SERGIO RUIZ-CARMONA
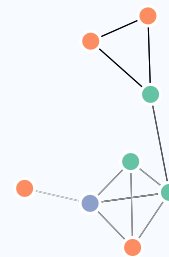
I am currently a Research Officer and Bioinformatician at the Baker Institute, under the supervision of professor Mike Inouye. My research interests are broad and involve mainly the relationship between genetic variants and their effect on protein structures.

I carried out my MSc and PhD in Barcelona in the Barril Lab, where I worked with different structure-based drug design methods with the aim to improve drug design for non-standard targets.

🎓 SELECTED EDUCATION

2017 | 2012

PhD in Biomedicine
Universitat de Barcelona 📍 Barcelona, ES

- Virtual Screening for novel MoA: Apps. and method developments
- Development and application of **structure-based drug discovery** methods
- Awards: **Extraordinary prize** for PhD Thesis and **Ramon Margalef award** for best publication

🏛 SELECTED POSITIONS

Today | 2019

Research Officer and Bioinformatician
Inouye Lab 📍 Melbourne, AU
Cambridge Baker Systems Genomics Initiative
Baker Heart and Diabetes Institute

- As part of the Baker Bioinformatics facility, I give bioinformatics, statistical and data analysis support to the whole Institute, mainly in projects related with cardiovascular diseases and diabetes

2019 | 2015

Associate Professor
Faculty of Pharmacy, Universitat de Barcelona 📍 Barcelona, ES

2017

EMBO Short-Term Fellow
Andreas Bender Lab, Unversity of Cambridge 📍 Cambridge, GB

- I spent 2 months in one of the main Pharmacogenomics groups in the world, where I used **gene-expression profiles** of different biological systems to study BRD4 and drug selectivity

📖 MAIN SCIENTIFIC OUTPUT

2021

Oxygen Pathway Limitations in Patients with Chronic Thromboembolic Pulmonary Hypertension
Circulation

- Erin J Howden *, **Sergio Ruiz-Carmona** *, [...] Andre La Gerche, Marion Delcroix and Guido Claessen
- Result of a Bioinformatics Core collaboration. Shiny app developed

2021

Loss of the long non-coding RNA OIP5-AS1 exacerbates heart failure in a sex-specific manner
iScience

- Aowen Zhuang, A Calkin, [...] **Sergio Ruiz-Carmona**, [...] and Brian G Drew
- Result of a Bioinformatics Core collaboration

2017

Dynamic undocking and the quasi-bound state as tools for drug discovery
Nature Chemistry

- **Sergio Ruiz-Carmona**, P Schmidtke, [...] Rod Hubbard and Xavier Barril
- **Highlighted in its issue cover**

2014

rDock: a fast, versatile and open source program for docking ligands to proteins and nucleic acids
PLoS Computational Biology

- **Sergio Ruiz-Carmona**, Daniel Alvarez-Garcia, [...] Xavier Barril, Rod Hubbard and S David Morley

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