

Marco Trevisan-Herraz, PhD



Researcher in computational biology

with a background in physics, proteomics and epigenomics
interested in understanding life from physics using computational models

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Key publications

tinyurl.com/MTH-GoogleScholar

orcid.org/0000-0002-7129-0602

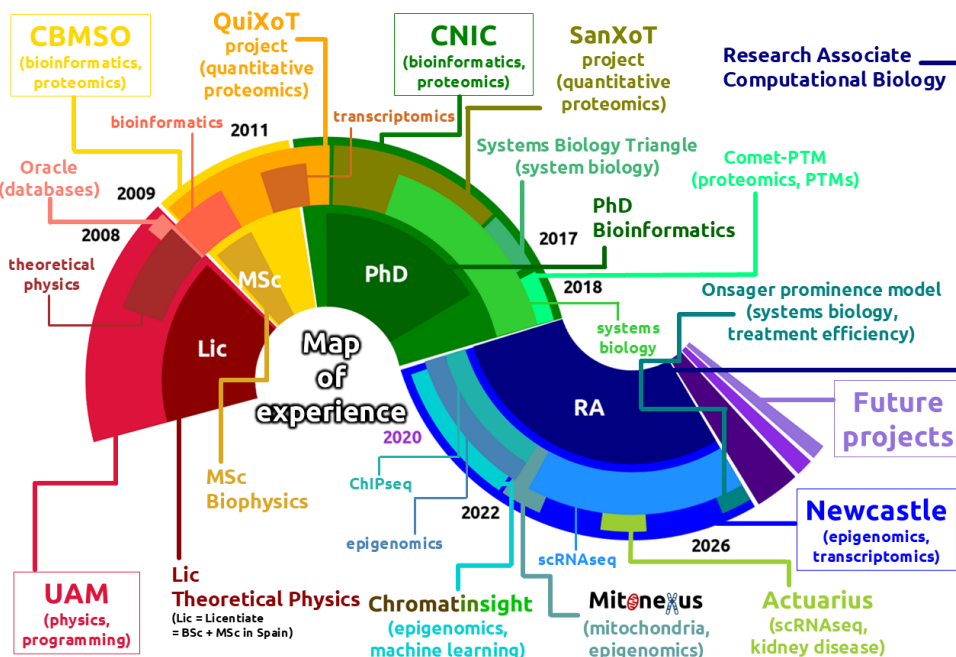
Marco Trevisan-Herraz, Caelinn James, David Juan, and Daniel Rico, «Evolutionary analysis of gene ages across TADs associates chromatin topology with whole-genome duplications», *Cell Reports*, 2024.

Trevisan-Herraz, M, et al, «SanXoT: a modular and versatile package for the quantitative analysis of high-throughput proteomics experiments», *Bioinformatics*, 2018.

Trevisan-Herraz, M, et al, «A novel systems-biology algorithm for the analysis of coordinated protein responses using quantitative proteomics», *Mol Cell Proteomics*, 2016.

Trevisan-Herraz, M, et al, «General Statistical Framework for Quantitative Proteomics by Stable Isotope Labeling», *J Proteome Res*, 2014.

	A1	A2	B1	B2	C1	C2	Mother tongue
Spanish							
Italian							
English							
Portuguese							
Esperanto							
Hungarian							
French							
German							
Finnish							



Education

Licenciate (BSc+MSc) Physics (2008)

MSc Biophysics (2010)

PhD Bioinformatics (2017)

Computational skills

Python

Visual C#

Visual Basic

Visual C++

MySQL

SQLite

R

Fortran

Bioinformatic skills

Computational epigenomics

Machine learning

Quantitative proteomics

Systems biology

Protein identification

Mass spectrometry

Biological databases

RNA-seq

PTMs

Core values

Creativity

Discovery

Learning

Synergy

Sharing