

# Resource Summary Report

Generated by [kravitz2](#) on Aug 1, 2026

## University of Malaga Andalusian Platform of Bioinformatics Core Facility

RRID:SCR\_017169

Type: Tool

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### Proper Citation

University of Malaga Andalusian Platform of Bioinformatics Core Facility  
(RRID:SCR\_017169)

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### 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, service resource, access 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:** 20260731T043010+0000

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### 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.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 9 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [kravitz2](#) .

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).

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.

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

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).

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.

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.