Post-doc position in computational physical-chemistry/biophysics
Institut de Biologie Physico Chimique (CNRS), Paris, France

Tags: molecular modeling, enzymatic activity, allostery, ancestral proteins

A post-doc position is available starting from February 2023. The candidate will work in the group of Dr. Fabio Sterpone in Paris, in the Laboratoire de Biochimie Théorique at the Institut de Biologie Physico-Chimique (http://www-lbt.ibpc.fr/); the research will focus on the study of functional motions in the protein family of malate and lactate dehydrogenases by applying computational methodologies. The investigation will support NMR measurements and biochemical essays done by collaborators.

The successful candidate must hold a PhD in Chemistry/Biophysics or related fields with a strong background in physical-chemistry/biophysics/statistical mechanics/bioinformatics. An extensive expertise in computer simulations of biomolecules and analysis of large-scale protein conformational changes is required. Proficiency in programming skills (Python) for post-processing are also highly desirable.

The research aims at individuating the functional modes in key representative members of the malate/lactate dehydrogenase protein family with the ultimate goal to single out the molecular basis at the origin of different functional regulations (allosteric vs non-allosteric enzymes). The study will also be extended to ancestral members of the family individuated via phylogenetic reconstruction. Further details and related publications can be found at: https://sites.google.com/site/sterponefabio/

The contract is offered for 24 months. The position is funded by the ANR (AlloSpace ANR-21-CE44-0034-01). The exact salary will depend on the candidate's experience as evaluated by the French Centre National de la Recherche (CNRS) salary grid.

The Laboratoire de Biochimie Théorique is an internationally recognized laboratory with the mission of developing and applying computational methodologies to solve biological relevant problems. The members are active in the fields of docking, atomistic and coarse-grained simulations tackling problems as protein/protein and protein/DNA interactions, dynamics and function of membrane proteins, protein folding and aggregation.

Interested applicants should send a detailed CV and have three reference letters.

Please follow the offer open call at:

Dr. Sterpone Fabio
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Institut de Biologie et Physico-Chimique, Paris, France

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