: "Computational analysis of high resolution Ribosome profiling detects thousands of high confidence ORFs and improves peptide identification"
May 2012	**BITS 2012 (University of Catania, Italy)**: "Quasi-Cellular Systems: Stochastic Simulation Analysis at Nanoscale Range"

Selected Poster Presentations and Courses

Dec 2019	**Bay Area RNA Conference**: (UCSF, San Francisco, USA) Poster: "RNP dynamics across the transcriptome during normal and misregulated translation"
Nov 2017	**RECOMB-ISCB Conference**: "Conference on Regulatory and Systems Genomics", (MSKCC New York, USA), Poster: "Detecting and quantifying translation on multiple RNA isoforms"
Feb 2016	**EMBL Course**: "Analysis and Integration of Transcriptome and Proteome Data" (EMBL, Heidelberg, Germany)
Oct 2014	**EMBO Conference**: "The Complex Life of mRNA" (EMBL, Heidelberg, Germany), Poster: "Genome-wide survey of translated loci using spectral analysis of footprint profiles"

Languages

Italian	Native speaker
English	Full Professional Proficiency
German	Elementary Proficiency
Turkish	Beginner level

Skills and competences

Computational	R/Bioconductor programming (advanced), R package development. Unix environment, HPC, Python programming (basic), Keras API.
Analysis	Genomic Data Analysis, Transcriptomics (advanced), Ribosome profiling (advanced), Proteomics, Spectral analysis (basic), Machine Learning.
Molecular Biology	Tissue culture, basic Molecular Biology techniques, RNA extraction, Polysome profiling, Next-gen sequencing technologies.
Other	Passionate about Molecular Biology, Data Analysis and Science in general. Handled multiple research projects independently and in collaborative environments. Outspoken and transparent person. Previously drummer in different Rock and Metal bands, recorded music albums and played live concerts in Italy and other countries.

Selected Publications

2020	**Lorenzo Calviello***, Antje Hirsekorn, and **Uwe Ohler***. Quantification of translation uncovers the functions of the alternative transcriptome. *Nature Structural and Molecular Biology*, 2020. doi: https://doi.org/10.1038/s41594-020-0450-4, *co-corresponding authors*
2020	David E Gordon, Gwendolyn M Jang, Mehdi Bouhaddou, Jiewei Xu, Kirsten Obernier, ..., Pedro Beltrao, Kevan Shokat, Brian K Shoichet, and Nevan J Krogan. **A SARS-CoV-2-Human Protein-Protein Interaction Map Reveals Drug Targets and Potential Drug-Repurposing.** *Nature*, 2020. doi: https://doi.org/10.1038/s41586-020-2286-9
2020	Chloe Chong, Markus Müller, HuiSong Pak, Dermot Harnett, ..., Uwe Ohler, George Coukos, and Michal Bassani-Sternberg. **Integrated Proteogenomic Deep Sequencing and Analytics Accurately Identify Non-Canonical Peptides in Tumor Immunopeptidomes.** *Nature Communications*, 2020. doi: https://doi.org/10.1038/s41467-020-14968-9
2019	Sebastiaan van Heesch, Franziska Witte, Valentin Schneider-Lunitz, ..., Uwe Ohler, Stuart A. Cook, and Norbert Hubner. **The Translational Landscape of the Human Heart.** *Cell*, 2019. doi: https://doi.org/10.1016/j.cell.2019.05.010
2019	**Lorenzo Calviello***, **Dominique Sydow***, Dermott Harnet, and Uwe Ohler. **RiboseQC: comprehensive analysis of cytoplasmic and organellar ribosome profiling data.** *bioRxiv*, 2019a. doi: https://doi.org/10.1101/601468, *co-first authors*
2019	**Lorenzo Calviello***, **Srivats Venkataramanan***, ..., Markus Landthaler, and Stephen Floor. **DDX3 depletion selectively represses translation of structured mRNAs.** *bioRxiv*, 2019b. doi: https://doi.org/10.1101/589218, *co-first authors*
2017	**Lorenzo Calviello** and Uwe Ohler. **Beyond Read Counts: Ribo-seq data analysis to understand the functions of the transcriptome.** *Trends in Genetics*, 2017. doi: http://dx.doi.org/10.1016/j.tig.2017.08.003
2017	Alessandra Zappulo, David van den Bruck, Camilla Ciolli Mattioli, Vedran Franke, ..., Altuna Akalin, and Marina Chekulaeva. **RNA localization is a key determinant of neurite-enriched proteome**. *Nature Communications*. doi: http://dx.doi.org/10.1038/s41467-017-00690-6
2016	Neelanjan Mukherjee, **Lorenzo Calviello**, Antje Hirsekorn, Stefano de Pretis, Mattia Pelizzola, and Uwe Ohler. **Integrative classification of human coding and non-coding genes based on RNA metabolism profiles**. *Nature Structural and Molecular Biology*, 2017. doi: doi: 10.1038/nsmb.3325, also featured in a News and Views article by Bedoya-Reina and Ponting: doi:10.1038/nsmb.3354
2016	Polly Yingshan Hsu, **Lorenzo Calviello**, Larry Wu Hsin-Yen, Li Fay-Wei, Carl J. Rothfels, Uwe Ohler, and Philipp N. Benfey. **Super-Resolution Ribosome Profiling Reveals Novel Translation Events in Arabidopsis**. *PNAS*, 2016. doi: doi: 10.1073/pnas.1614788113
2015	**Lorenzo Calviello**, Neelanjan Mukherjee, Emanuel Wyler, Henrik Zauber, Antje Hirsekorn, Matthias Selbach, Markus Landthaler, Benedikt Obermayer, and Uwe Ohler. **Detecting actively translated open reading frames in ribosome profiling data**. *Nature Methods*, 2015. doi: doi:10.1038/nmeth.3688, also featured in a News and Views article by Baranov and Michel: doi:10.1038/nmeth.3738
2015	Sebastian Mackowiak, Henrik Zauber, ..., Nikolaus Rajewsky, Stefan Kempa, Matthias Selbach, and Benedikt Obermayer. **Extensive identification and analysis of conserved small ORFs in animals**. *Genome Biology*, 2015. doi: 10.1186/s13059-015-0742-x
2013	**Lorenzo Calviello**, Pasquale Stano, Fabio Mavelli, Pier Luigi Luisi, and Roberto Marangoni. **Quasi-cellular systems: stochastic simulation analysis at nanoscale range**. *BMC Bioinformatics*, 2013. doi: 10.1186/1471-2105-14-S7-S7

References

Stephen Floor, Assistant Professor	Postdoctoral Advisor stephen.floor@ucsf.edu Department of Cell and Tissue Biology University of California San Francisco
Uwe Ohler, Professor	PhD Advisor uwe.ohler@mdc-berlin.de Laboratory of Computational Regulatory Genomics Berlin Institute for Medical Systems Biology Max Delbrück Center for Molecular Medicine Berlin, Berlin
Markus Landthaler, Professor	Collaborator and PhD Thesis Reviewer markus.landthaler@mdc-berlin.de Laboratory of RNA Biology and Posttranscriptional Regulation Berlin Institute for Medical Systems Biology Max Delbrück Center for Molecular Medicine Berlin, Berlin
Neelanjan Mukherjee, Assistant Professor	Collaborator neelanjan.mukherjee@ucdenver.edu Biochemistry and Molecular Genetics RNA Bioscience Initiative University of Colorado Anschutz Medical Campus