CV

MARCO ORLANDO

Personal information

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Experience

1 October 2025 - present

MSCA Post-Doc Research fellow at laboratory for Environmental and Life Sciences of the **University of Nova Gorica** (Slovenia). Supervisor: prof. Ario de Marco. I work in a protein design project to generate, validate and optimize protein binders towards antigen of biomedical relevance. Such project involves the use of AI-based methods and aims to provide a user-friendly workflow for designing binders and lead-optimize them in case of working with hard antigens for which high-throughput experimental systems are not available.

24 September 2025

Lecturer of the *de novo* nanobody design session, within the “Nanobodies Workshop: Binder Recovery by In Silico and In Vitro Panning” (https://indico.ijs.si/event/2966/).

1 Jun 2022 - 30 September 2025

Post-Doc Research fellow at the laboratory of protein engineering and industrial enzymology at the Department of Biotechnologies and Biosciences of the **University of Milano-Bicocca** (Italy). Lab head and supervisor: prof. Marina Lotti. I am combining different computational tools, including end-to-end deep learning methods, to study structural and functional proprieties of enzymes from their primary sequences deposited in public genomic and metagenomic databases. My aim is to build and test a predictive sequence-based bioinformatics workflow to be used to select a “small-but-smart” set of biocatalysts that have maximal probabilities to be soluble and active on the hydrolysis of specific types of polymers.

9 Oct 2023 - present

48 h Tutor for the course “**Biochemistry**” held by Prof. Marina Lotti, during the academic years 2023/2024 (32 h) and 2024/2025 (16 h) at the Department of Biotechnologies and Biosciences of the **University of Milano-Bicocca**, Milan (Italy).

Oct 2024

6 h lecturer “Protein structure prediction: AlphaFold and beyond” for the students of “Protein Engineering” in the master’s course “Biotechnology for the bio-based and health industry" at the University of Insubria, in academic years 2022/2023, 2023/2024, 2024/2025.

6 Jun 2024

2 h lecturer "Next-generation Bioinformatics approaches to predict structural, stability and functional properties of proteins and their variants" for the students of "Nuove frontiere nella biocatalisi" in the master's course "Biotecnologie per le biorisorse e lo sviluppo ecosostenibile" at the University of Verona, in academic year 2023/2024.

6 May 2024

2 h lecturer "Protein structure prediction: AlphaFold and beyond" for the students of "Biologia Computazionale" in "Biologia" master at the University of Milano-Bicocca, in academic year 2023/2024.

11-12 Jul 2024

4 h workshop lecturer "**Protein engineering: how artificial intelligence is democratizing the *de novo* design of proteins and enzymes**" for the students of the PhD Course in Molecular, Industrial and Environmental Biotechnologies at the Department of Biotechnology, University of Verona

1 Oct 2021 - 30 Sep 2022

Adjunct Professor, **frontal** and **laboratory lessons** of the module "**Data Science**" (3 cfu, 24 h) of the course "**Biostatistics and Data Science**" (https://www.uninsubria.it/ugov/degreecourse/155227, 6 cfu) during the academic year 2021/2022 at the Department of Biotechnologies and Life Sciences of the **University of Insubria**, Italy. "Cultore della materia" for the course "Biochemistry and Bioinformatics (SSD BIOS-07) of the bachelor's in Biotechnology in the same University.

1 Sep 2020 - 31 May 2022

Post-Doc Research fellow at the laboratory **The Protein Factory 2.0** at the Department of Biotechnologies and Life Sciences of the **University of Insubria** (Varese, Italy). Lab head: prof. Loredano Pollegioni, Supervisor: prof. Gianluca Molla. I worked on three projects:

i. The engineering of PET hydrolyzing enzymes, both in wet lab (enzyme production in E. coli, protein purification, kinetic analysis on model substrates and biophysical analysis by circular dichroism) and *in silico* (evolutive, docking and dynamic modelling analyses). I created and applied a bioinformatics workflow to engineer a PET hydrolase with improved PET hydrolase activity (https://www.theproteinfactory2.it/plastic-biodegradation).

ii. The analysis of the sequence space and evolution of succinic semialdehyde dehydrogenase (SSADH) enzymes deposited in public databases, in collaboration with prof. Mariarita Bertoldi from University of Verona (Italy).

iii. Optimization of protocols for lipids and proteins extraction from Black Soldier Fly (*Hermetia illucens*) biomass reared on organic waste (https://www.theproteinfactory2.it/valorizationorganicwaste).

1 Jan 2020 - 31 Aug 2020

Research scholarship at the laboratory of protein engineering and industrial enzymology at the Department of Biotechnologies and Biosciences of the **University of Milano-Bicocca** (Lab head and supervisor: prof. Marina Lotti). I worked with lysozyme enzymes that have a relatively high activity at low temperature, by employing and comparing experimental and computational approaches. My aim in this project was to study the cold-related properties of enzymes by biochemical and biophysical approaches in comparison to their molecular evolution and predicted *in silico* features from models and simulations.

1 Nov 2016 - 31 Oct 2019

PhD student in **Biology and Biotechnology** at the Department of Biotechnologies and Biosciences of the University of Milano-Bicocca, Milan (Italy), in the laboratory of protein engineering and industrial enzymology (Lab head and supervisor: prof. Marina Lotti). Qualification obtained on 31st January 2020 by discussing the thesis with the title "Biochemical and biophysical analysis of two Antarctic lysozyme endolysins and *in silico* exploration of glycoside hydrolase 19 sequence space".

Oct 2018 - Jan 2019

Adjunct Professor, **laboratory lessons** (24 h) of the course "**Structures and Molecular Interactions**" held by Prof. Luca De Gioia, during the academic year 2018/2019 at the Department of Biotechnologies and Biosciences of the University of Milano-Bicocca, Milan (Italy).

Education & training

May 2019 - 5 Jul 2019

Visiting PhD student in the laboratory of Juergen Pleiss at the Institute of Biochemistry and Technical Biochemistry of Stuttgart (Germany). I worked on a joint project on setting-up a new SQL-based database of a glycoside hydrolase family (https://gh19ed.biocatnet.de/). Bioinformatics tools have been used for analyzing the sequence space, the structures, and study protein evolution; previous information from experimental literature was integrated. The aims of the project were building a new, extended, family classification, finding sequence patterns for predicting activity specificity and detecting evolutionary trends in structural elements.

21 Oct - 22 Nov 2018

Visiting PhD student in the Innovation Unit at the Elvesys microfluidics innovation center, Paris (France). I got an update on the possible applications of droplet-based microfluidics technique, and I had the

	opportunity to observe and operate with fluid flows under a microscope in presence of experts in the field of droplet-based microfluidics.
25, 27, 29 Jun 2018	Course “Foundamentals of Biostatistics” organized by “Scuola di Dottorato” of the University of Milano-Bicocca, Milan (Italy).
4 - 8 Sep 2017	Summer school “Towards a Bio-based Economy: science innovation, economics, education” at the University of Milano-Bicocca, Milan (Italy).
4 Jul 2017	Seminar lesson and laboratory “A field trip in Metagenomics” organized by the PhD course in “Tecnologie Convergenti per I Sistemi Biomolecolari” of the University of Milano-Bicocca, Milan (Italy)
Oct 2013 - Mar 2016	Master’s degree in Evolutionary Biology, 110/110 cum laude, at the University of Padova, Padova (Italy). During my thesis internship, I spent a year in the laboratory of Evolutionary Biology of Arthropods at the Department of Biology (University of Padova, Italy). I was trained in the use of stereo- and light- microscopes for describing morphological characters of arthropods and combine them with computational analysis of nucleotide sequences of nuclear and mitochondrial molecular markers to delimit species by integrative taxonomy.
Oct 2010 - Jul 2013	Bachelor’s degree in Biology, 110/110 cum laude, at the University of Padova, Padova (Italy).

Research interests

Computational tools play a major role in experimental planning, especially when dealing with the study of mechanisms underlying biological complexity, which is the results of non-addictive interactions between genes, proteins, their structures up to phenotypes and entire communities.

I am interested in the development and application of bioinformatics tools, including those obtained by unsupervised and supervised artificial intelligence-based models, for improving the prediction of protein properties at molecular level, helping in planning experiments to understand their interaction with other protein and non-protein systems, and for generating tailored *de novo* designed proteins. This is hot topic research in the biomedical context: predicting the molecular properties responsible for disease dynamics due to dysfunctional human proteins or pathogen proteins and their variants will permit the diagnosis and design protein-based treatments of such diseases; moreover, there is a rising demand for new industrial enzymes for recycling of synthetic polymers and biopolymers. In both cases computational tools are useful to propose fit-for-purpose (stability, enzymatic activity, selective binding affinity to a specific target, ...) nature-derived protein variants or *de novo* protein designs, accelerating lab-based screenings.

Although I am more oriented towards bioinformatic tasks, I also worked in a lab in which I performed experimental validation over computational predictions, enjoying the contact with multi-disciplinary skills and knowledge backgrounds. From this experience, I learned to make an efficient integration of different expertise to approach issues, identify correct scientific questions and manage practical, also economical, aspects of research.

Skills

Mother tongue

Italian.

Other languages

English; C1 level of CEFR in understanding (listening/reading), writing and expression (spoken interaction/spoken production).

***In silico* expertise**

Advanced use of Linux-based operating systems (Ubuntu distributions) and bash shell and Python 3.x programming language. Advanced use of browser-based code editors (Jupyter notebooks, Google Colab) and code versioning software (Github). Advanced use of Microsoft Office and Origin packages for documents and plots production in a Microsoft Windows environment. Advanced use of computational tools for predicting the effect of point mutations on protein activity or/and stability (i. e., FoldX, Rosetta commons package). Advanced use of Modeller package for homology modelling of proteins and of recent deep-learning approaches for the structure prediction of biomolecules (i.e., AlphaFold, Boltz, OmegaFold, RoseTTAFold, ESM model series, IgFold) and for the *de novo* design of protein backbones (i.e., RFDiffusion), sequences conditioned on backbones (i.e., ProteinMPNN), protein-protein and protein-ligand complexes (i.e., GENzyme, [-AA], BindCraft, PocketGen, DiffAb). Advanced use of software for protein structure visualization (Pymol, Visual Molecular Dynamics, Chimera[X]). Advanced use of GROMACS and good use of OpenMM packages for preparing and performing/analyzing molecular dynamics simulations of protein systems, also in interaction with small organic/inorganic ligands, in a water solvent with ions at constant pH and temperature. Advanced use of tools for genomic data annotation and function prediction (prokka and operon Mapper packages with custom Hidden Markov Model-based annotation), software for building multi-alignment of homologue DNA/RNA/protein sequences and/or structures (i.e., Mafft, T-coffee, Clustal-X, Muscle, Foldseek), and for trimming unreliable aligned positions (i.e., Aliscore, ZORRO, Guidance 2). Recently protein search became multimodal with sequence-structure-text models like ProTrek, for which I started to explore possible improvements over classical string level dynamic programming-based alignments. Deep expertise in reconstructing and dating the molecular evolution of genes and proteins (IQTREE, TNT, PhyML, RAxML, MrBayes, Beast, Bali-phy). Good knowledge of Statistica Statsoft for descriptive presentation of data and statistical analysis of quantitative and meristic morphological data. Expertise in DNA-based species delimitation tools and DNA barcoding methods. Basic use of Mesquite and R package for the implementation of some functions of the tools mentioned above. Basic knowledge of Microsoft SQL Server for storing and annotating biological sequence data from public databases, and of Cytoscape platform for biological networks visualization. Basic use of QGIS for plotting geo-referenced points on a map.

Lab expertise Taking morphometric measures and working with multi-stacks photos captured at stereo- and light-microscopes. Molecular biology for PCR-based mutagenesis and setting recombinant protein production in *E. coli*. Biochemical techniques for the purification (i.e., IMAC) and the functional characterization of enzymes. Use of circular dichroism and tryptophan intrinsic fluorescence for biophysical characterization of proteins. Growth inhibition plate assays. Soxhlet extraction by petroleum ether. Chemical methods for the extraction of proteins from biomasses (TCA precipitation, pH-dependent solubilization and precipitation, Osborne fractionation).

Congresses

11 - 13 Nov 2024	European RosettaCon at Biocenter, University of Copenhagen, Denmark.
29 Jun - 3 Jul 2024	The 48th FEBS congress “Mining biochemistry for human health and well-being” at Milan (Italy).
28 - 31 Mar 2023	“Novel Enzymes 2023” at Greifswald (Germany).
15 - 16 Dec 2022	Evolutionary Cell Biology Workshop at Die Heinrich-Heine-Universität Düsseldorf (Germany).
5 - 8 Sep 2022	EMBO workshop “When predictions meet experiments: The future of structure determination” at Palazzo Branciforte, Palermo (Italy).

9 - 25 Feb 2022	23rd Bologna Winter School "Structural Bioinformatics in the era of AlphaFold2". 24 hours Online Event.
4 - 7 Sep 2019	16th International Conference on Computational Intelligence methods for Bioinformatics and Biostatistics, held at the University of Bergamo, Bergamo (Italy).
1 - 4 Sep 2019	8th Congress of the "Italian Society of Evolutionary Biology" (SIBE or ISEB) at the "Orto Botanico" at the University of Padova, Padova (Italy).
25 - 27 Aug 2019	Meeting "Perspectives in bioinformatics: data mining and scale bridging" in Söllerhaus, Hirschegg (Austria).
3 - 5 Jul 2019	Workshop "Nature as a teacher: big data, complex systems, new chemistry", held at the *Tagungshotel* campus.guest of the University of Stuttgart, Stuttgart (Germany).
14 - 15 Feb 2019	Workshop "Understanding complexity in life sciences" at the Department of Earth and Environmental Sciences, University of Milano-Bicocca, Milan (Italy).
16 - 20 Sep 2018	12th International Congress of "Extremophiles" at Hotel Continental Ischia, Ischia, Naples (Italy).
28 - 30 May 2018	Congress "Proteine 2018" held in the "Silos di Ponente" of "Polo di Santa Marta", University of Verona, Verona (Italy).
28 - 31 Aug 2017	7th Congress of the "Italian Society of Evolutionary Biology" (SIBE or ISEB) at the Department of Science of the University of Roma Tre, Rome (Italy). I received an update on the major topics and methods currently applied in evolutionary research activities, and the new techniques for teaching biological disciplines.
4 Apr 2017	Conference "Digital Revolution: come cambierà la nostra vita", held at the University of Milano-Bicocca. It is a special edition of the "13th world conference Science and Society: science for a better life".
31 Aug-3 Sep 2015	6th Congress of the "Italian Society of Evolutionary Biology" (SIBE or ISEB) at the University of Bologna, Bologna (Italy).

Meeting Contributions

28 Jan 2025	(Oral) Orlando M. A benchmark of Deep Learning approaches for annotating the substrate specificity of glycoside hydrolase enzymes from nature. WIDEnzymes workshop. Politecnico di Milano, Lecco Campus (Italy).
11 - 13 Nov 2024	(Poster) Orlando M., Marchetti, A., Mangiagalli, M., Bombardi, L., Fusco, S., Lotti, M. *In silico* tools to mine glycoside hydrolase enzymes from nature. European RosettaCon at Biocenter, University of Copenhagen, Denmark.
29 Jun - 3 Jul 2024	(Poster) Orlando M., Marchetti, A., Mangiagalli M., Bombardi, L., Fusco, S., Lotti, M. An *in silico* workflow for mining glycoside hydrolase enzymes from nature. The 48th FEBS congress "Mining biochemistry for human health and well-being" at Milan (Italy)
22 Sep 2023	(Oral) Orlando M., Lotti M., An *in-silico* workflow based on deep learning methods for sequence-based screening of enzymes: the case of Glycoside Hydrolase 3 family. 7th meeting of Young Biochemists in Lombardy, Brescia (Italy).
28 - 31 Mar 2023	(Poster) Orlando M., Lotti M., A structure-based *in silico* workflow for the predictive exploration of substrate specificity in enzyme families. Congress "Novel Enzymes 2023" at Greifswald (Germany).
15 - 16 Dec 2022	(Oral) Orlando M., Can deep learning allow to scale up evolutionary studies on the substrate specificity of enzymes? The case of "PET degrading" enzymes. Evolutionary Cell Biology Workshop at Die Heinrich-Heine-Universität Düsseldorf (Germany).
1 - 4 Sep 2019	(Poster) Orlando M., Buchholz P. C. F., Lotti M., Pleiss J., Diversity and evolution of glycoside hydrolases family 19 revised by sequence space mining. 8th Congress of the "Italian Society of Evolutionary Biology" at Padova (Italy).
25 - 27 Aug 2019	(Oral) Orlando M., Introduction to "FuncLib": next-generation automatic design of multipoint mutations at enzyme active sites. Meeting "Perspectives in bioinformatics: data mining and scale bridging" at Hirschegg (Austria).
3 - 5 Jul 2019	(Poster and flash presentation) Orlando M., Buchholz P. C. F., Lotti M., Pleiss J., Diversity and evolution of glycoside hydrolases family 19 revised by sequence space mining. Workshop "Nature as a teacher: big data,

complex systems, new chemistry" at Stuttgart (Germany).

16 - 20 Sep 2018 (Poster) Orlando M., Pucciarelli S., Lotti M., Biochemical and sequence signatures of cold-activity in Antarctic glycoside hydrolase enzymes. 12th International Congress of "Extremophiles" at Ischia, Naples (Italy).

20 - 22 Sep 2018 (Oral) Lotti M., Brocca S., Mangiagalli M., Pischedda A., Orlando M., Maione S., De Pascale D., Pucciarelli S., Nardini M., Braslavsky I., "Cold Biotechnology": enzymes and anti-freeze proteins from Antarctic organisms. 59th Congress Italian Society of Biochemistry and Molecular Biology at Caserta (Italy).

28 - 30 May 2018 (Poster) Orlando M., Maione S., Mangiagalli M., Pischedda A., Valtorta R., Mondo D., Pennati M., Brocca S., Pucciarelli S., Lotti M., Biochemical and structural features of enzymes from an Antarctic metagenome. Proteine 2018 at Verona (Italy).

1 - 4 Jul 2018 (Oral) Lotti M., Brocca S., Mangiagalli M., Pischedda A., Orlando M., Maione S., De Pascale D., Pucciarelli S., Nardini M., Braslavsky I., "Enzymes and ice binding proteins from Antarctic organisms". 18th European Congress on Biotechnology at Geneva (Switerland).

30 Aug - 2 Sep 2016 (Oral) of my Master's thesis work at the first national joint congress of "Società Italiana di Ecologia"- "Unione Zoologica Italiana"- "Società Italiana di Biogeografia" (SITE-UZI-SIB) at the University of Milano-Bicocca, Milan (Italy).

Tutoring activity

Oct 2023 - Nov 2024 I supervised a master's student from the University of Milano-Bicocca.

Sep 2020 - Sep 2021 I supervised a bachelor's and a master's student from the University of Insubria.

Jul 2020 I provided a 4-hours online course to four students of the bachelor's in biotechnologies at the University of Milano-Bicocca. The topic was computational prediction of protein function, fast modelling and annotation of uncharacterized protein sequences (glycosyl hydrolase enzyme class) from metagenomic open reading frames.

Jul 2018 I supervised for a month Hüseyin Okan Soykam, a visiting Master Student from Yeditepe University. We worked on gene annotations and bioinformatic analysis on coding protein sequences.

Publications

(Article) Testa, E., Barbera, V., Fasoli, E., Giese, U., Belviso, M. R., Rossini, P., Bruno, D., Tettamanti, G., Orlando, M., Molla G., Casartelli, M. & Galimberti, M. (2025). Electroconductive Bionanocomposites from Black Soldier Fly Proteins for Green Flexible Electronics. *ACS Sustainable Chemistry & Engineering*. **DOI: 10.1021/acssuschemeng.4c08242**.

(Article) Orlando, M., Marchetti, A., Bombardi, L., Lotti, M., Fusco, S., & Mangiagalli, M. (2025). Polysaccharide degradation in an Antarctic bacterium: Discovery of glycoside hydrolases from remote regions of the sequence space. *International Journal of Biological Macromolecules*, 140113. **DOI: 10.1016/j.ijbiomac.2025.140113**.

(Article) Cesaro, S., Orlando, M., Bettin, I., Longo, C., Spagnoli, G., de Laureto, P. P., ... & Bertoldi, M. (2025). A crucial active site network of titratable residues guides catalysis and NAD+ binding in human succinic semialdehyde dehydrogenase. *Protein Science*. **DOI: 10.1002/pro.70024**.

(Article) Bruno, D., Orlando, M., Testa, E., Miino, M. C., Pesaro, G., Miceli, M., ... & Tettamanti, G. (2025). Valorization of organic waste through black soldier fly: On the way of a real circular bioeconomy process. *Waste Management*. **DOI: 10.1016/j.wasman.2024.10.030**.

(Article) Salini, A., Zuliani, L., Gonnelli, P. M., Orlando, M., Odoardo, A., Ragno, D., Aulitto, M., Zaccone, C., Fusco, S. (2024). Plastic-Degrading Microbial Consortia from a Wastewater Treatment Plant. *International Journal of Molecular Sciences.* **DOI: 10.3390/ijms252312747**.

(Article) Bombardi, L., Orlando, M., Aulitto, M., Fusco, S. (2024) Thermophilic Hemicellulases Secreted by Microbial Consortia Selected from an Anaerobic Digester. *International Journal of Molecular Sciences* **DOI: 10.3390/ijms25189887**.

(Article) Riva, D., Orlando, M., Rabattoni, V., Pollegioni, L. (2024) On the quaternary structure of human D-3-phosphoglycerate dehydrogenase. *Protein Science*. **DOI: 10.1002/pro.5089**

(Article) Marchetti, A., Orlando, M., Bombardi, L., Fusco, S., Mangiagalli M., Lotti, M. (2024) Evolutionary history and activity towards oligosaccharides and polysaccharides of GH3 glycosidases from an Antarctic marine bacterium. *International Journal of Biological Macromolecules*. **DOI: 10.1016/j.ijbiomac.2024.133449**

(Article) Murtas, G., Zerbini, E., Rabattoni, V., Motta, Z., Caldinelli, L., Orlando, M., Marchesani, F., Campanini, B., Sacchi, S., Pollegioni, L. (2023). Biochemical and cellular studies of three human 3 - phosphoglycerate dehydrogenase variants responsible for pathological reduced L - serine levels. *BioFactors*. **DOI: 10.1002/biof.2002**

(Article) Bonato, L., Bortolin, F., De Zen, G., Decker, P., Lindner, E. N., Orlando, M., Spelda, J., Voigtländer, k., Wesener, T. (2023). Towards elucidating species diversity of European inland Strigamia (Chilopoda: Geophilomorpha): a first reassessment integrating multiple lines of evidence. *Zoological Journal of the Linnean Society*. **DOI: 10.1093/zoolinnean/zlad070**

(Review) Orlando, M., Molla, G., Castellani, P., Pirillo, V., Torretta, V., Ferronato, N. (2023). Microbial enzyme biotechnology to reach plastic waste circularity: current status, problems and perspectives. *International Journal of Molecular Sciences*. **DOI: 10.3390/ijms24043877**

(Article) Pirillo, V., Orlando, M., Battaglia, C., Pollegioni, L., Molla, G. (2023). Efficient polyethylene terephthalate degradation at moderate temperature: a protein engineering study of LC-cutinase highlights the key role of residue 243. *The FEBS Journal*. **DOI: doi.org/10.1111/febs.16736**

(Article) Marchetti, A., Orlando, M., Mangiagalli, M., Lotti, M. (2022). A cold active esterase enhances mesophilic properties through Mn2+ binding. *The FEBS Journal*. **DOI: 10.1111/febs.16661**

(Article) Pirillo, V., Orlando M., Tessaro, D., Pollegioni, L., Molla, G. (2022). An Efficient Protein Evolution Workflow for the Improvement of Bacterial PET Hydrolyzing Enzymes. *International Journal of Molecular Sciences*. **DOI: 10.3390/ijms23010264**

(Article) Orlando, M., Buchholz C. F., P., Lotti, M., Pleiss, J. (2021). The GH19 Engineering Database: sequence diversity, substrate scope, and evolution in glycoside hydrolase family 19. *Plos One*. **DOI: 10.1371/journal.pone.0256817**

(Article) Orlando, M., Fortuna, S., Oloketuyi, S., Bajc, G., Goldenzweig, A., de Marco, A. (2021). CDR1 composition can affect nanobody recombinant expression yields. *Biomolecules*. **DOI: 10.3390/biom11091362**

(Article) Ubbiali D., Orlando M., Kovačič M., Iacobucci C., Semrau M. S., Bajc G., Fortuna S., Ilc G., Medagli B., Oloketuyi S., Storici P., Sinz A., Grandori R., de Marco A. (2021). An anti-HER2 nanobody binds to its antigen HER2 via two independent paratopes. *International Journal of Biological Macromolecules*. **DOI: 10.1016/j.ijbiomac.2021.04.032**

(Article) Orlando M., Pucciarelli S., Lotti M. (2021). Endolysins from Antarctic Pseudomonas Display Lysozyme Activity at Low Temperature. *Marine Drugs*. **DOI: 10.3390/md18110579**

(Article) Mangiagalli M., Lapi M., Maione S., Orlando M., Brocca S., Pesce A., Barbiroli A., Camilloni C., Pucciarelli S., Lotti M., Nardini M. (2021). The co-existence of cold activity and thermal stability in an Antarctic GH42 β-galactosidase relies on its hexameric quaternary arrangement. *The FEBS Journal*. **DOI: 10.1111/febs.15354**

(Review) Mangiagalli M., Brocca S., Orlando M., & Lotti M. (2020). The “cold revolution”. Present and future applications of cold-active enzymes and ice-binding proteins. *New Biotechnology*. **DOI: 10.1016/j.nbt.2019.09.003**

(Article) Bonato L., Orlando M., Zapparoli M., Fusco G., & Bortolin F. (2017). New insights into Plutonium, the least known of the European large scolopenders (Chilopoda): occurrence, evolution and morphology. *Zoological Journal of the Linnean Society*. **DOI: 10.1093/zoolinnean/zlw026**

(Article) Bonato L., Bortolin F., Drago L., Orlando M., & Dànyi L. (2017). Evolution of Strigamia centipedes (Chilopoda): a first molecular assessment of phylogeny and divergence times. *Zoologica Scripta*. **DOI: 10.1111/zsc.12234**

03/10/2025 Marco Orlando