ibmb
Institut de Biologia Molecular de Barcelona
CSIC

28th October 2020

Postdoctoral position in Computational Protein Design

A postdoctoral position is available at the recently established Protein Design and Modeling lab from the Molecular Biology Institute of Barcelona (IBMB). The institute is located in the Barcelona Science Park, a major hub for biological research and biotech companies, and affiliated to the Spanish National Research Council (CSIC). Our goal in the lab is to design proteins from first principles and tailored to desired structures, circumventing the engineering limitations of natural proteins. We combine computational protein design with biochemical and structural biology techniques to create new proteins for current challenges in biotechnology and therapeutics.

This position will involve the computational design of de novo ligand-binding protein folds, with a particular interest on developing binding-induced conformational responses. This will lay the basis for custom-designing conformational switches responding to small-molecules in biosensing and synthetic biology applications. The project will be carried out in close collaboration with biochemists performing the experimental characterization of the designed proteins.

We are looking for a highly motivated scientist with initiative and strong interest in protein structure and engineering. The candidate must have prior experience in some areas of protein molecular modeling (molecular dynamics, protein structure prediction, protein design, ligand-binding interactions and/or Rosetta modeling). Sound understanding of protein expression, biochemistry and/or high-resolution structure determination techniques is a plus.

This is a one-year position that could be renewed depending on funding availability. The starting date is flexible, and can be between December 1st (2020) and March 1st (2021).

If you are keen on joining a growing team of protein scientists working on ambitious and multidisciplinary projects please send your CV and/or questions to Enrique Marcos (embcri@ibmb.csic.es) as soon as possible.

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