Fecha del CVA	30/01/2020

Parte A. DATOS PERSONALES

Nombre y Apellidos	Jose Maria Carazo Garcia		
DNI	25959269C	Edad	61
Núm. identificación del investigador	Researcher ID	E-9234-2016	
	Scopus Author ID	35500936300	
	Código ORCID	0000-0003-0788-8447	

A.1. Situación profesional actual

Organismo	Consejo Superior de Investigaciones Científicas		
Dpto. / Centro	Estructura de Macromoleculas / Centro Nacional de Biotecnología		
Dirección			
Teléfono	639197980	Correo electrónico	carazo@cnb.csic.es
Categoría profesional	Full Professor	Fecha inicio	2005
Espec. cód. UNESCO	120000 - Matemáticas; 240401 - Bioestadística; 240600 - Biofísica; 241500 - Biología molecular		
Palabras clave	Biología estructural; Bioinformática		

A.2. Formación académica (titulo, institución, fecha)

Licenciatura/Grado/Doctorado	Universidad	Año
Doctor en Ciencias Biológicas	Universidad Autónoma de Madrid	1984
Licenciado en Ciencias Físicas	Universidad de Granada	1981

A.3. Indicadores generales de calidad de la producción científica

h- index: 49 (ISIWeb of Science-January 30, 2020)

Publications: 288

Period (2016 - 2018): 37 (16 - Q1, 11- Q2, 8 - Q3, 2 -NA)

Citations: 8260

XMIPP & SCIPION Software download: 3500 times in just the last two years.

3DBionotes more than 1700 unique IP mark in the last year.

Other Experience and Professional Memberships:

2003-2014 Principal Founder of the CNB spin-off Integromics, developing software in Bioinformatics, becoming Perkin-Elmer genomics software offer in 2014

2014- Structural Biology Grid (SBGrid), Member of the Scientific Advisory Board (SAB)

2015–2019 European Synchrotron Radiation Facility, Member of the Science Advisory Committee (SAC)

2015- Australian Centre of Excellence for Advanced Molecular Imaging, Member of the International Scientific Advisory Committee (ISAC)

2016- National Center for Protein Science (CAS), Shanghai, Member of the Top User Program

Parte B. RESUMEN LIBRE DEL CURRÍCULUM

I specialize in the area of Structural Biology, with a very strong additional component of data management and data analysis. In this way, I am part of two key European Research Infrastructures: INSTRUCT (for Structural Biology) and ELIXIR (for BioInformatics), effectively bridging the world of data management and analysis with the one of the elucidation of the three-dimensional structure of Biological Macromolecules, paving the way to drug design. My impact in the field can be estimated quoting my more than 8260 citations (h index 49), according to ISI Web of Science on January 30, 2020, the 3500 different users from all over the world that have downloaded our software suites XMIPP and Scipion in the last two years, the 1700 unique users of a new software 3DBionotes since March 2017 or the 7 International projects I am partner of, including an ERC Synergy grant. Note that due to space restrictions, in the CV only papers from 2016 have been considered (this corresponds to the start date of the current MINECO project, FLEX3D)

I would like to highlight our strategic involvement in the development of the very much used EMDataBank (EMDB) (started from the European Union "Bioimage" project that I coordinated from 1996 to 1999), one of the most unique and undisputed resources for structural information to date. Naturally, structure has to be necessarily complemented by other approaches, a position that explains our continued effort in information integration at all levels, with 3DBionotes, our information integration software, being selected in 2019 as one of very few ELIXIR Recommended Interoperability Resources.

I know very well the area of software development both in the public and the Corporate world, and the Bioinformatics company that was spinned off from my group in 2003, called Integromics, was an example of information integration during the more than a decade long it was active, winning the first National Prize of La Caixa Emprendedor XXI 2007 and the Frost and Sullivan 2008 Prize to the Most Innovative European Bioinformatics Company, before being acquired in 2014 by the US multinational Perkin Elmer.

Parte C. MÉRITOS MÁS RELEVANTES (ordenados por tipología)

C.1. Publicaciones

1 Martínez M; et al. 2020. Integration of Cryo-EM Model Building Software in Scipion.Journal of chemical information and modeling. ISSN 1549-9596.

2 Vilas JL; et al. 2020. Measuring local-directional resolution and local anisotropy in cryo-EM maps.Nature communications. 11, pp.55.

3 Vilas JL; et al. 2020. Re-examining the spectra of macromolecules. Current practice of spectral quasi B-factor flattening.Journal of structural biology. pp.107447. ISSN 1047-8477.

4 Peschiera I; et al. 2020. Structural basis for cooperativity of human monoclonal antibodies to meningococcal factor H-binding protein.Communications biology. 2, pp.241.

5 Segura J; et al. 2019. 3DBIONOTES v3.0: crossing molecular and structural biology data with genomic variations.Bioinformatics (Oxford, England). 35, pp.3512-3513. ISSN 1367-4803.

6 Ramírez-Aportela E; et al. 2019. Automatic local resolution-based sharpening of cryo-EM maps.Bioinformatics (Oxford, England). ISSN 1367-4803.

7 Busselez J; et al. 2019. Cryo-Electron Tomography and Proteomics studies of centrosomes from differentiated quiescent thymocytes.Scientific reports. 9, pp.7187.

8 Ramírez-Aportela E; et al. 2019. DeepRes: a new deep-learning- and aspect-based local resolution method for electron-microscopy maps.IUCrJ. 6, pp.1054-1063.

9 Maluenda D; et al. 2019. Flexible workflows for on-the-fly electron-microscopy single-particle image processing using Scipion.Acta crystallographica. Section D, Structural biology. 75, pp.882-894.

10 Peschiera I; et al. 2019. Structural basis for cooperativity of human monoclonal antibodies to meningococcal factor H-binding protein.Communications biology. 2, pp.241.

11 Sorzano COS; et al. 2019. Survey of the analysis of continuous conformational variability of biological macromolecules by electron microscopy.Acta crystallographica. Section F, Structural biology communications. 75, pp.19-32.

12 Sorzano COS; et al. 2018. A Survey of the Use of Iterative Reconstruction Algorithms in Electron Microscopy.BioMed research international. 2017, pp.6482567. ISSN 2314-6133.

13 Sorzano COS; et al. 2018. A new algorithm for high-resolution reconstruction of single particles by electron microscopy.Journal of structural biology. 204, pp.329-337. ISSN 1047-8477.

14 Vilas JL; et al. 2018. Advances in image processing for single-particle analysis by electron cryomicroscopy and challenges ahead.Current opinion in structural biology. 52, pp.127-145. ISSN 0959-440X.

15 Sanchez-Garcia R; et al. 2018. BIPSPI: a method for the prediction of partner-specific protein-protein interfaces.Bioinformatics (Oxford, England). 35, pp.470-477. ISSN 1367-4803.

16 Sorzano COS; et al. 2018. Blind estimation of DED camera gain in Electron Microscopy.Journal of structural biology. 203, pp.90-93. ISSN 1047-8477.

17 Sanchez-Garcia R; et al. 2018. Deep Consensus, a deep learning-based approach for particle pruning in cryo-electron microscopy.IUCrJ. 5, pp.854-865.

18 Sacristan C; et al. 2018. Dynamic kinetochore size regulation promotes microtubule capture and chromosome biorientation in mitosis.Nature cell biology. 20, pp.800-810. ISSN 1465-7392.

19 Marabini R; et al. 2018. Map challenge: Analysis using a pair comparison method based on Fourier shell correlation.Journal of structural biology. 204, pp.527-542. ISSN 1047-8477.

20 Vilas JL; et al. 2018. MonoRes: Automatic and Accurate Estimation of Local Resolution for Electron Microscopy Maps.Structure (London, England : 1993). 26, pp.337-344.e4. ISSN 0969-2126.

21 Heymann JB; et al. 2018. The first single particle analysis Map Challenge: A summary of the assessments.Journal of structural biology. 204, pp.291-300. ISSN 1047-8477.

22 Gómez-Blanco J; et al. 2018. Using Scipion for stream image processing at Cryo-EM facilities.Journal of structural biology. 204, pp.457-463. ISSN 1047-8477.

23 Jiménez A; et al. 2018. Validation of electron microscopy initial models via small angle X-ray scattering curves.Bioinformatics (Oxford, England). 35, pp.2427-2433. ISSN 1367-4803.

24 Segura J; et al. 2017. 3DBIONOTES v2.0: a web server for the automatic annotation of macromolecular structures.Bioinformatics (Oxford, England). 33, pp.3655-3657. ISSN 1367-4803.

25 Sanchez-Garcia R; et al. 2017. 3DCONS-DB: A Database of Position-Specific Scoring Matrices in Protein Structures.Molecules (Basel, Switzerland). 22.

26 Ljubetič A; et al. 2017. Design of coiled-coil protein-origami cages that self-assemble in vitro and in vivo.Nature biotechnology. 35, pp.1094-1101. ISSN 1087-0156.

27 Alvarez-Cabrera AL; et al. 2017. Electron Microscopy Structural Insights into CPAP Oligomeric Behavior: A Plausible Assembly Process of a Supramolecular Scaffold of the Centrosome.Frontiers in molecular biosciences. 4, pp.17.

28 Martínez M; et al. 2017. Gene signature associated with benign neurofibroma transformation to malignant peripheral nerve sheath tumors.PloS one. 12, pp.e0178316.

29 Albanese P; et al. 2017. Pea PSII-LHCII supercomplexes form pairs by making connections across the stromal gap.Scientific reports. 7, pp.10067.

30 Vargas J; et al. 2017. Quantitative analysis of 3D alignment quality: its impact on soft-validation, particle pruning and homogeneity analysis.Scientific reports. 7, pp.6307.

31 Conesa Mingo P; et al. 2017. Scipion web tools: Easy to use cryo-EM image processing over the web.Protein science : a publication of the Protein Society. 27, pp.269-275. ISSN 0961-8368.

32 Cuenca-Alba J; et al. 2017. ScipionCloud: An integrative and interactive gateway for large scale cryo electron microscopy image processing on commercial and academic clouds.Journal of structural biology. 200, pp.20-27. ISSN 1047-8477.

33 Tabas-Madrid D; et al. 2016. 3DBIONOTES: A unified, enriched and interactive view of macromolecular information.Journal of structural biology. 194, pp.231-4. ISSN 1047-8477.

34 Segura J; et al. 2016. 3DIANA: 3D Domain Interaction Analysis: A Toolbox for Quaternary Structure Modeling.Biophysical journal. 110, pp.766-75. ISSN 0006-3495.

35 Sorzano CO; et al. 2016. A review of resolution measures and related aspects in 3D Electron Microscopy.Progress in biophysics and molecular biology. 124, pp.1-30. ISSN 0079-6107.

36 Koning RI; et al. 2016. Asymmetric cryo-EM reconstruction of phage MS2 reveals genome structure in situ.Nature communications. 7, pp.12524.

37 Jonić S; et al. 2016. Denoising of high-resolution single-particle electron-microscopy density maps by their approximation using three-dimensional Gaussian functions.Journal of structural biology. 194, pp.423-33. ISSN 1047-8477.

38 Conesa JJ; et al. 2016. Intracellular nanoparticles mass quantification by near-edge absorption soft X-ray nanotomography.Scientific reports. 6, pp.22354.

39 Vargas J; et al. 2016. Particle alignment reliability in single particle electron cryomicroscopy: a general approach.Scientific reports. 6, pp.21626.
40 de la Rosa-Trevín JM; et al. 2016. Scipion: A software framework toward integration, reproducibility and validation in 3D electron microscopy.Journal of structural biology. 195, pp.93-9. ISSN 1047-8477.
41 Sanchez Sorzano CO; et al. 2016. StructMap: Elastic Distance Analysis of Electron Microscopy Maps for Studying Conformational Changes.Biophysical journal. 110, pp.1753-1765. ISSN 0006-3495.
42 Marabini R; et al. 2016. The Electron Microscopy eXchange (EMX) initiative.Journal of structural biology. 194, pp.156-63. ISSN 1047-8477.
43 Abrishami V; et al. 2015. A fast iterative convolution weighting approach for gridding-based direct Fourier three-dimensional reconstruction with correction for the contrast transfer function.Ultramicroscopy. 157, pp.79-87. ISSN 0304-3991.
44 Sorzano CO; et al. 2015. A statistical approach to the initial volume problem in Single Particle Analysis by Electron Microscopy.Journal of structural biology. 189, pp.213-9. ISSN 1047-8477.
45 Abrishami V; et al. 2015. Alignment of direct detection device micrographs using a robust Optical Flow approach.Journal of structural biology. 189, pp.163-76. ISSN 1047-8477.
46 Marabini R; et al. 2015. CTF Challenge: Result summary.Journal of structural biology. 190, pp.348-59. ISSN 1047-8477.
47 Sorzano CO; et al. 2015. Cryo-EM and the elucidation of new macromolecular structures: Random Conical Tilt revisited.Scientific reports. 5, pp.14290.
48 Otón J; et al. 2015. Measurement of the modulation transfer function of an X-ray microscope based on multiple Fourier orders analysis of a Siemens star.Optics express. 23, pp.9567-72.
49 Carazo JM; et al. 2015. Three-dimensional reconstruction methods in Single Particle Analysis from transmission electron microscopy data.Archives of biochemistry and biophysics. 581, pp.39-48. ISSN 0003-9861.
50 Segura J; et al. 2015. Using neighborhood cohesiveness to infer interactions between protein domains.Bioinformatics (Oxford, England). 31, pp.2545-52. ISSN 1367-4803.

C.2. Proyectos

1 HighResCells: A synergistic approach toward understanding receptor signaling in the cell at very high resolution European Union - H2020. Jose Maria Carazo Garcia. (Centro Nacional de Biotecnología). 01/03/2019-28/02/2024. 1.726.457 €.
2 TOMOXLIVER: Estudio de la disfunción del hepatocito desde un abordaje multidisciplinar. Comunidad de Madrid. Carazo JM (Coordinador). (Centro Nacional de Biotecnología). 01/01/2018-31/12/2022. 111.205 €.
3 EOSC-Life: Providing an open collaborative space for digital biology in Europe European Union - H2020. 01/03/2019-28/02/2022. 507.940 €.
4 Plataforma de Bioinformática Instituto de Salud Carlos III. Carazo JM. (Centro Nacional de Biotecnología). 01/01/2018-31/12/2020. 150.975 €.
5 731005, Instruct Ultra: Releasing the full potential of Instruct to expand and consolidate infrastructure services for integrated structural life science research UE. Jose Maria Carazo Garcia. (Centro Nacional de Biotecnología). 01/01/2017-31/12/2020. 200.000 €.
6 654248, CORBEL: Coordinated Research Infrastructures Building Enduring Life-science services UE. Jose Maria Carazo Garcia. (Centro Nacional de Biotecnología). 01/09/2015-31/08/2018. 195.679 €.

C.3. Contratos

Collaboration Agreement FEI/ThermoFisher for Single Particle Reconstruction (SPR) FEI/ThermoFisher. Jose Maria Carazo Garcia. 03/10/2017-03/10/2020.

C.4. Patentes