

# Dr Javier Sánchez Utgés

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## Education

<b>PhD</b>	<b>University of Dundee</b> , Structural Bioinformatics	Sept 2020 – Mar 2025
	<ul style="list-style-type: none"> <li>Supervised 7 students across BSc, MSc and PhD degrees</li> <li>Student Representative of Computational Biology Division</li> <li>Thesis: <i>"Computational methods for the characterisation and evaluation of protein-ligand binding sites"</i></li> </ul>	
<b>MSc</b>	<b>Universitat Pompeu Fabra</b> , Bioinformatics for Health Sciences	Sept 2018 – July 2020
	<ul style="list-style-type: none"> <li>Grade: 9.3/10</li> <li>9-month Internship at the <a href="#">Barton Group</a>, University of Dundee</li> <li>Thesis: <i>"Ankyrin repeats in context with population variation"</i></li> </ul>	
<b>BSc</b>	<b>Universitat Autònoma de Barcelona</b> , Genetics	Sept 2014 – July 2018
	<ul style="list-style-type: none"> <li>Grade: 8.4/10</li> <li>9-month Erasmus exchange at University of Dundee</li> <li>Dissertation: <i>"Methods for the detection and estimation of selection acting upon the genome"</i></li> </ul>	

## Experience

<b>University of Dundee</b> , Postdoctoral Research assistant	Dundee, Scotland Mar 2025 – June 2025
<b>The Association of the British Pharmaceutical Industry (ABPI)</b> , Intern	London, England Aug 2022 – Nov 2022
<ul style="list-style-type: none"> <li>Improved the Interactive Resources for Schools website of the <a href="#">ABPI</a></li> </ul>	
<b>IBE-CSIC-UPF</b> , Intern	Barcelona, Spain July 2017 – Sept 2017
<ul style="list-style-type: none"> <li>Internship at the <a href="#">Calafell Lab</a> on Forensic and Population Genetics</li> </ul>	

## Publications

<b>LIGYSIS-web: a resource for the analysis of protein-ligand binding sites</b>	May 2025
<b>Utgés JS</b> , MacGowan SA, Barton GJ <a href="https://doi.org/10.1093/nar/gkaf411">10.1093/nar/gkaf411</a> (Nucleic Acids Research)	
<b>Comparative evaluation of methods for the prediction of protein-ligand binding sites</b>	Nov 2024
<b>Utgés JS</b> , Barton GJ <a href="https://doi.org/10.1186/s13321-024-00923-z">10.1186/s13321-024-00923-z</a> (Journal of Cheminformatics)	
<b>Classification of likely functional class for ligand binding sites identified from fragment screening</b>	Mar 2024
<b>Utgés JS</b> , MacGowan SA, Ives CM, Barton GJ <a href="https://doi.org/10.1038/s42003-024-05970-8">10.1038/s42003-024-05970-8</a> (Communications Biology)	
<b>Ankyrin repeats in context with human population variation</b>	Aug 2021
<b>Utgés JS</b> , Tsenkov MI, Dietrich NJM, MacGowan SA, Barton GJ <a href="https://doi.org/10.1371/journal.pcbi.1009335">10.1371/journal.pcbi.1009335</a> (PLOS Computational Biology)	

## Projects

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### 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

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### ELIXIR 3DBioInfo Annual General Meeting | ISCB 3DSIG

Mar 2025

Talk: *"Computational methods for the characterisation and evaluation of protein-ligand binding sites"*

Barcelona, Spain

### ISCB ISMB 2024

July 2024

Poster: *"LIGYSIS: a resource for the analysis of ligand binding sites"*

Montreal, Canada

### 3DBioInfo | ICSB 3DSIG | ELIXIR Czech Republic Community Meeting

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

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**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

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**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

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**PhD Supervisor:** [Prof Geoff Barton](#) 

**MSc Secondary Supervisor:** [Dr Stuart MacGowan](#) 

**PIPS Supervisor:** [Dr Andrew Croydon](#) 

**BSc Dissertation Supervisor:** [Prof Antonio Barbadilla](#) 