

**OFERTA PROYECTO PARA AYUDAS PARA CONTRATOS PREDOCTORALES
PARA LA FORMACIÓN DE DOCTORES 2017**
(Enviar a dpe@csic.es)

REFERENCIA PROYECTO
BIO2016-76400-R
INVESTIGADOR PRINCIPAL (IP)
JOSE MARIA CARAZO GARCIA
TÍTULO PROYECTO
FLEX3D: ANALISIS EN ALTO RENDIMIENTO DE LA FLEXIBILIDAD ESTRUCTURAL TANTO POR CRIO MICROSCOPIA ELECTRONICA COMO POR CRIO MICROSCOPIA DE RAYOS X BLANDOS
ÁREA CIENTÍFICA
BIOLOGÍA FUNDAMENTAL Y DE SISTEMAS
CENTRO/INSTITUTO
CENTRO NACIONAL DE BIOTECNOLOGIA
PROVINCIA/COMUNIDAD AUTÓNOMA
MADRID
CORREO ELECTRÓNICO IP
carazo@cnb.csic.es
WEBSITE GRUPO DE INVESTIGACIÓN O CENTRO/INSTITUTO
http://biocomp.cnb.csic.es/

RESUMEN PROYECTO/PROJECT SUMMARY

Europe has taken a lead position in Structural Biology, especially in Electron Microscopy under cryogenic conditions (cryoEM), by enabling platforms that allow experimentalists to have access to high-end equipment and services, such as Instruct (<https://www.structuralbiology.eu>) and iNext (<http://www.inext-eu.org>).

In this regard, the Instruct Image Processing Center in Madrid (<http://i2pc.cnb.csic.es>) is a European and world reference center both for the development of computational infrastructures as well as image processing algorithms. The position offered in this proposal would tackle the heterogeneity/flexibility problem in macromolecular structural elucidation at several levels:

- 1) Determination of several starting volumes, solving in this way the initial volume problem in the case of highly heterogeneous datasets.
- 2) Development of fast 2D classification algorithms capable of dealing with increasingly larger datasets (currently in the order of several hundred thousand images and rapidly growing to the millions of particles, posing a bottleneck in the processing capabilities of cryoEM).
- 2) Development of 3D classification algorithms able to deal with strongly imbalanced classes. Note, that macromolecular mixtures in which one of the populations is much smaller than the rest may go unnoticed and blur the final result.

Collectively, this work will solve one of the major current bottlenecks in biomedical Electron Microscopy, allowing this technique to become a high-resolution, high throughput approach, with the additional capability of being able to analyze the dynamics of the conformational changes taking place in the macromolecule.