NAME	POSITION TITLE
Marta Biagioli, Ph.D. ORCID: 0000-0001-8295-8025	Associate professor, NeuroEpigenetics Laboratory http://www.cibio.unitn.it/184/neuroepigenetics-laboratory https://biagiolilab.wordpress.com/author/martabiagioli/ Department of Cellular, Computational and Integrative Biology (CIBio), University of Trento (ITALY)

EDUCATION/TRAINING

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	MM/YY	FIELD OF STUDY
University of Pisa, Pisa (ITALY)	M.Sc. (Laurea) - Honors	10/1999	*Molecular Biology*
University of Pisa, Pisa (ITALY)	Ph.D. - Honors	04/2003	*Molecular Biotechnology*
International School for Advanced Studies (I.S.A.S – S.I.S.S.A.), Trieste, Italy	Postdoctoral fellow	From 07/2003 To 07/2009	*Neurobiology and Functional Genomics* Lab Dr. S. Gustincich
Center for Human Genetics Research, Massachusetts General Hospital and Harvard Medical School, Boston (USA)	Postdoctoral fellow Senior	From 07/2009 To 07/2014	*Human Genetics* Lab Drs M.E. MacDonald and J.F. Gusella

A. Positions, Honors

Positions, Employment and Career Breaks

2014-2017 Instructor, Department CIBio, University of Trento, (ITALY)
2017-2020 Assistant Professor, Department CIBio, University of Trento, (ITALY)
2020-present Associate Professor in Genetics, Department CIBio, University of Trento, (ITALY)

Honors and Awards (most recents)

2015 Selected for NARSAD Research Partner Program, "Jan and Stefan Abrams Investigator"
2016 Marie Skłodowska-Curie actions (European Community) Reintegration Fellowship
2016 Member of TRAIN – "Trentino Autism Initiative" [http://www.unitn.it/ateneo/55368/train-trentino-autism-initiative]
2017 Human Biology Fellowship, Huntington's Disease Society of America – HDSA
2022 5X1000 – University of Trento fundraising campaign – "*Neuro Spy, tracking dying neurons"*

B. Contribution to science

1) Understanding non-coding RNA function in neurologic diseases

We explored the contribution of small non-coding RNA (miRNAs) as molecular mediators of huntingtin fundamental role during normal organism development, **analyzing a series of hypomorphic mutations of the mouse Huntington's disease (HD) gene orthologue [Murthy, Tebaldi et al., Biagioli (last and corresponding author), 2019. *PLoS Genet* 15(3): e1007765]. Lately, the emerging field of circRNA biology in brain functions strongly attracted my attention. Circular RNAs, single-stranded RNA molecules produced by back-splicing events, are, largely enriched in the brain and contributing to synaptic activity and brain metabolism. Thus, we decided to address the question of the role of circRNA in Huntington's Disease, looking both at genome-wide phenotypes induced by the *Htt* mutations and, specifically and at the specific *Htt* locus. These hypotheses granted the support of the Huntington's Society of Canada, HDSA (Human Biology project, 2017) and EHDN (Seed Money 2018). The first publication describing the importance of alternative splicing and back-splicing alterations for HD pathologic process is currently under revision at *PLOS Genetics* and available in Biorxiv at this link: https://www.biorxiv.org/content/10.1101/2021.12.27.474266v1.**

2) Epigenetics alterations in neurologic conditions.

The knowledge of epigenetics mechanisms is crucial not only to better understand normal brain development and function, but also to dissect chromatin pathways malfunctioning in diseases. **I started to investigate epigenetic/chromatin, using ChIP-seq and RNA-seq technologies, while I was a postdoc at Harvard Medical School in Boston, working in the laboratory of Dr. Marcy MacDonald. Through these genome-wide approaches and using mouse HD genetic models, I proved a functional interaction between huntingtin protein (wild-type and mutant) and the polycomb-repressive complex 2 (PRC2), specifically affecting neuronal networks during development. The results were summarized in Biagioli*, Ferrari* et al. *Human Molecular Genetics* (2015). 24 (9): 2442-2457.** On the other hand, I explored the transcriptional networks that CHD8, the

chromodomain helicase DNA-binding protein 8, regulates in neural progenitor cells by reducing its expression and then integrating transcriptome sequencing with genome-wide CHD8 binding (Sugathan, **Biagioli** et al., 2014. *PNAS* 111, 42: E4468-E4477.). Lately, I focused on the characterization of chromatin changes following CHD8 suppression. A publication describing these results is currently under revision at *Nucleic Acid Research* and available at this bioRxiv link: https://doi.org/10.1101/2020.03.14.992032.

3) Vulnerability of specific neuronal population to genetic mutations

As a postdoctoral fellow at S.I.S.S.A. in Trieste (ITALY), I addressed the question of why dopaminergic neurons of the *substantia nigra* are uniquely sensitive to Parkinson's Disease. From the study, we found unexpected expression of α- and β-globin transcripts and proteins whose function relates to oxygen and mitochondrial homeostasis (**Biagioli M.**, Pinto M. et al., 2009 *PNAS*, 106 (36) 15454-15459; DOI: 10.1073/pnas.0813216106). **I applied my previous expertise to investigate the selective neuronal vulnerability of medium-sized spiny neurons in the context of HD mutation. Particularly, through an integrative effort to combine cutting edge methods to visualize, isolate and profile single neurons and analysis of RNA-seq datasets, we characterize the molecular sensitizers that render dopamine-receptor 2 neurons most susceptible to HD mutation. This project, funded by a MSCA-reintegration fellowship from the EU community, supported the publication of a recent review published in *Front. Cell. Neurosci.* and sparkled international collaborations with bioinformatic groups (Dr. Thierry Voet, KU Leuven, Belgium), leading expert in the field of single-cell RNA-seq and DNA-seq. New publication describing these data is currently in preparation.**

Complete List of Published Work could be found here: https://pubmed.ncbi.nlm.nih.gov/?term=Biagioli+Marta&show_snippets=off

Selected Peer-reviewed Publications [Google Scholar_April 2022_Total Citations 2785_H-index 19]

1. Michele Arnoldi, Giulia Zarantonello, Stefano Espinoza, Stefano Gustincich, Francesca Di Leva, **Marta Biagioli** (2022). Design and Delivery of SINEUP: A New Modular Tool to Increase Protein Translation. *Methods Mol Biol*, 2434:63-87.
2. Giulia Zarantonello, Michele Arnoldi, Michele Filosi, Toma Tebaldi, Giovanni Spirito, Anna Barbieri, Stefano Gustincich, Remo Sanges, Enrico Domenici, Francesca Di Leva, **Marta Biagioli** (2021). Natural SINEUP RNAs in Autism Spectrum Disorders: *Front Genet*, 12:745229.
3. Guendalina Bergonzoni, Jessica Döring and **Marta Biagioli**. 'D1R- and D2R-Medium-Sized Spiny Neurons Diversity: Insights Into Striatal Vulnerability to Huntington's Disease Mutation'. *Frontiers in Celular Neuroscience*, 10 February 2021.
4. Vidya Murthy, Toma Tebaldi, Toshimi Yoshida, Serkan Erdin, Teresa Calzonetti, Ravi Vijayvargia, Takshashila Tripathi, Emanuela Kerschbamer, Ihn Sik Seong, Alessandro Quattrone, Michael E. Talkowski, James F. Gusella, Katia Georgopoulos, Marcy E. MacDonald, **Marta Biagioli**. 'Hypomorphic mutation of the mouse Huntington's disease gene orthologue'. *PLoS Genetics* 2019 Mar 21;15(3): e1007765.
5. The HD iPSC Consortium - Ryan G Lim, Lisa L Salazar, Daniel K Wilton [….**Marta Biagioli**.....] and Clive N Svendsen. Developmental alterations in Huntington's disease neural cells and pharmacological rescue in cells and mice. *Nature Neuroscience*, 2017. 20(5):648-660. DOI: 10.1038/nn.4532.
6. **Marta Biagioli** (*), Francesco Ferrari (*), Eric M. Mendenhall, Yijing Zhang, Serkan Erdin, Ravi Vijayvargia, Sonia M. Vallabh, Nicole Solomos, Poornima Manavalan, Ashok Ragavendran, Fatih Ozsolak, Jong Min Lee, Michael E. Talkowski James F. Gusella, Marcy E. MacDonald, Peter J. Park and Ihn Sik Seong. *Htt* CAG repeat expansion confers on mutant huntingtin pleiotropic gains of function in chromatin regulation. *Human Molecular Genetics* (2015). 24 (9): 2442-2457. (*) These contributed equally to this work.
7. Sugathan Aarathi (*), **Marta Biagioli** (*), Christelle Golzio (*), Serkan Erdin (*), Ian Blumenthal, Poornima Manavalan, Ashok Ragavendran Harrison Brand, Diane Lucente, Judith Milese, Steven D. Sheridan, Alexei Stortchevoi, Manolis Kellis, Stephen J. Haggarty, Nicholas Katsanis, James F. Gusella, and Michael E. Talkowski. CHD8 regulates neurodevelopmental pathways associated with autism spectrum disorder in neural progenitors. *Proceedings of the National Academy of Sciences* (2014) 111, 42: E4468-E4477. (*) These authors contributed equally to this work.
8. Carrieri C. (*), Cimatti L. (*), **Biagioli M.**, Beugnet A., Zucchelli S., Fedele S., Pesce E., Ferrer I., Collavin L., Santoro C., Forrest A.R.R., Carninci P., Biffo S., Stupka E. and Gustincich S. Long non-coding antisense RNA controls UchL1 translation through the 5' overlapping region and an embedded SINEB2 repeat. (*) These authors contributed equally to this work. *Nature*. 2012 Nov 15;491(7424):454-7.