

Dr. Brian Jiménez García

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Personal

Name: Brian Jiménez García

Born: October 5, 1984

Place of birth: Barcelona, Spain

Nationality: Spanish

Contact

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Languages

- Mother tongues: Spanish and Catalan
- Fluent in English
- Basic knowledge: French, Japanese

Education

Universitat de Barcelona (University of Barcelona)

Doctor of Philosophy (PhD), Bioinformatics and Computational Biology, 2011 - 2016 (Cum Laude)

Universitat de Barcelona (University of Barcelona)

MSc, Biomedicine, 2010 - 2011

École polytechnique fédérale de Lausanne (EPFL)

Stage, Biocomputing, 2007 - 2008

Universitat Politècnica de Catalunya (BarcelonaTech)

Engineering, Computer Science, 2002 - 2008

Work experience

Postdoctoral Researcher at Bonvin Lab (Utrecht University)

May 2018 - Present

Postdoctoral researcher at Bonvin Lab (<http://www.bonvinlab.org/>).

Postdoctoral Researcher at Barcelona Supercomputing Center

July 2016 – April 2018

Postdoctoral researcher at the Protein Interactions and Docking group and INB computational bioinformatics node. Development of protein-DNA docking tools for the MuG H2020 project (<http://www.multiscalegenomics.eu>).

Course Instructor at Universitat Oberta de Catalunya (UOC)

October 2015 - Present

Programming for bioinformatics lecturer in the *Bioinformatics and Biostatistics* master's degree (<http://estudis.uoc.edu/ca/masters-universitaris/bioinformatica-bioestadistica/presentacio>).

PhD Candidate at Barcelona Supercomputing Center

June 2010 - July 2016 (6 years 2 months)

PhD student at the Protein Interactions and Docking Group.

Student visitor at National Institute of Biomedical Innovation

May 2013 – August 2013 (4 months)

Collaboration between Mizuguchi Laboratory (National Institute of Biomedical Innovation) and Protein Interactions and Docking Group (Barcelona Supercomputing Center).

Software Engineer at CELLS (Spanish Synchrotron)

September 2008 - June 2010 (1 year 10 months)

Zope/Plone development.

Sysadmin internship at Automatic Control Department BarcelonaTech

May 2005 - August 2006 (1 year 4 months)

GNU/Linux administrator.

Memberships

- Python Software Foundation
- Spanish Society for Biochemistry and Molecular Biology (SEBBM)

Grants and Awards

- 2012 - FPI pre-doctoral grant (4 years, Spanish Ministry of Economy and Competitiveness)
- 2012 - IUBMB-FEBS Sevilla 2012 international congress travel grant
- 2013 – Short Stays for Research Staff – FPI (Spanish Ministry of Economy and Competitiveness)
- 2013 – AlgoSB Winter School travel grant
- 2015 – SEBBM travel grant
- 2016 – First conference of Research Software Engineers speaker travel grant
- 2018 – Seal of excellence awarded to ProtDNADockChallenge "Addressing Protein-DNA Interactions Docking Challenges" proposal and submitted under the Horizon 2020's Marie Skłodowska-Curie actions call H2020-MSCA-IF-2017.

Courses

2011

- NVIDIA Programming and Tuning Massively Parallel 2011 Systems summer school (Barcelona, Spain)
- Stanford-Sweden multiresolution Molecular simulation 2011 workshop (Uppsala, Sweden)
- HPC-PRACE Winter School (Nicosia, Cyprus)

2013

- Algorithms in Structural Biology Winter School (Toulouse, France)

2014

- 13th VI-HPS Tuning Workshop @ BSC (Barcelona, Spain)
- PATC Programming ARM based prototypes (Barcelona, Spain)

2015

- Programming Distributed Computing Platforms with COMPSs (Barcelona, Spain)

Publication list

Google Scholar: <https://scholar.google.es/citations?hl=en&user=eVN1WVYAAAAJ>

ORCID: orcid.org/0000-0001-7786-2109

2017

LightDock: a new multi-scale approach to protein–protein docking

B Jiménez-García, J Roel-Touris et al.

Bioinformatics 34 (1), 49-55

pyDockDNA: a new approach for protein-DNA docking

LA Rodríguez-Lumbreras, B Jiménez-García, J Fernández-Recio

Barcelona Supercomputing Center, Book of abstracts, 49-49

IRaPPA: Information retrieval based integration of biophysical models for protein assembly selection.

IH Moal, D Barradas-Bautista, B Jiménez-García, M Torchala et al.

Bioinformatics 33 (12), 1806-1813

2016

pyDock scoring for the new modeling challenges in docking: Protein–peptide, homo-multimers, and domain–domain interactions

C Pallara, B Jiménez-García, M Romero, IH Moal, J Fernández-Recio

Proteins: Structure, Function, and Bioinformatics

Prediction of homoprotein and heteroprotein complexes by protein docking and template-based modeling: A CASP-CAPRI experiment

MF Lensink, S Velankar, A Kryshtafovych, SY Huang et al.

Proteins: Structure, Function, and Bioinformatics 84 (S1), 323-348

2015

Updates to the integrated protein–protein interaction benchmarks: docking benchmark version 5 and affinity benchmark version 2

T Vreven, IH Moal, A Vangone, BG Pierce, PL Kastiris, M Torchala et al.

Journal of molecular biology 427 (19), 3031-3041

pyDockSAXS: protein–protein complex structure by SAXS and computational docking

B Jiménez-García, C Pons, DI Svergun, P Bernadó, J Fernández-Recio

Nucleic acids research 43 (W1), W356-W361

pyDock performance in 5th CAPRI edition: from docking and scoring to binding affinity predictions and other challenges

C Pallara, B Jiménez-García, M Romero, J Fernández-Recio

BSC Doctoral Symposium (2nd: 2015: Barcelona), 99-100

CCharPPI web server: computational characterization of protein–protein interactions from structure

IH Moal, B Jiménez-García, J Fernández-Recio

Bioinformatics 31 (1), 123-125

2014

Blind prediction of interfacial water positions in CAPRI

MF Lensink, IH Moal, PA Bates, PL Kastritis, ASJ Melquiond, E Karaca et al.

Proteins: Structure, Function, and Bioinformatics 82 (4), 620-632

2013

Expanding the frontiers of protein–protein modeling: from docking and scoring to binding affinity predictions and other challenges

C Pallara, B Jiménez-García, L Pérez-Cano, M Romero-Durana et al.

Proteins: Structure, Function, and Bioinformatics 81 (12), 2192-2200

Community-wide evaluation of methods for predicting the effect of mutations on protein–protein interactions

R Moretti, SJ Fleishman, R Agius, M Torchala, PA Bates, PL Kastritis et al.

Proteins: Structure, Function, and Bioinformatics 81 (11), 1980-1987

pyDockWEB: a web server for rigid-body protein-protein docking using electrostatics and desolvation scoring

B Jiménez-García, C Pons, J Fernández-Recio

Bioinformatics, btt262

2012

Integration of protein-protein docking tools for multi-scale approach to complex structural prediction

B Jimenez-Garcia, J Fernandez-Recio

The Febs Journal 279, 532

A protein-RNA docking benchmark (II): Extended set from experimental and homology modeling data

L Pérez-Cano, B Jiménez-García, J Fernández-Recio

Proteins: Structure, Function, and Bioinformatics 80 (7), 1872-1882

2007

Centipede robot locomotion

B Jimenez, A Ikspeert

Master project, ecole polytechnique federale de Lausanne

Congress contributions

Posters

2016

B Jiménez-García, J Fernández-Recio (2016) High-performance computational tools for the characterization of protein-protein interactions. BIFI2016. Zaragoza (Spain).

B Jiménez-García, J Roel, J Fernández-Recio (2016) LightDock: a novel protein-protein docking framework for the new challenges in the interactomics era. 6th CAPRI evaluation meeting. Tel-Aviv (Israel).

2015

B Jiménez-García, J Fernández-Recio (2015) LightDock: a novel protein-protein docking framework for the new challenges in the interactomics era. SEBBM2015. Valencia (Spain).

2013

B Jiménez-García, C Pallara, D Triki, J Fernández-Recio (2013) PyDock version 3: improvements for high-performance docking and general applicability for non-peptidic molecules. CAPRI 5th. Utrecht (Netherlands).

2012

B Jiménez-García, C Pons, J Fernández-Recio (2012) pyDockWEB: a new web-server for energy-based protein-protein docking. XII Congress SBE. Barcelona (Spain).

B Jiménez-García, J Fernández-Recio (2012) Integration of protein-protein docking tools for multi-scale approach to complex structural prediction. IUBMB-FEBS. Seville (Spain).

Oral communications

2016

B Jiménez-García (2016) LightDock: a novel protein-protein docking framework for the new challenges in the interactomics era. Intelligent Pharma. Barcelona (Spain).

2015

B Jiménez-García (2015) Development and optimization of high-performance computational tools for protein-protein docking. Life Sciences Seminars (BSC). Barcelona (Spain).

B Jiménez-García (2015) LightDock: a novel protein-protein docking framework for the new challenges in the interactomics era. III Bioinformatics and Computational Biology Symposium (BIB). Barcelona (Spain).

2014

B Jiménez-García (2014) Swarm intelligence. Jornada d'Investigadors Predoctorals Interdisciplinària (JIPI). Barcelona (Spain).

B Jiménez-García (2014) Development and optimization of high-performance computational tools for protein-protein docking. BSC Days. Barcelona (Spain).

2013

B Jiménez-García (2013) Computational approaches to protein-protein docking. National Institute of Biomedical Innovation. Osaka (Japan).

Conference organization

- Course instructor of the EMBO practical course on “Integrative modelling of biomolecular interactions”, Barcelona, Spain, July 4-9, 2016.
- Bioinformatics section chairman of the “1st Biomed PhD Day Symposium”, Barcelona, Spain, December 7, 2016.
- Course instructor of the EMBO practical course on “Integrative modelling of biomolecular interactions”, Barcelona, Spain, 2018, TBA.