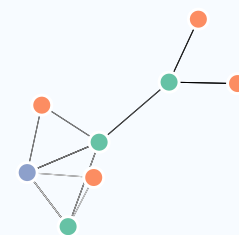


SERGIO RUIZ-CARMONA

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.



View this resume [online](#)

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
Baker Heart and Diabetes Institute
 - I am working in a project that overlaps Structural Biology and Genomics, in collaboration with David Ascher's Lab. Mainly, I am trying to understand how rare missense variants alter protein structures and can induce different diseases

2019
|
2015

 - Associate Professor**
Faculty of Pharmacy, Universitat de Barcelona 📍 Barcelona, ES
 - Classes in Pharmacy, Food Science and Nutrition degrees (total 400h)

2016
|
2011

 - Predoctoral Researcher**
Barril Lab, Universitat de Barcelona 📍 Barcelona, ES
 - Master's and PhD research projects in the Xavier Barril Lab

MAIN SCIENTIFIC OUTPUT

- 2021
- Oxygen Pathway Limitations in Patients with Chronic Thromboembolic Pulmonary Hypertension**
Circulation
Read it [here](#)
 - Erin J Howden *, **Sergio Ruiz-Carmona** *, [...] Andre La Gerche, Marion Delcroix and Guido Claessen

2020

 - Var2Prot: A new tool to unravel the 3D structural effect of genetic variants**
[Lorne Proteins 2020](#) 📍 Lorne, AUS
Oral Communication

2017

 - Dynamic undocking and the quasi-bound state as tools for drug discovery**
Nature Chemistry
Read it [here](#)
 - 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
Read it [here](#)
 - Sergio Ruiz-Carmona**, Daniel Alvarez-Garcia, [...] Xavier Barril, Rod Hubbard and S David Morley

CONTACT

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🐦 [@RuizCSergio](#)
🔗 [sruizcarmona](#)
in [Sergio Ruiz](#)
🌐 [ruizsergio.com](#)

PROGRAMMING

SKILLS



OTHER SKILLS

Highly experienced in:

computational biology
and drug design
bioinformatics and
biostatistics
data visualization
experimental techniques

Recently involved in NGS data
analysis and genomics
prediction

MORE INFO

See full CV at
[ruizsergio.com/cv](#) for a more
complete list of positions,
publications and more



Source code available in [github](#)
Last updated on May 19, 2021