

Resource Summary Report

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University of Malaga Andalusian Platform of Bioinformatics Core Facility

RRID:SCR_017169

Type: Tool

Proper Citation

University of Malaga Andalusian Platform of Bioinformatics Core Facility
(RRID:SCR_017169)

Resource Information

URL: <http://www.scbi.uma.es/site/>

Proper Citation: University of Malaga Andalusian Platform of Bioinformatics Core Facility
(RRID:SCR_017169)

Description: Provides assistance in computing, nanotechnology, and biological fields. Provides scientific support and resources to the UMA research groups, public institutions and private companies.

Abbreviations: SCBI, scbi

Synonyms: Universidad de Malaga, scbi, UMA, Plataforma Andaluza de Bioinformatica, University of Malaga, SCBI, Supercomputing and Bioinnovation Center

Resource Type: core facility, data or information resource, access service resource, service resource

Keywords: bioinformatics, computing, nanotechnology, biology, data

Availability: Open

Resource Name: University of Malaga Andalusian Platform of Bioinformatics Core Facility

Resource ID: SCR_017169

Record Creation Time: 20220129T080334+0000

Record Last Update: 20260808T042841+0000

Ratings and Alerts

No rating or validation information has been found for University of Malaga Andalusian Platform of Bioinformatics Core Facility.

No alerts have been found for University of Malaga Andalusian Platform of Bioinformatics Core Facility.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 13 mentions in open access literature.

Listed below are recent publications. The full list is available at [dkNET](#) .

Rautio IV, et al. (2026) Prefrontal cortex encodes behavior states decoupled from motor execution. Cell reports, 45(4), 117138.

Rogério F, et al. (2025) ?Long-distance gene flow and recombination shape the evolutionary history of a maize pathogen. IMA fungus, 16, e138888.

García-Criado F, et al. (2025) Advancing edge-based clustering and graph embedding for biological network analysis: a case study in RASopathies. Briefings in bioinformatics, 26(4).

García-Criado F, et al. (2025) Integrative Transcriptomic and Network-Based Analysis of Neuromuscular Diseases. International journal of molecular sciences, 26(19).

Martorell-Marugán J, et al. (2024) Explainable deep neural networks for predicting sample phenotypes from single-cell transcriptomics. Briefings in bioinformatics, 26(1).

Cordoba-Caballero J, et al. (2024) Exploring miRNA-target gene pair detection in disease with coRmiT. Briefings in bioinformatics, 25(2).

Díaz-Santiago E, et al. (2024) Better understanding the phenotypic effects of drugs through shared targets in genetic disease networks. Frontiers in pharmacology, 15, 1470931.

Becerra S, et al. (2023) Chromosome-level analysis of the Colletotrichum graminicola genome reveals the unique characteristics of core and minichromosomes. Frontiers in microbiology, 14, 1129319.

Rojano E, et al. (2022) Assigning protein function from domain-function associations using DomFun. BMC bioinformatics, 23(1), 43.

Pagano-Márquez R, et al. (2022) Deepening the knowledge of rare diseases dependent on angiogenesis through semantic similarity clustering and network analysis. Briefings in bioinformatics, 23(4).

Nuñez R, et al. (2022) Transcriptional changes in dendritic cells underlying allergen specific induced tolerance in a mouse model. *Scientific reports*, 12(1), 2797.

Jabato FM, et al. (2021) Gene expression analysis method integration and co-expression module detection applied to rare glucide metabolism disorders using ExpHunterSuite. *Scientific reports*, 11(1), 15062.

Guerrero-Sánchez VM, et al. (2021) Changes in the transcript and protein profiles of *Quercus ilex* seedlings in response to drought stress. *Journal of proteomics*, 243, 104263.