

AVVISO DI SEMINARIO

Il giorno **25 Marzo 2024** alle ore **14.00**

Dr. Giuliano Sciara

researcher at BBF for INRAE, the French Research Institute for Agriculture, Food and Environment (Marseille, FR)

(ospite di Prof. Francesco Musiani e Prof. Stefano Ciurli)

terrà un seminario dal titolo:

Beyond the coupled distortion model: structural analysis of the single domain, green mononuclear cupredoxinAcoP

Area tematica: Structural biology

in presenza:

Aula 1, via Belmeloro 6, Bologna BO

e in streaming:

https://teams.microsoft.com/l/meetupjoin/19%3aN09c0NlyEssBnF7ObCyDOQwkgDWm1qdd9f7F2nJV9fw1%40thread.tacv2/1631519 544944?context=%7b%22Tid%22%3a%22e99647dc-1b08-454a-bf8c-699181b389ab%22%2c%22Oid%22%3a%225a941351-ef41-4aa4-8771fa50a6d62ca1%22%7d

Colleghi e studenti sono cordialmente invitati

ABSTRACT

Cupredoxins are the perfect model proteins to dissect and understand the structure-function relationship in T1 centres. In the last decades the Coupled Distortion Model (CDM) has been the only reference to describe the structure-function relationship in T1 centres. The discovery of novel cupredoxins demonstrates their high diversity, with variations in term of copper-binding ligands, copper centre geometry, redox potential, as well as biological function. AcoP is a periplasmic cupredoxin belonging to the iron respiratory chain of an acidophilic bacterium [1]. It presents original features, including high resistance to acidic pH and a green-type copper center of high redox potential [2]. In this study [3], structural and biophysical characterization of wild type AcoP and of two Cu-ligand mutants (H166A and M171A) confirms that the active centre of AcoP is highly constrained. Comparative analysis with other cupredoxins of known structures, suggests that in AcoP the second coordination sphere might be the main determinant of active centre rigidity, due to the presence of an extensive hydrogen bond network. Crystallographic structures of native reduced (1.65 Å resolution) and oxidized AcoP, confirmed by EXAFS data, unveil unusual Cu-ligand distances, presenting both T1 and T1.5 features. This finding suggests that for AcoP the CDM might not hold valid. Finally we show that for other cupredoxins as well, the properties described do not fit well the CDM, and propose that alternative models describing Cu centre geometries need to be developed, while the importance of rack-induced contributions should not be underestimated. Figure 1: cupredoxins vs the CDM.

- [1] M. Roger et al., PLoS One. 2014, 9, e98941.
- [2] M. Roger et al., BBA Bioenerg. 2017, 1858, 351-359.
- [3] M. Roger et al., Dalton Trans. 2024, 53, 1794-1808.

BIOGRAPHICAL SKETCHES

Giuliano Sciara graduated in Biology at the University of Bologna in 1999 under the supervision of Prof. Stefano Luciano Ciurli with a thesis on protein NMR. Since then, structural biology and the structure-function relationship in proteins has become the core of his research activity, pursued with a PhD in protein crystallography at the Department of Biochemistry of Sapienza University, Rome from 2000 to 2003, under the supervision of Prof. Beatrice Vallone and Prof. Maurizio Brunori. He pursued the study of diverse types of biological macromolecules, such as gas and electron carriers, enzymes, membrane proteins and large viral assemblies, during post-doctoral works carried out at the Laboratories: AFMB - CNRS "Architecture and Function of Biological Macromolecules" (2005-09; Dr. Christian Cambilleau, Marseille-FR); Dept. of Physiology - Columbia University (2010-13; Prof. Filippo Mancia, New York-US); BIP "Bioénergétique et Ingénierie des Protéines" and BBF "Biodiversity and Biotechnology of Fungi" (2013-2016; Dr. Marie-Thérèse Giudici-Orticoni and Dr. Jean-Guy Berrin, Marseille-FR). In January 2017 he was appointed researcher at BBF for INRAE, the French Research Institute for Agriculture, Food and Environment, with a focus on both fundamental aspects of enzyme studies and their application, for the development of sustainable and eco-friendly technologies.