

BIOGRAPHICAL SKETCH

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NAME Carazo, Jose Maria	POSITION TITLE Full Professor		
eRA COMMONS USER NAME josemaricarazo			
EDUCATION/TRAINING <i>(Begin with baccalaureate or other initial professional education, such as nursing, and include postdoctoral training.)</i>			
INSTITUTION AND LOCATION	DEGREE <i>(if applicable)</i>	YEAR(s)	FIELD OF STUDY
University of Granada, Spain	Ms.C	1981	Physics
University Autonoma, Madrid, Spain	Ph.D	1984	Structural Biology

A. Positions and Honors.

Positions and Employment

1981-1984	Pre-doctoral fellow, IBM Research Center, Madrid, Spain
1985-1986	Post-doctoral fellow, Centro de Biología Molecular Severo Ochoa, Madrid, Spain
1987-1988	Research Affiliate II, New York S. Dept. of Health
1989-	Head of the Biocomputing Unit, National Center of Biotechnology, Madrid, Spain
1990-2000	Tenure Scientist National, Center of Biotechnology, Madrid, Spain
2001-2002	Senior Research Scientist, National Center of Biotechnology, Madrid, Spain
1998-2001	Deputy Director for Research, National Center of Biotechnology, Madrid,
2002-2003	Deputy Director for Research Planning and Monitoring, Science and Technology Ministry
1995-2003	Adj. Professor of Computer Science, Autonoma University, Madrid, Spain
2003-2004	Senior Research Scientist National Center of Biotechnology, Madrid, Spain
2005 -	Full Professor, National Center of Biotechnology, Madrid, Spain

Other Experience and Professional Memberships

1997-2001	President of the Spanish Microscopy Society.
2005-	Senior member of the IEEE Computer Society

Honors

1984	PhD Excellence Award by the Spanish Academy of Science.
1986	Okazato Research Award, by JEOL.
1998	Rhone-Poulenc Excellence Award by the French Academy of Science

B. Selected peer-reviewed publications (in chronological order since 2003, from 162 total).

1. N. Jiménez-Lozano, M. Chagoyen, J. Cuenca-Alba and J.M. Carazo. FEMME database: topologic and geometric information of macromolecules. *J Struct Biol.*, 2003: 144:104-113.
2. M.G. Gomez-Lorenzo, M. Valle, J. Frank, C. Gruss, C.O.S. Sorzano, X.S. Chen, L.E. Donate and J.M. Carazo. Large T antigen on the simian virus 40 origin of replication: a 3D snapshot prior to DNA replication. *EMBO J*, 2003: 22:6205-6213. PMID: PMC291853.
3. J.M. Carazo. Accessing information on the conformational flexibility of molecular machines. *Structure*, 2004: 12:170-171.
4. R. Marabini, C.O.S. Sorzano, S. Matej, J.J. Fernández, J.M. Carazo and G.T. Herman. 3D reconstruction of 2D crystals in real space, *IEEE Transactions on Image Processing* 2004: 13:549-561.

5. C.O.S. Sorzano, S. Jonić, C. El-Bez, J.M. Carazo, S. De Carlo, P. Thévenaz and M. Unser. A multiresolution approach to orientation assignment in 3D electron microscopy of single particles. *J Struct Biol*, 2004:146:381-392.
6. C.O.S. Sorzano, R. Marabini, J. Velázquez-Muriel, J.R. Bilbao-Castro, S.H. Scheres, J.M. Carazo and A. Pascual-Montano. XMIPP: a new generation of an open-source image processing package for electron microscopy. *J Struct Biol*, 2004: 148:194-204.
7. J.A. Velázquez-Muriel, C.O.S. Sorzano, S.H. Scheres and J.M. Carazo. SPI-EM: towards a tool for predicting CATH superfamilies in 3D-EM maps. *J Mol Biol*, 2005: 345:759-771.
8. S.H.W. Scheres, M. Valle, R. Nuñez, C.O.S. Sorzano, R. Marabini, G.T. Herman and J.M. Carazo. Maximum-likelihood multi-reference refinement for electron microscopy images, *Journal of Molecular Biology*, 2005: 348:139-149.
9. S.H.W. Scheres, M. Valle and J.M. Carazo. Fast maximum-likelihood refinement of electron microscopy images. *Bioinformatics*, 2005: 21 Suppl 2:ii243-244.
10. Y. Gómez-Llorente, R.J. Fletcher, X.S. Chen, J.M. Carazo and C. San Martín. Polymorphism and double hexamer structure in the archaeal minichromosome maintenance (MCM) helicase from *Methanobacterium thermoautotrophicum*. *J Biol Chem*, 2005: 280:40909-15.
11. R.J. Fletcher, J. Shen, Y. Gómez-Llorente, C.S. Martín, J.M. Carazo and X.S. Chen. Double hexamer disruption and biochemical activities of *Methanobacterium thermoautotrophicum* MCM. *J Biol Chem*, 2005: 280:42405-42410.
12. P. Carmona-Saez, M. Chagoyen, A. Rodriguez, O. Trelles, J.M. Carazo and A. Pascual-Montano. Integrated analysis of gene expression by Association Rules Discovery. *BMC Bioinformatics*, 2006: 7:54. PMID: PMC1386712.
13. A. Pascual-Montano, J.M. Carazo, K. Kochi, D. Lehmann and R.D. Pascual-Marqui. Nonsmooth nonnegative matrix factorization (nsNMF). *IEEE Trans Pattern Anal Mach Intell*, 2006: 28:403-415.
14. M. Valle, X.S. Chen, L.E. Donate, E. Fanning and J.M. Carazo. Structural basis for the cooperative assembly of large T antigen on the origin of replication. *J Mol Biol*, 2006: 357:1295-1305.
15. R. Núñez-Ramírez, Y. Robledo, P. Mesa, S. Ayora, J.C. Alonso, J.M. Carazo and L.E. Donate. Quaternary polymorphism of replicative helicase G40P: structural mapping and domain rearrangement. *J Mol Biol*, 2006: 357:1063-1076.
16. J.A. Velazquez-Muriel, M. Valle, A. Santamaría-Pang, I.A. Kakadiaris and J.M. Carazo. Flexible fitting in 3D-EM guided by the structural variability of protein superfamilies. *Structure*, 2006: 14:1115-1126.
17. A. Pascual-Montano, P. Carmona-Saez, M. Chagoyen, F. Tirado, J.M. Carazo and R.D. Pascual-Marqui. bioNMF: a versatile tool for non-negative matrix factorization in biology. *BMC Bioinformatics*, 2006: 7:366. PMID: PMC1550731.
18. S.H.W. Scheres, H. Gao, M. Valle, G.T. Herman, P.P.B. Eggermont, J. Frank and J.M. Carazo. Disentangling conformational states of macromolecules in 3D-EM through likelihood optimization, *Nature Methods*, 2007: 4:27-29.
19. P. Carmona-Saez, M. Chagoyen, F. Tirado, J.M. Carazo, A. Pascual-Montano. GENECODIS: a web-based tool for finding significant concurrent annotations in gene lists. *Genome Biol*, 2007:8:R3. PMID: PMC1839127.
20. R. Núñez-Ramírez, M. Velten, G. Rivas, P. Polard, J.M. Carazo and L.E. Donate. Loading a ring: structure of the *Bacillus subtilis* DnaB protein, a co-loader of the replicative helicase. *J Mol Biol*, 2007: 367:764-769.
21. X. Agirrezabala, J.A. Velázquez-Muriel, P. Gómez-Puertas, S.H. Scheres, J.M. Carazo and J.L. Carrascosa. Quasi-atomic model of bacteriophage t7 procapsid shell: insights into the structure and evolution of a basic fold. *Structure*, 2007:15:461-472.
22. J.A. Velazquez-Muriel and J.M. Carazo. Flexible fitting in 3D-EM with incomplete data on superfamily variability. *J Struct Biol*, 2007: 158:165-181.
23. J.R. Macía, N. Jiménez-Lozano and J.M. Carazo. Integrating electron microscopy information into existing Distributed Annotation Systems. *J Struct Biol*, 2007: 158:205-213.
24. H. Tidow, R. Melero, E. Mylonas, S.M. Freund, J.G. Grossmann, J.M. Carazo, D.I. Svergun, M. Valle and A.R. Fersht. Quaternary structures of tumor suppressor p53 and a specific p53 DNA complex. *Proc Natl Acad Sci U S A*, 2007: 104:12324-12329. PMID: PMC1941468.
25. S.H. Scheres, R. Núñez-Ramírez, Y. Gómez-Llorente, C. San Martín, P.P. Eggermont and J.M. Carazo. Modeling experimental image formation for likelihood-based classification of electron microscopy data. *Structure*, 2007: 15:1167-1177. PMID: PMC2277044.

26. C.O.S. Sorzano, S. Jonic, R. Núñez-Ramírez, N. Boisset and J.M. Carazo. Fast, robust, and accurate determination of transmission electron microscopy contrast transfer function. *J Struct Biol*, 2007: 160:249-262.
27. S.H. Scheres, R. Núñez-Ramírez, C.O.S. Sorzano, J.M. Carazo and R. Marabini. Image processing for electron microscopy single-particle analysis using XMIPP. *Nat Protoc*, 2008;3:977-990. NIHMSID: NIHMS152971.
28. F. Abascal, P. Carmona-Saez, J.M. Carazo and A. Pascual-Montano. ChIPCodis: mining complex regulatory systems in yeast by concurrent enrichment analysis of chip-on-chip data. *Bioinformatics*, 2008: 24:1208-1209.
29. M. Chagoyen, J.M. Carazo and A. Pascual-Montano. Assessment of protein set coherence using functional annotations. *BMC Bioinformatics*, 2008: 9:444. PMID: PMC2588600.
30. A.S. Brewster, G. Wang, X. Yu, W.B. Greenleaf, J.M. Carazo, M. Tjajadia, M.G. Klein and X.S. Chen. Crystal structure of a near-full-length archaeal MCM: functional insights for an AAA+ hexameric helicase. *Proc Natl Acad Sci U S A*, 2008: 105:20191-20196. PMID: PMC2629282.
31. R. Nogales-Cadenas, F. Abascal, J. Díez-Pérez, J.M. Carazo and A. Pascual-Montano. CentrosomeDB: a human centrosomal proteins database. *Nucleic Acids Res*, 2009: 37(Database issue):D175-D180. PMID: PMC2686521.
32. J.R. Bilbao-Castro, R. Marabini, C.O.S. Sorzano, I. García, J.M. Carazo and J.J. Fernández. Exploiting desktop supercomputing for three-dimensional electron microscopy reconstructions using ART with blobs. *J Struct Biol*, 2009: 165:19-26.
33. J.A. Velázquez-Muriel, M. Rueda, I. Cuesta, A. Pascual-Montano, M. Orozco and J.M. Carazo. Comparison of molecular dynamics and superfamily spaces of protein domain deformation. *BMC Struct Biol*, 2009: 9:6. PMID: PMC2666742.
34. C.O.S. Sorzano, A. Otero, E.M. Olmos and J.M. Carazo. Error analysis in the determination of the electron microscopical contrast transfer function parameters from experimental power Spectra. *BMC Struct Biol*, 2009 :9:18. PMID: PMC2683171.
35. C.O.S. Sorzano, C. Messaoudi, M. Eibauer, J.R. Bilbao-Castro, R. Hegerl, S. Nickell, S. Marco and J.M. Carazo. Marker-free image registration of electron tomography tilt-series. *BMC Bioinformatics*, 2009: 10:124. PMID: PMC2694187.
36. S.H.W. Scheres, M. Valle, P. Grob, E. Nogales and J.M. Carazo. Maximum likelihood refinement of electron microscopy data with normalization errors. *J Struct Biol*, 2009: 166:234-240. PMID: PMC2693001.
37. M. Vazquez, P. Carmona-Saez, R. Nogales-Cadenas, M. Chagoyen, F. Tirado, J.M. Carazo and A. Pascual-Montano. SENT: semantic features in text. *Nucleic Acids Res*. 2009: 37(Web Server issue):W153-W159. PMID: PMC2703940.
38. R. Nogales-Cadenas, P. Carmona-Saez, M. Vazquez, C. Vicente, X. Yang, F. Tirado, J.M. Carazo and A. Pascual-Montano. GeneCodis: interpreting gene lists through enrichment analysis and integration of diverse biological information. *Nucleic Acids Res*, 2009: 37(Web Server issue):W317-W322. PMID: PMC2703901.
39. S.H.W. Scheres and J.M. Carazo. Introducing robustness to maximum-likelihood refinement of electron-microscopy data. *Acta Crystallogr D Biol Crystallogr*, 2009: 65(Pt 7):672-678. PMID:PMC2703573.
40. S. Nickell, F. Beck, S.H.W. Scheres, A. Korinek, F. Förster, K. Lasker, O. Mihalache, N. Sun, I. Nagy, A. Sali, J.M. Plitzko, J.M. Carazo, M. Mann and W. Baumeister. Insights into the molecular architecture of the 26S proteasome. *Proc Natl Acad Sci U S A*. 2009 Jul 21;106(29):11943-7.; PMID: PMC2715492.
41. C.O.S. Sorzano, E. Recarte, M. Alcorlo, J.R. Bilbao-Castro, C. San-Martín, R. Marabini and J.M. Carazo. Automatic particle selection from electron micrographs using machinelearning techniques. *J Struct Biol*, 2009: 167:252-260. NIHMSID: NIHMS152972.
42. N. Jiménez-Lozano, J. Segura, J.R. Macías, J. Vega and J.M. Carazo. aGEM: an integrative system for analyzing spatial-temporal gene-expression information. *Bioinformatics*, 2009: 25:2566-2572. PMID: PMC2752607.

C. Research Support

Ongoing Research Support

CSD2006-00023 Serrano (Coordinator of 9 research groups) 11/01/06 – 11/01/11
 Spanish Ministry of Education and Sciences (MEC)

Centrosome – 3D

Large collaborative project on the structural-functional relationships of the centrosome.

Role: PI

S-GEN-0166-2006 Carazo (Coordinator of six research groups) 01/01/07 – 12/31/11

Community of Madrid

Hacia la proteómica funcional: una aproximación conjunta desde la proteómica, la bioinformática y la biología estructural

Large interdisciplinary project on the centrosome differential and structural proteomics.

Role: PI

BIO2007 - 67150 – Carazo (Coordinator of three research groups) 10/01/07 – 10/01/10

Spanish Ministry of Education and Sciences (MEC)

Análisis de grandes cantidades de imágenes de microscopía electrónica tridimensional: Desarrollo de métodos y aplicación al análisis del replisoma.

A structural biology Project focused in the large scale processing of 3DEM images, and its application to the characterization of the replisome

Role: PI

PIF08-020-2: Carazo (Coordinator of three research groups) 09/01/08 – 08/31/10

Spanish High Research Council (CSIC)

Tomografía de Rayos X: Una herramienta de integración entre biología molecular y celular.

Multidisciplinary project around the Spanish X-ray Tomography synchrotron beam line

Role: PI

UE (CE: FP7-202047) Rolf Ziesche (Coordinator of 12 groups) 04/01/08 – 03/31/13

European Union

Resolve chronic inflammation and achieve healthy ageing by understanding non-regenerative repair.

Our work in this large consortium is on data management and data analysis of proteomics data

Role: PI

2R01 HL070472-05 Herman (PI) 9/1/05-8/31/10

NIH

Image Processing in Biological 3D Electron Microscopy

A multidisciplinary approach is proposed to apply image-processing techniques to problem areas of 3D electron microscopy of complex biological macromolecules.

Role: Co-Investigator

Completed Research Support

UE (FP6-502828) Andreas Engel (Coordinator of a large network) 05/01/04 – 05/07/09

European Union

EU Network of Excellence in “New electron microscopy approaches for studying protein complexes and cellular supramolecular architecture”

Large collaborative project among leading European 3DEM research groups

Role: Co-Investigator