

CURRICULUM VITAE

MARCO TREVISAN-HERRAZ



Personal details

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Education

Physics Licenciatae (≈BSc+MSc, Licenciado en Ciencias Físicas), with specialisation in Theoretical Physics, at the Universidad Autónoma de Madrid (qualification obtained on: 7th October 2008).

Biophysics MSc (Máster en Biofísica) at the Universidad Autónoma de Madrid (qualification obtained on: 16th April 2010)

Master Thesis: «*GO connect: A Systems Biology Software for Automated Search and Visualisation of High Throughput Quantitative Proteomics Data*», presented in October 2009, regarding a software I developed in Visual C# to use biological databases in MySQL, associated to experiments in proteomics. The software performed system biology analyses for the comprehension and analysis of experimental results, and was used in the Laboratory of Chemistry of Proteins at the Centro de Biología Molecular «Severo Ochoa».

PhD in Biochemistry, Molecular Biology, Biomedicine and Biotechnology (area of Bioinformatics) at the Universidad Autónoma de Madrid (thesis defended on 27th March 2017).

PhD Thesis: «*Advances in Bioinformatics: Contributions to High-Throughput Proteomics-Based Identification, Quantification and Systems Biology*», the thesis consists of the presentation of three relevant bioinformatic problems I solved while working at the Cardiovascular Proteomics Laboratory of Prof. Jesús Vázquez, at CNIC, regarding the improvement of peptide identification algorithms, the statistics of quantitative proteomics experiments, and the systems biology analysis in high-throughput proteomics experiments.

Professional experience

Nov 2025 - Current position	Research Associate at Prof Gavin Richardson research group (at the Newcastle University Biosciences Institute), on computational biology projects regarding research in cardiovascular ageing and regeneration, where I'm creating a model to evaluate the effectiveness of treatments using RNA-seq datasets (both bulk and single cell).
Nov 2021 - Oct 2024	Research Associate in several groups at Newcastle University, including the Wellcome Centre for Mitochondrial Research , with funding I obtained for my <i>Mitonexus Project</i> , to explore the relationship between mitochondrial haplogroups and epigenomic histone marks using large datasets on ChIP-seq data. I also worked in this period on a research project for the analysis of big datasets of single cell RNAseq experiments in cancer and ageing, as well as in John Sayer's group analysing data for kidney disease research.
Sep 2018 - Oct 2021	Research Associate at Daniel Rico's laboratory (Newcastle University, UK), in a project funded by the Wellcome Trust Seed Award in Science to investigate the epigenomic basis of sex differences in immune system cells using computational approaches like <i>Chromatinsight</i> , a model I created to analyse epigenomics data with machine learning algorithms.
Oct 2011 - Aug 2018	Bioinformatics technician (2011-2018) and part-time pre-doctoral researcher (2012-2017) at the Laboratory of Cardiovascular Proteomics of Prof Jesús Vázquez at the Spanish National Centre for Cardiovascular Research (CNIC). FPI grant holder between 2012 and 2014. Published 11 papers on bioinformatics in proteomics in this period, including the <i>SanXoT</i> project, the <i>Systems Biology Triangle</i> , and <i>Comet-PTM</i> , whose model and software are (as of 2026) still in use and development in the proteomics community.
Dec 2008 - Sep 2011	Bioinformatics technician at the Laboratory of Chemistry of Proteins of Prof Jesús Vázquez at the Centro de Biología Molecular «Severo Ochoa». During this period I also obtained my MSc in Biophysics, while I created statistical models and their associated software for proteomics.

Selection of publications

Full list	Google scholar: https://scholar.google.es/citations?user=fABl17MAAAAJ ORCID: http://orcid.org/0000-0002-7129-0602
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Publication stats (as of 23rd June 2026)

Total peer-reviewed articles: 20 (4 as first author)

Total citations (according to Google Scholar): 1084

h-index (on Google Scholar): 13

Aug 2025	Praveen Dhondurao Sudhindar, [...], <u>Marco Trevisan-Herraz</u> , et al, «Urinary renal epithelial cells for NPHP1 phenotyping and personalized therapeutic response», <i>Journal of Cell Science</i> , 2025
Jul 2025	Praveen Dhondurao Sudhindar, [...], <u>Marco Trevisan-Herraz</u> , et al, «Urine-derived renal epithelial cells for deep phenotyping and transcriptomic response to therapy in Fabry disease», <i>Clinical Science</i> , 2025.

Sep 2024	Estefanía Núñez, [...], <u>Marco Trevisan-Herraz</u> , et al, «A Multiplexed Quantitative Proteomics Approach to the Human Plasma Protein Signature», <i>Biomedicines</i> , 2024
Jul 2024	Brigid Davidson, [...], <u>Marco Trevisan-Herraz</u> , et al, «Evolutionarily conserved enhancer-associated features within the MYEOV locus suggest a regulatory role for this non-coding DNA region in cancer», <i>Frontiers in Cell and Developmental Biology</i> , 2024.
Apr 2024	<u>Marco Trevisan-Herraz</u> , Caelinn James, David Juan, and Daniel Rico, «Evolutionary analysis of gene ages across TADs associates chromatin topology with whole-genome duplications», <i>Cell Reports</i> , 2024.
Jul 2022	Aneta Mikulasova, Daniel Kent, <u>Marco Trevisan-Herraz</u> , et al, «Epigenomic translocation of H3K4me3 broad domains over oncogenes following hijacking of super-enhancers», <i>Genome Research</i> , 2021.
Mar 2020	Elena Bonzon-Kulichenko, [...] <u>Marco Trevisan-Herraz</u> , et al, «Improved integrative analysis of the thiol redox proteome using filter-aided sample preparation», <i>Journal of Proteomics</i> , 2020.
Sep 2018	<u>Marco Trevisan-Herraz</u> , et al, «SanXoT: a modular and versatile package for the quantitative analysis of high-throughput proteomics experiments», <i>Bioinformatics</i> , 2018.
Sep 2017	<u>Marco Trevisan-Herraz</u> , et al, «QuiXoT: quantification and statistics of high-throughput proteomics by stable isotope labelling», <i>bioRxiv</i> , 2017
May 2016	<u>Marco Trevisan-Herraz</u> , Fernando García-Marqués, et al, «A novel systems-biology algorithm for the analysis of coordinated protein responses using quantitative proteomics», <i>Mol Cell Proteomics</i> , 2016.
Dec 2014	Elena Bonzon-Kulichenko, [...] <u>Marco Trevisan-Herraz</u> , et al, «Revisiting peptide identification by high-accuracy mass spectrometry: problems associated to the use of narrow mass precursor windows», <i>J Proteome Res</i> , 2014
Jan 2014	<u>Marco Trevisan-Herraz</u> , Pedro Navarro, et al, «General Statistical Framework for Quantitative Proteomics by Stable Isotope Labeling», <i>J Proteome Res</i> , 2014.
Jan 2011	Elena Bonzon-Kulichenko, [...] <u>Marco Trevisan-Herraz</u> , et al, «A robust method for quantitative high-throughput analysis of proteomes by 18O labeling», <i>Mol Cell Proteomics</i> , 2011.

Selection of computational skills

Python	11 years, developing software packages from scratch for proteomics, epigenomics and systems biology . Used regularly at CNIC (Spanish National Cardiovascular Research Centre, Madrid), and other research laboratories.
R	7 years, developing methodologies and performing analyses on proteomics (at CNIC), computational epigenomics and single cell RNA-seq (at Newcastle University).
Linux, Unix	8 years, including Ubuntu , in particular for the management of genomics projects, which require dealing with Linux-only applications.
Databases	MySQL, SQLite : 5 years, managing the databases of Gene Ontology and treating Proteome Discoverer's MSF files, to be used in parallel with the in-house development of proteomics software packages.

Teaching experience

2019 – 2024	Participation in the module CSC8309 “Genome Scale Data Analytics”, led by Dr Cockell (MSc of Bioinformatics, Newcastle University).
2019 – 2024	Participation in the module CMB2000 “Essential biomedical research skills”, led by Dr Armstrong (Medical School, Newcastle University).
2020	Participation in the module BMS3025 “Bioinformatics”, led by Dr Phillip Aldridge (Medical School, Newcastle University).
2017	Participation in the module "Proteomics" (MSc Bioinformatics, Universidad Autónoma de Madrid), led by Prof. Díaz-Uriarte.
2009 – 2017	Participation in the module "Proteomics" (Degree in Biotechnology, at Universidad Francisco de Vitoria, Madrid), led by Prof. Vázquez.

Selection of data analysis and bioinformatic skills

Artificial Intelligence and Machine learning	3 years, identifying differential patterns in histone marks in genomic regions using large ChIP-seq datasets, as a Research Associate at Dr Rico's Computational Epigenomics Laboratory, Newcastle University.
Computational epigenomics: Chromatinsight, Mitonexus	3 years, working with large datasets from ChIP-seq experiments (Blueprint project), to identify sex differences in the immune system, during my work as a Research Associate at Dr Rico's Computational Epigenomics Laboratory, Newcastle University.
Computational transcriptomics	3 years, analysing large RNA-seq datasets from the Blueprint project, while working at Dr Rico's Computational Epigenomics Laboratory (2 years).
Computational genomics	6 months, working at the Wellcome Centre for Mitochondrial Research, to identify the mitochondrial variants in the Blueprint datasets, in a collaboration with Dr Hudson.
Systems Biology	8 years, especially developing the Systems Biology Triangle method (see <i>Mol Cell Proteomics</i> published in May 2016, where I am co-first author), as part of the SanXoT software package. I also developed software for systems biology in MSc Thesis (see Education section).
Biological databases	16 years, related to projects in epigenomics, proteomics, systems biology, and transcriptomics, such as Encode, Ensembl, UniProt, Gene Ontology, KEGG, Ingenuity Pathway Analysis, SGD and other.
Identification of proteins: Proteome Discoverer, SEQUEST	10 years, mainly for peptide identification, and in parallel with the development from scratch of software packages and models for quantitative proteomics (SanXoT and QuiXoT). Also for an in-house developed software (pRatio) for the validation of these peptide identifications. Including deep management of MSF files.
Quantitative proteomics: QuiXoT, SanXoT	9 years, being the main focus of my doctoral thesis. In the context of the development of the abovementioned QuiXoT and SanXoT software packages for quantitative proteomics, the latter fully developed by me, and used in many projects at CNIC, including the €22 million funded PESA Project (see <i>J Proteome Res</i> published in Jan 2014).
Post-translational modifications	In general, in the context of protein identification and quantification, and, more specifically in the development and maintenance of the Comet-PTM project (2 years).

Research funding and funded projects

Fellowships, grants and internal research funding

Dec 2023 - Nov 2024	Co-Investigator on <i>Stop codon read-through compounds for the treatment of polycystic kidney disease</i> (PI: Prof John Sayer; additional Co-I: Dr Shalabh Srivastava). Northern Counties Kidney Research Fund award 20/01 ; approximately £15,000 total project funding.
Mar 2023 - Feb 2024	Co-Investigator on <i>Assessing the use of nonsense read-through compounds for the treatment of polycystic kidney disease</i> (PI: Prof John Sayer). PKD Charity Small Grant ; £10,000 total project award.
Oct 2021 - Mar 2022	Project originator and lead of the <i>Mitonexus Project</i> , investigating relationships between mitochondrial genetic variation and nuclear chromatin structure. Secured internal bridging support from the Newcastle University Faculty of Medical Sciences , with additional support from the former Wellcome Centre for Mitochondrial Research , following shortlisting for a BBSRC postdoctoral fellowship .
2010 - 2014	Individual award holder of a Spanish Ministry of Science and Innovation FPI Predoctoral Fellowship , BES-2010-036506 , linked to project BIO2009-07990 , <i>Desarrollo de técnicas de proteómica de segunda generación para el estudio profundo del proteoma dinámico: aplicación en Proteómica Cardiovascular</i> . Approximately €68,154 total public funding, including remuneration and estimated Social Security contributions.

Participation in funded research projects

Sep 2018 - Oct 2021	Research Associate on <i>Sex-dependent gene regulation in immune cells</i> , funded by a Wellcome Trust Seed Award in Science (206103/Z/17/Z) ; PI and award holder: Dr Daniel Rico.
2012 - 2018	Researcher on Spanish national research projects BIO2012-37926 and BIO2015-67580-P , supporting proteomics research and the development and application of <i>SanXoT</i> and related methodologies.
2013 - Aug 2018	Researcher participating in the ProteoRed PRB2 and PRB3 programmes , Spanish Proteomics Network awards IPT13/0001 and IPT17/0019 , supporting the proteomics research infrastructure.

Hobbies & interests

My core values (creativity, discovery, learning, synergy, and sharing) drive both my professional and personal life. Combining them with my passion for science and mathematical thinking, arise many activities that develop my strategic thinking and mentorship skills. For example, I led science shows for kids and the weekly chess club (both at my kids' school). In addition, I love engaging in creative writing, programming challenges, scientific illustration, creation of board games, and travelling with my kids.