

Resource Summary Report

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University of Liege Interdisciplinary Cluster for Applied Genoproteomics Bioinformatics Core Facility

RRID:SCR_017163

Type: Tool

Proper Citation

University of Liege Interdisciplinary Cluster for Applied Genoproteomics Bioinformatics Core Facility (RRID:SCR_017163)

Resource Information

URL: http://www.giga.uliege.be/cms/c_151663/fr/giga-genomcis-lab-manager

Proper Citation: University of Liege Interdisciplinary Cluster for Applied Genoproteomics Bioinformatics Core Facility (RRID:SCR_017163)

Description: Core provided by interdisciplinary center of biomedical research of Liege University. Develops and applies computational methods to extract information from large sets of biological and biomedical data.

Abbreviations: GIGA

Synonyms: , Bioinformatics Facility, Bioinformatics Core Facility, University of Liege, GIGA, Interdisciplinary Cluster for Applied Genoproteomics

Resource Type: core facility, access service resource, service resource

Keywords: bioinformatics, center, biomedical, data, computational, service

Resource Name: University of Liege Interdisciplinary Cluster for Applied Genoproteomics Bioinformatics Core Facility

Resource ID: SCR_017163

Record Creation Time: 20220129T080333+0000

Record Last Update: 20260808T190642+0000

Ratings and Alerts

No rating or validation information has been found for University of Liege Interdisciplinary Cluster for Applied Genoproteomics Bioinformatics Core Facility.

No alerts have been found for University of Liege Interdisciplinary Cluster for Applied Genoproteomics Bioinformatics Core Facility.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 5 mentions in open access literature.

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

Alhindi T, et al. (2026) Genome-Wide Identification and Analysis of the MADS-Box Gene Family in *Tectona grandis* (Teak), a Member of the Lamiaceae Family. *Genes*, 17(2).

Nickles GR, et al. (2026) Tracing the origins of crmA megasynthase through lichen genomes. *Current biology : CB*, 36(13), 3354.

Lin X, et al. (2021) Chromosomal-Level Genome Assembly of Silver Sillago (*Sillago sihama*). *Genome biology and evolution*, 13(2).

Alhindi T, et al. (2021) Genome-Wide Identification and Analysis of the MADS-Box Gene Family in American Beautyberry (*Callicarpa americana*). *Plants (Basel, Switzerland)*, 10(9).

Jiang JJ, et al. (2016) Insights into long noncoding RNAs of naked mole rat (*Heterocephalus glaber*) and their potential association with cancer resistance. *Epigenetics & chromatin*, 9, 51.