# Giancarlo Croce

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## Research Interests

I work at the intersection of biology, machine learning, and statistical modeling. I develop data-driven algorithms to model T cells interactions with cancer cells, with the aim of expediting personalized cancer immunotherapies. Previously, I developed statistical physics-inspired methods to model protein structures, evolution and interactions from their amino acid sequences.

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## Positions

JAN 2020 - CURRENT
LAUSANNE (SWITZERLAND)

**Postdoctoral Researcher**
**Marie Skłodowska-Curie Individual Fellow MT-PoINT project**
University of Lausanne - Ludwig center for cancer research
Computational Cancer Biology Lab -  David Gfeller Lab

OCT 2016 - OCT 2019,
PARIS (FRANCE)

**Ph.D. Fellow**
Sorbonne University, Computational and Quantitative Biology Lab  (LCQB)
Thesis: Towards a genome-scale coevolutionary analysis
Supervisor: Martin Weigt. Co-supervisor: Olivier Tenaillon

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## Education

SEP 2014 - JUN 2016,
PARIS (FRANCE)

**MSc in theoretical and statistical physics**
École Normale Supérieure, Paris,
• M2 thesis: *Out of equilibrium dynamics of spin glass models*
Supervisor: Cristina Toninelli
• M1 thesis: Adaptive *Cluster expansion for Ising model*
Supervisors: Simona Cocco, Francesco Zamponi

SEP 2011 - JUL 2014,
PAVIA (ITALY)

**BSc in physics**
Thesis: Symmetries in quantum mechanics, Casimir Operators
Supervisor: Prof. Claudio Dappiaggi

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## Publications

**Croce, G.**, Bobisse, S., Moreno, D. L., Schmidt, J., Guillame, P., Harari, A., & Gfeller, D. (2023). Deep learning predictions of TCR-epitope interactions reveal epitope-specific chains in dual alpha T cells. bioRxiv, 2023-09.

Racle, J., Guillaume, P., Schmidt, J., Michaux, J., Larabi, A., Lau, K., ... & Gfeller, D. (2023). Machine learning predictions of MHC-II specificities reveal alternative binding mode of class II epitopes. Immunity, 56(6), 1359-1375.

Gfeller, D., Schmidt, J., **Croce, G.**, Guillaume, P., Bobisse, S., Genolet, R., ... & Harari, A. (2023). Improved predictions of antigen presentation and TCR recognition with MixMHCpred2. 2 and PRIME2. 0 reveal potent SARS-CoV-2 CD8+ T-cell epitopes. Cell Systems, 14(1), 72-83.

Camviel, N., Wolf, B., **Croce, G.**, Gfeller, D., Zoete, V., & Arber, C. (2022). Both APRIL and antibody-fragment-based CAR T cells for myeloma induce BCMA downmodulation by trogocytosis and internalization. Journal for Immunotherapy of Cancer, 10(11).

Vigué, L.\*, **Croce, G.**\*, Petitjean, M., Ruppé, E., Tenaillon, O., & Weigt, M. (2022). Deciphering polymorphism in 61,157 Escherichia coli genomes via epistatic sequence landscapes. Nature Communications, 13(1), 4030.

Rodriguez-Rivas, J.\*, **Croce, G.**\*, Muscat, M., & Weigt, M. (2022). Epistatic models predict mutable sites in SARS-CoV-2 proteins and epitopes. Proceedings of the National Academy of Sciences, 119(4), e2113118119.

Muscat, M., **Croce, G.**, Sarti, E., & Weigt, M. (2020). FilterDCA: interpretable supervised contact prediction using inter-domain coevolution. PLoS computational biology, 16(10), e1007621.

**Croce, G.**, Gueudré, T., Ruiz Cuevas, M. V., Keidel, V., Figliuzzi, M., Szurmant, H., & Weigt, M. (2019). A multi-scale coevolutionary approach to predict interactions between protein domains. PLoS computational biology, 15(10), e1006891.

Cocco, S.\*, **Croce, G.**\*, & Zamponi, F.\* (2019). Adaptive cluster expansion for Ising spin models. The European Physical Journal B, 92, 1-17.

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**Grants and awards**

Jul 2021 - Jul 2023 Marie Sklodowska-Curie Individual Fellowship 2020 for the MT-PoINT (Motif in T cells for the Prediction of INTeractions) project at the interface between data science and immunology

Apr 2020 - Jun 2021 Sorbonne University - SU-COVID19-FSI project: Data-driven models of SARS-CoV-2 sequences: Mutational effects, selective constraints, and potential drug targets

Jan 2019 - Mar 2019 Visiting researcher at University of L'Havana (Cuba) funded by the INFERNET project: new algorithms for inference and optimization from large-scale biological data

Oct 2016 - Nov 2019 Ph.D. grant funded by *Labex Calsimlab - Data, computing and simulation.* Calsimlab is a cluster of excellence for research (PIA2 laboratoires d'excellence)

Sep 2014 - Jun 2016 Two-years master scholarship funded by ICFP-ENS Labex. The ICFP-ENS master is specifically intended for outstanding international students wishing to obtain a first-class education in physics

Sep 2011 - Sep 2014 Student at Collegio Ghislieri - a 450-year-old Italian institution - that is committed to providing housing and financial support to outstanding students enrolled at the University of Pavia.

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## Recent talks

Set 2023 - Basel (Switzerland)
Basel Computational Biology Conference - Big data in biology promises and challenges

April 2023 - Antwerp (Belgium)
The Third Antwerp TCR meeting - international experts discuss T cells from the TCR perspective.

April 2023 - Lausanne (Switzerland)
Biological Evolution Across Scales: Mathematical modeling and statistical inference

Aug 2022 - Cargese (France)
Physics and Computation in Immunology

Jun 2022 - Paris (France)
QBIO-IARANA Innate and Adaptive Recognition of Antigens and Neoantigens

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## Students

Jan 2020 - Sep 2020   Richie Yat-Tasi Wan - M2 Master Project. Now PhD student at the Technical University of Denmark

Jan 2022 - Jan 2023   Daniel Hafez - M2 Master Project.

Jun 2023 - Sep 2023  Animesh Awasth      - Undergraduate student (The School of Biology Summer Undergraduate Research Programme). Now PhD student at the Medical University of Vienna

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## Teaching

Dec 2021 - Introduction to Cancer Genomics - PhD class

Sep-Nov 2022 - introduction to clinical bioinformatics

Sep-Nov 2023 - introduction to clinical bioinformatics

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## Reviewing activities

Reviewer for Bioinformatics, Immunoinformatics, Plos ONE, Nature Methods, Nature Biotechnology, Cell Genomics

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## Languages

- **Italian**: Native speaker
- **English**: Fluent
- **French**: Fluent