

Publication list

Google Scholar: scholar.google.com/citations?user=9e1m3-AAAAAJ

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ResearchGate: https://www.researchgate.net/profile/Brian_Jimenez-Garcia

Bold indicates first author or co-author. A star (*) indicates correspondence author.

2020

Structural characterization of protein-protein interactions with pyDockSAXS.

B Jiménez-García, P Bernadó, J Fernández-Recio,

Methods in Molecular Biology - Structural Bioinformatics (in press)

2019

pyDockEneRes: per-residue decomposition of protein-protein docking energy

M Romero-Durana, B Jiménez-García, J Fernández-Recio,

Bioinformatics, btz884, <https://doi.org/10.1093/bioinformatics/btz884>

Integrative modeling of protein-protein interactions with pyDock for the new docking challenges

M Rosell, LA Rodríguez-Lumbreras, M Romero-Durana, B Jiménez-García, L Díaz, J Fernandez-Recio

Proteins: Structure, Function, and Bioinformatics (2019)

Blind prediction of homo-and hetero-protein complexes: The CASP13-CAPRI experiment.

MF Lensink, *et al.* (including B Jiménez-García)

Proteins: Structure, Function, and Bioinformatics (2019)

Aprendiendo a programar. Nuevos retos, nuevas propuestas

B Jiménez-García, C Pérez Solà, P Andrio Balado, MJ Marco Galindo

Actas de las Jenui 4, 71-78 (Spanish)

Modeling Antibody-Antigen Complexes by Information-Driven Docking

F Ambrosetti, B Jiménez-García, J Roel-Touris, AMJJ Bonvin

Structure (2019)

MuGVRE. A virtual research environment for 3D/4D genomics

L Codo *et al.* (including B Jiménez-García)

BioRxiv <https://doi.org/10.1101/602474>

LightDock goes information-driven

J Roel Touris, AMJJ Bonvin, **B Jiménez-García***

Bioinformatics (2019)

PRODIGY-crystal: a web-tool for classification of biological interfaces in protein complexes

B Jiménez-García, K Elez, PI Koukos, AMJJ Bonvin, A Vangone

Bioinformatics (2019)

2018

SKEMPI 2.0: an updated benchmark of changes in protein–protein binding energy, kinetics and thermodynamics upon mutation

J Jankauskaitė, **B Jiménez-García**, J Dapkūnas, J Fernández-Recio, IH Moal

Bioinformatics 35 (3), 462-469

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, et al. (including B Jiménez-García)

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 85 (3), 487-496

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

MF Lensink, et al. (including B Jiménez-García)

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, et al. (including B Jiménez-García)

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 Fernandez-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, et al. (including B Jiménez-García)

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, et al. (including B Jiménez-García)

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

2012

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

B Jimenez-García, 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, *École polytechnique fédérale de Lausanne*

Conference contributions

Posters

2019

B Jiménez-García, J Roel-Touris, AMJJ Bonvin (2019) Information-driven macromolecular docking with LightDock. NWO CHAINS. Veldhoven (The Netherlands).

B Jiménez-García, J Roel-Touris, AMJJ Bonvin (2019) Shedding Light on data-driven docking. SEBBM Conference. Madrid (Spain).

B Jiménez-García, J Roel-Touris, F Ambrosetti, AMJJ Bonvin (2019) Shedding Light on data-driven docking. 7th CAPRI Meeting. Hinxton (United Kingdom).

B Jiménez-García, PI Koukos, ME Trellet, J Schaarschmidt, AMJJ Bonvin (2019) Data-Driven Structural Bioinformatics: The HADDOCK/WeNMR Ecosystem. EOSC-Hub Week. Prague (Czech Republic).

B Jiménez-García, PI Koukos, ME Trellet, J Schaarschmidt, AMJJ Bonvin (2019) Data-Driven Structural Bioinformatics: The HADDOCK/WeNMR Ecosystem. EGI AAI Conference. Amsterdam (The Netherlands).

2018

B Jiménez-García, PI Koukos, ME Trellet, J Schaarschmidt, AMJJ Bonvin (2018) Data-Driven Structural Bioinformatics: The HADDOCK Ecosystem. UBC 5th Symposium. Utrecht (The Netherlands).

B Jiménez-García, PI Koukos, ME Trellet, J Schaarschmidt, AMJJ Bonvin (2018) Data-Driven Structural Bioinformatics: The HADDOCK Ecosystem. NWO CHAINS. Veldhoven (The Netherlands).

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

2019

B Jiménez-García (2019) Structural biology in the cloud powered by the WeNMR thematic services: A success story of 10 years. EOSC-Hub Week. Prague (Czech Republic).

B Jiménez-García (2019) Flash-talk on Shedding Light on data-driven docking. 7th CAPRI Meeting. Hinxton (United Kingdom).

2018

B Jiménez-García (2018) The road to software development in the reproducible scientific research context. Barcelona Supercomputing Center Seminars. Barcelona (Spain).

B Jiménez-García (2018) PyDock practical. EMBO Practical Course on Integrative modelling of biomolecular interactions. Barcelona (Spain).

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, Health and Nutrition. Osaka (Japan).