

# Giancarlo Croce

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## Research Interests

My research combines biology, machine learning, and statistical modeling to tackle key challenges in immunology and protein science. I develop computational tools to model how T cells recognize and eliminate cancerous or infected cells, with the goal of advancing personalized cancer immunotherapies. Another aspect of my research focuses on designing methods that leverage protein sequence data to uncover evolutionary patterns and predict protein-protein interactions.

## Professional experience

JAN 2020 - CURRENT  
LAUSANNE (SWITZERLAND)

**Postdoctoral fellow**, *University of Lausanne - Ludwig center for cancer research*  
**Marie Skłodowska-Curie Individual Fellowship** [MT-PolINT project](#)  
Cancer Immune Recognition Lab - [David Gfeller Lab](#)

## Education

OCT 2016 - OCT 2019,  
PARIS (FRANCE)

**PhD, Computational biology**, *Sorbonne University*  
Computational and Quantitative Biology Lab  
Thesis: [Towards a genome-scale coevolutionary analysis](#)  
Supervisor: Martin Weigt. Co-supervisor: Olivier Tenaillon

SEP 2014 - JUN 2016,  
PARIS (FRANCE)

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

SEP 2011 - JUL 2014,  
PAVIA (ITALY)

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

## Grants and awards

Jul 2021 - Jul 2023 Marie Skłodowska-Curie Individual Fellowship 2020 for the [MT-PolINT](#) (Motif in T cells for the Prediction of INteractions) project at the interface between data science and immunology

Jun 2024 - Selected to participate in the [73rd Lindau Nobel Laureate Meeting](#), engaging with Nobel Laureates and leading scientists.

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. supporting grant funded by *Labex Calsimlab - Data, computing and simulation*.

Sep 2014 - Jun 2016 Two-year master's scholarship for international students from the École Normale Supérieure, Paris.

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

## Teaching experience

### Courses:

Fall 2024 - Write a review - course for master students

Sep-Nov 2022/2023/2024 - Introduction to clinical bioinformatics - for undergraduate students

Dec 2021 - Introduction to Cancer Genomics - for PhD students

### Student supervisor:

Master's thesis: Jikaël Ntoko, Daniel Hafez, Richie Yat-Tasi Wan

Master's and Bachelor's Projects: Alice Chiozza, Cailyn Mae Ong, Yebeen Kim, Animesh Awasth

## Recent talks

Jan 2025 - University of Cologne (Germany)

Collaborative Research Center 1310 - Predictability in Evolution

Oct 2024 - University of Lausanne (Switzerland)

Talk at the department of computational biology.

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

## Reviewing activities

Reviewer for Nature Communications, Bioinformatics, Cell Systems, Cell Genomics, Immunoinformatics, Plos Computational Biology, Plos ONE

## Languages

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

# Publication list

## Select Publications

**Croce, G.**, Bobisse, S., Moreno, D. L., Schmidt, J., Guillaume, P., Harari, A., Gfeller, D. (2024). *Deep learning predictions of TCR-epitope interactions reveal epitope-specific chains in dual alpha T cells*. Nature Communications, 15(1), 3211. <https://doi.org/10.1038/s41467-024-47461-8>

**Croce, G.**, Lani, R., Tardivon, D., Bobisse, S., de Tiani, M., Bragina, M., Perez, M. A. S., Schmidt, J., Guillaume, P., Zoete, V., Harari, A., Rufer, N., Hebeisen, M., Dunn, S., Gfeller, D. (2024). *Phage display enables machine learning discovery of cancer antigen specific TCRs*. Accepted for publication in Science Advances. bioRxiv. <https://doi.org/10.1101/2024.06.27.600973>

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. <https://doi.org/10.1073/pnas.2113118119>

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. <https://doi.org/10.1038/s41467-022-31643-3>

**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. <https://doi.org/10.1371/journal.pcbi.1006891>

## Additional Publications

Nielsen M., Eugster A., Jensen M. F., Goel M., Tiffeau-Mayer A., Pelissier A., Valkiers S., Rodríguez Martínez M., Meynard-Piganeau B., Greiff V., Mora T., Walczak A. M., **Croce G.**, Moreno D. L., Gfeller D., Meysman P., Barton J.(2024). *Lessons Learned from the Immrep23 TCR-Epitope Prediction Challenge*. Immunoinformatics. <https://doi.org/10.1016/j.immuno.2024.100045>

Racle, J., Guillaume, P., Schmidt, J., Michaux, J., Larabi, A., Lau, K., Perez, M. A. S., **Croce, G.**, Genolet, R., Coukos, G. (2023). *Machine learning predictions of MHC-II specificities reveal alternative binding mode of class II epitopes*. Immunity, 56(6), 1359-1375.e13. <https://doi.org/10.1016/j.immuni.2023.03.009>

Gfeller, D., Schmidt, J., **Croce, G.**, Guillaume, P., Bobisse, S., Genolet, R., Queiroz, L., Cesbron, J., Racle, J., 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.e5. <https://doi.org/10.1016/j.cels.2022.12.002>

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), e004711. <https://doi.org/10.1136/jitc-2022-005091>

Muscat, M., **Croce, G.**, Sarti, E., Weigt, M. (2020). *FilterDCA: Interpretable supervised contact prediction using inter-domain coevolution*. PLoS Computational Biology, 16(10), e1007621. <https://doi.org/10.1371/journal.pcbi.1007621>

Cocco, S.\*, **Croce, G.\***, Zamponi, F.\* (2019). *Adaptive cluster expansion for Ising spin models*. The European Physical Journal B, 92, 1-17. <https://doi.org/10.1140/epjb/e2019-100313-9>