



Alejandro Matia

Postdoctoral Scholar, Molecular and Cellular Physiology

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BIO

Alejandro Matia conducted his PhD research at the Spanish National Research Council (CSIC), employing multi-omic technologies such as CRISPR genetic screens to detect new host factors in Poxvirus infections. His interest in Bioinformatics led to the creation of MaGplotR, a tool designed for the analysis of multiple genetic screens. Alejandro also has experience in long-read sequencing, and he has sequenced different viral genomes such as Vaccinia virus, Monkeypox virus and SARS-CoV-2. Alejandro was a visiting scientist at the Chan Zuckerberg Biohub (San Francisco) where he conducted single cell transcriptomics experiments with Poxvirus. Currently, Alejandro leverages his omics expertise to unravel the intricate mechanisms of opioid receptor physiology.

BOARDS, ADVISORY COMMITTEES, PROFESSIONAL ORGANIZATIONS

- Member, International Society for Computational Biology (ISCB) (2023 - present)
- Member, European Virus Bioinformatics Center (EVBC) (2023 - present)

PROFESSIONAL EDUCATION

- Doctor of Philosophy, Universidad Autonoma De Madrid (2023)
- Master of Science, Universidad Autonoma De Madrid (2018)
- Bachelor of Science, Universidad Autonoma De Madrid (2017)
- Master of Science, University Pablo De Olavide (2022)
- PhD, Universidad Autónoma de Madrid , Virology
- Masters, Universidad Pablo de Olavide , Bioinformatics
- Masters, Universidad Autonoma de Madrid , Biotechnology

STANFORD ADVISORS

- Ruth Huttenhain, Postdoctoral Faculty Sponsor

Publications

PUBLICATIONS

- **Spatio-temporal analysis of Vaccinia virus infection and host response dynamics using single-cell transcriptomics and proteomics** *bioRxiv*
Matia, A., McCarthy, F., Woosley, H., Turon-Lagot, V., Platzer, S. W., Liu, J., Lorenzo, M. M., Borja, M., Shetty, K., Winkler, J., Elias, J. E., Blasco, R., Arias, et al
2024
- **Identification of #2 microglobulin, the product of B2M gene, as a Host Factor for Vaccinia Virus Infection by Genome-Wide CRISPR genetic screens.** *PLoS pathogens*
Matía, A., Lorenzo, M. M., Romero-Estremera, Y. C., Sánchez-Puig, J. M., Zaballo, A., Blasco, R.

2022; 18 (12): e1010800

- **Tools for the targeted genetic modification of poxvirus genomes.** *Current opinion in virology*

Matía, A., Lorenzo, M. M., Blasco, R.

2020; 44: 183-190

- **Vaccinia Virus Strain MVA Expressing a Prefusion-Stabilized SARS-CoV-2 Spike Glycoprotein Induces Robust Protection and Prevents Brain Infection in Mouse and Hamster Models.** *Vaccines*

Lorenzo, M. M., Marín-López, A., Chiem, K., Jimenez-Cabello, L., Ullah, I., Utrilla-Trigo, S., Calvo-Pinilla, E., Lorenzo, G., Moreno, S., Ye, C., Park, J. G., Matía, A., Brun, et al

2023; 11 (5)

- **MaGplotR: a software for the analysis and visualization of multiple MaGeCK screen datasets through aggregation** *bioRxiv*

Matia, A., Lorenzo, M. M., Peng, D.

2023