David Moyano Palazuelo

PhD | Computational Biology & Bioinformatics

Passionate about science, technology & solving complex problems with code

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dmoypal

Computational biologist with expertise in essential gene analysis and evolutionary bioinformatics. Author of high-impact publications and creator of innovative web resources for the scientific community. Proven track record in international research collaborations and algorithm development.

publications/

- Rivas-Marin E.*, Moyano-Palazuelo D.*, et al. (2023). Essential gene complement of P. limnophila. Nature Communications 14, 7224
- [2] Henriques V., Moyano-Palazuelo D., et al. (2025). Verrucomicrobium spinosum essential genome and the divergence of cell division in the PVC superphylum. iScience 28(8), 113037

Both authors contributed equally

research experience/_

2025-2026 Postdoctoral Researcher

CABD, Sevilla - UNAM, México

Conducting independent research in computational biology and bacterial genomics. Developing bioinformatics tools and databases for the scientific community.

Jun-Sep 2024 Visiting Researcher - MobLilex Program

Institute Pasteur de Lille, France

International collaboration on bacterial genomics within the European research framework.

2022-2023 Research Fellow - REFRACT Project

UNAM, México

Developed ultrafast tandem repeat detection algorithm for large-scale genomic analysis.

2022-2025 Predoctoral Researcher

CABD, Sevilla

Leading research on PVC gene evolution and essential gene complement analysis.

T awards_and_grants/

- [2024] MobLilex Doctoral Fellowship Institut Pasteur de Lille, France
- [2022-2023] REFRACT Project Fellowship MSCA RISE European Project, UNAM, México
- [2022-2026] Predoctoral Contract Junta de Andalucía Fellowship, CABD, Sevilla
- [2021-2022] CSIC JAE Intro Fellowship Research Training Program, CABD, Sevilla
- [2019] Research Initiation Grant Universidad Pablo de Olavide, CABD, Sevilla

conferences/_

- [2024] VI PVC Meeting Lille, France | Oral: "Orthologous groups in the superphylum PVC"
- [2023] Workshop "Computational Methods for Tandem Repeat Proteins" Montpellier, France | Oral: "T-REx algorithm for tandem repeat detection"
- [2023] ISMB/ECCB 2023 Lyon, France | Poster: "T-REx. A Tandem Repeat Explorer algorithm"
- [2023] 19th ISCB Student Council Symposium Lyon, France
- [2022] REFRACT Hackathon Padova, Italy | Code session
- [2022] V PVC Meeting Bergen, Norway | Oral: "Essential gene complement of P. limnophila"

key_projects/

Current PVC_Database/

biocomputo.ibt.unam.mx:8083

Comprehensive web platform for exploring Planctomycetota-Verrucomicrobiota-Chlamydiota superphylum

data. Stack: Python, JavaScript, Web Dev

2023 TraDIS_P.limnophila/

GitHub: dmoypal/TraDIS_in_P.limnophila

Automated pipeline for processing transposon insertion sequencing data and predicting essential

genes. Languages: Python, R

2024 TraDIS_V.spinosum/

GitHub: dmoypal/TraDIS_in_V.spinosum

Complete analytical workflow for essential gene prediction using TraDis methodology. Languages:

Python, R

education/

2021-2025 PhD in Microbiology & Bioinformatics

Universidad Pablo de Olavide

Thesis: "Analysis of the evolutionary history of PVC genes"

2019-2021 Master's in Biomedical Engineering

Universidad de Sevilla Digital Health specialization

2015-2019 Bachelor's in Biotechnology

Universidad Pablo de Olavide

Graduated with honors

</>> tech_stack/.









Professional (B2+)