Javier Sánchez Utgés

utges03@gmail.com | 07878 459945 | ORCID | LinkedIn | GitHub | Google Scholar

Education

PhD **University of Dundee**, Structural Bioinformatics — Sept 2020 – present

- PIPS Internship at ABPI
- Supervised 7 students across BSc, MSc and PhD degrees
- Reviewer of contributions for ISMB 2024: 3DSIG
- Student Representative of Computational Biology Division

MSc **Universitat Pompeu Fabra**, Bioinformatics for Health Sciences — Sept 2018 – July 2020

- Grade: 9.3/10
- Honours: *Introduction to Perl*
- 9-month Internship at the Barton Group, University of Dundee
- MSc Thesis: *"Ankyrin repeats in context with population variation"*

BSc **Universitat Autònoma de Barcelona**, Genetics — Sept 2014 – July 2018

- Grade: 8.4/10
- Honours: *Bioinformatics*, *Molecular Structure & Interactions*
- 12-month Erasmus exchange at University of Dundee
- Dissertation: *"Methods for the detection and estimation of selection acting upon the genome"*

Experience

The Association of the British Pharmaceutical Industry (ABPI), Intern — London, England, Aug 2022 – Nov 2022

- Improved the Interactive Resources for Schools website of the ABPI

IBE-CSIC-UPF, Intern — Barcelona, Spain, July 2017 – Sept 2017

- Internship at the Calafell Lab on Forensic and Population Genetics

Publications

Comparative evaluation of methods for the prediction of protein-ligand binding sites — Nov 2024

Utgés JS, Barton GJ

10.1186/s13321-024-00923-z (Journal of Cheminformatics)

Classification of likely functional class for ligand binding sites identified from fragment screening — Mar 2024

Utgés JS, MacGowan SA, Ives CM, Barton GJ

10.1038/s42003-024-05970-8 (Communications Biology)

Ankyrin repeats in context with human population variation — Aug 2021

Utgés JS, Tsenkov MI, Dietrich NJM, MacGowan SA, Barton GJ

10.1371/journal.pcbi.1009335 (PLOS Computational Biology)

Projects

LIGYSIS-web LIGYSIS-web

- A Python Flask Web Application to explore protein-ligand binding sites
- Tools: Python, JavaScript, HTML, CSS
- Packages: Flask, 3DMol.js, Chart.js

LBS-comparison LBS-comparison

- The largest benchmark of ligand binding site prediction methods.
- Tools: Python, P2Rank, fpocket, IF-SitePred, POVME
- Packages: BioPython, Pandas, Sklearn

FRAGSYS FRAGSYS

- A pipeline for the analysis of fragment screening-derived binding sites
- Tools: Python, Bash, Jalview, OC
- Packages: Matplotlib, Pandas, Seaborn

ANK-analysis ANK-analysis

- The most comprehensive analysis of Ankyrin repeats
- Tools: Python, ClustalO, Chimera, AMPS, gnomAD
- Packages: ProIntVar, ProteoFAV, VarAlign

Conferences

ISCB ISMB 2024 July 2024
Poster: *"LIGYSIS: a resource for the analysis of ligand binding sites"*
Montreal, Canada

3D-BioInfo | ICSB 3D-SIG | ELIXIR Czech Republic Community Meeting in Structural Bioinformatics Nov 2023
Poster: *"LIGYSIS: a resource for the analysis of ligand binding sites"*
Prague, Czech Republic

ISCB ECCB/ISMB 2023 July 2023
Poster: *"Characterising the human protein-ligand interactome"*
Lyon, France

EMBO VizBi 2023 Mar 2023
Poster + flash talk: *"Predicting function in ligand binding sites"*
Heidelberg, Germany

ISCB ECCB 2022 Sept 2022
Poster: *"Fragment screening in context with human population variation"*
Sitges, Spain

European Society for Evolutionary Biology Symposium June 2021
Talk: *"Tandem Repeats: methods and roles in molecular evolution"*
Online

Assets

Languages: Python, Bash, R, JavaScript, HTML, CSS.

Software: Jalview, ChimeraX, PyMol, Clustal, HMMER.

Skills: Protein sequence and structure analysis, machine learning, web development, workflow generation, method benchmarking, version control, scientific writing, supervision, team work.

Languages

Spanish and Catalan: Mother tongue

English: Advanced level, C1 (Grade A, First Certificate in English)

German: Advanced level, B2 (5 years at Official Language School)

French: Basic level

References

PhD Supervisor: Prof Geoff Barton

MSc Secondary Supervisor: Dr Stuart MacGowan

PIPS Supervisor: Dr Andrew Croydon

BSc Dissertation Supervisor: Prof Antonio Barbadilla