

## Jacopo Vertemara

### Personal Data

Date of birth 27-04-1989, Italian citizenship

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### Education and Training

March 2018, he obtained PhD in Biotechnology and Bioscience at the University of Milano-Bicocca under the supervision of Luca De Gioia. The PhD thesis titled “Computational modelling of macromolecules: prediction of 3D structure, catalytic activity and dynamics features of proteins” is focused on computational techniques, in particular Quantum Mechanics and Molecular Dynamics methods, to investigate the relation between structure and activity of macromolecules.

October 2013, he obtained master’s degree in biotechnology and Bioscience at the University of Milano-Bicocca, with a degree thesis on the characterization of the hydrolytic mechanism using Density Functional Theory of a *de novo* design carbonic anhydrase under the supervision of Prof. Luca De Gioia.

### Employment and research experience

Since April 2018 he has a post-doc fellowship at the Department of Biotechnology and Bioscience at University of Milano-Bicocca with project about using of accelerated molecular dynamics simulations to study the rearrangement of protein complexes involved in the pathways of DNA double strand break repair.

The main research activity has been focused on the characterization at atomistic resolution using MD approach of effects of amino acid substitutions in Mre11 and Rad50 subunits of the MRX complex in *S. Cerevisiae*.

From March 2014 to February 2015 he has a research scholarship at Associazione la Nostra Famiglia IRCCS E. Medea to identify functional genetic polymorphisms in genes of biomedical interest and to detect variants that affect human phenotypes. In this period, he developed statistical and bioinformatic tools in R-script to manage genomic elements annotation, sequences and positional genomic features and to keep track of genomic variations.

### Scientific Production

The scientific activity has led to the overall production as author/coauthor of 16 articles on international peer reviewed journals.

H-index (scopus) 7.

### Publications

- 1) Mozzi A, Forni D, Cagliani R, Pozzoli U, **Vertemara J**, Bresolin N, Sironi M. Albuminoid genes: evolving at the interface of dispensability and selection. *Genome Biol Evol.* 2014 Oct 27;6(11):2983-97. doi: 10.1093/gbe/evu235.
- 2) Forni D, Mozzi A, Pontremoli C, **Vertemara J**, Pozzoli U, Biasin M, Bresolin N, Clerici M, Cagliani R, Sironi M. Diverse selective regimes shape genetic diversity at ADAR genes and at their coding targets. *RNA Biology.* *RNA Biology* 12:2, 149--161; February 2015; © 2015 Taylor & Francis Group, LLC
- 3) Pontremoli C, Mozzi A, Forni D, Cagliani R, Pozzoli U, Menozzi G, **Vertemara J**, Bresolin N, Clerici M, Sironi M. Natural selection at the brush-border: adaptations to carbohydrate diets in humans and other mammals. *Genome Biol. Evol.* 7(9):2569–2584. doi:10.1093/gbe/evv166

- 4) Visentin C, Pellistri F, Natalello A, **Vertemara J**, Bonanomi M, Gatta E, Penco A, Relini A, De Gioia L, Airoidi C, Regonesi M E and Tortora P. Epigallocatechin-3-gallate and related phenol compounds redirect the amyloidogenic aggregation pathway of ataxin-3 towards non-toxic aggregates and prevent toxicity in neural cells and *Caenorhabditis elegans* animal model. *Human Molecular Genetics*, 2017, Vol. 26, No. 17 3271–3284
- 5) Bertini L, Alberto M E, Arrigoni F, **Vertemara J**, Fantucci P, Bruschi M, Zampella G, De Gioia L, On the photochemistry of  $\text{Fe}_2(\text{edt})(\text{CO})_4(\text{PMe}_3)_2$ , a [FeFe]-hydrogenase model: A DFT/TDDFT investigation, *Quantum chemistry*, 2017 DOI: 10.1002/qua.25537
- 6) Cassani C, Gobbin E, **Vertemara J**, Wang W, Marsella A, Sung P, Tisi R, Zampella G, Longhese MP. Structurally distinct Mre11 domains mediate MRX functions in resection, end-tethering and DNA damage resistance. *Nucleic Acids Res.* 2018 Feb 6. doi: 10.1093/nar/gky086
- 7) Keable SM, **Vertemara J**, Zadornyy OA, Eilers BJ, Danyal K, Rasmussen AJ, De Gioia L, Zampella G, Seefeldt LC, Peters JW. Structural characterization of the nitrogenase molybdenum-iron protein with the substrate acetylene trapped near the active site. *J Inorg Biochem.* 2018 Mar;180:129-134. doi: 10.1016/j.jinorgbio.
- 8) Forni D, Cagliani R, Pontremoli C, Pozzoli U, **Vertemara J**, De Gioia L, Clerici M and Sironi M. Evolutionary Analysis Provides Insight Into the Origin and Adaptation of HCV. *HCV Origin and Evolution* published: 01 May 2018, doi: 10.3389/fmicb.2018.00854
- 9) Gobbin E, Cassani C, **Vertemara J**, Wang W, Mambretti F, Casari E, Sung P, Tisi R, Zampella G & Longhese M P. The MRX complex regulates Exo1 resection activity by altering DNA end structure. *The EMBO Journal*, 2018 | Accepted 30 May 2018, DOI 10.15252/embj.201798588 | Received 7 November 2017 | Revised 24 May
- 10) Gobbin E, **Vertemara J**, Longhese M P, Local unwinding of double-strand DNA ends by the MRX complex promotes Exo1 processing activity. *Molecular & Cellular Oncology*, 2018 DOI: 10.1080/23723556.2018.1511208
- 11) Cassani C, **Vertemara J**, Bassani M, Marsella A, Tisi R, Zampella G, Longhese M P, The ATP-bound conformation of the Mre11–Rad50 complex is essential for Tel1/ATM activation. *Nucleic acids research*, 2019 doi: 10.1093/nar/gkz038
- 12) Bonetti, D; Rinaldi, C; **Vertemara, J**; Notaro, M; Pizzul, P; Tisi, R; Zampella, G; Longhese, MP. DNA binding modes influence Rap1 activity in the regulation of telomere length and MRX functions at DNA ends. *Nucleic acids research*, 2019 doi: 10.1093/nar/gkz1203
- 13) Tisi, R., **Vertemara, J.**, Zampella, G., Longhese, M.P., Functional and structural insights into the MRX/MRN complex, a key player in recognition and repair of DNA double-strand breaks. *Computational and Structural Biotechnology Journal* Volume 18, 2020, Pages 1137-1152 <https://doi.org/10.1016/j.csbj.2020.05.013>
- 14) F. Arrigoni, F. Rizza, **J. Vertemara**, R. Breglia, C. Greco, L. Bertini, G. Zampella, L. De Gioia, Rational Design of  $\text{Fe}_2(\mu\text{-PR}_2)_2(\text{L})_6$  Coordination Compounds Featuring Tailored Potential Inversion, *ChemPhysChem* 2020, Volume 21, N. 20, pag 2279-2292.
- 15) Frascotti G, Galbiati E, Mazzucchelli M, Pozzi M, Salvioni L, **Vertemara J**, Tortora P. The Vault Nanoparticle: A Gigantic Ribonucleoprotein Assembly Involved in Diverse Physiological and Pathological Phenomena and an Ideal Nanovector for Drug Delivery and Therapy. *Cancers (Basel)*. 2021 Feb 9;13(4):707. doi: 10.3390/cancers13040707. PMID: 33572350; PMCID: PMC7916137.

### Teaching

2016 – present: tutor of laboratory of General and Inorganic Chemistry

2017 – present: tutor of laboratory of the course “Interazioni ligando-macromolecola”

2017 – present: tutor of laboratory of the course “Strutture e interazioni molecolari”.

### Awards

2020 Premio Giovani Talenti dell'Università degli studi di Milano-Bicocca, Edizione 2020. (Secondo posto)