David Moyano Palazuelo

PhD | Computational Biology & Bioinformatics

Passionate about science, technology & solving complex problems with code

✉ moyanopalazuelo@gmail.com   in /d-moyano-palazuelo   🌐 dmoypal.github.io
🆔 0000-0002-5400-3659   ⭘ dmoypal   🐦 moyanopalazuelo

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/

[1] 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

⚗ 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.	

🏆 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

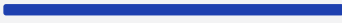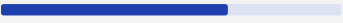• [2022] **V PVC Meeting** — Bergen, Norway | Oral: "Essential gene complement of P. limnophila"

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Current	**PVC_Database/**	
	biocomputo.ibt.unam.mx:8083	
	Comprehensive web platform for exploring Planctomycetota–Verrucomicrobiota–Chlamydiota su- perphylum 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. Lan- guages: 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	

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Programming Languages

🐍 Python — Proficient	JS JavaScript — Intermediate
® R — Advanced	>_ Bash — Advanced

Bioinformatics & Analysis

⚗ Phylogennetics — Proficient	☰ Comparative Genomics — Advanced
⧗ Omics — Proficient	✔ Essential Gene Analysis — Proficient

Development & Infrastructure

git Git/GitHub — Advanced	▤ HPC/SLURM — Advanced
🐳 Docker — Intermediate	🌐 Web APIs — Intermediate

Databases & Resources

NCBI Suite	AlphaFold DB
UniProt	KEGG

🌐 languages

🏳 **Spanish**	🌐 **English**
Native	Professional (B2+)