

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

MACiE

RRID:SCR_013296

Type: Tool

Proper Citation

MACiE (RRID:SCR_013296)

Resource Information

URL: <http://www.ebi.ac.uk/thornton-srv/databases/MACiE/>

Proper Citation: MACiE (RRID:SCR_013296)

Description: MACiE, which stands for Mechanism, Annotation and Classification in Enzymes, is a collaborative project on enzyme reaction mechanisms. MACiE currently contains 223 fully annotated enzyme reaction mechanisms, which comprise 218 EC numbers (161 EC sub-subclasses) and 310 distinct CATH codes. It is a joint effort between the Mitchell Group at the Unilever Centre for Molecular Informatics part of the University of Cambridge and the Thornton Group at the European Bioinformatics Institute.

Abbreviations: MACiE

Synonyms: The MACiE Database, Annotation and Classification in Enzymes, Mechanism

Resource Type: data or information resource, database

Keywords: bio.tools

Resource Name: MACiE

Resource ID: SCR_013296

Alternate IDs: biotools:macie, nif-0000-03093

Alternate URLs: <https://bio.tools/macie>

Record Creation Time: 20220129T080315+0000

Record Last Update: 20260905T133205+0000

Ratings and Alerts

No rating or validation information has been found for MACiE.

No alerts have been found for MACiE.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 8 mentions in open access literature.

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

Mondragon-Estrada E, et al. (2025) Noncoding variants and sulcal patterns in congenital heart disease: Machine learning to predict functional impact. *iScience*, 28(2), 111707.

Han Y, et al. (2023) Multitrait genome-wide analyses identify new susceptibility loci and candidate drugs to primary sclerosing cholangitis. *Nature communications*, 14(1), 1069.

Miltenberger-Miltenyi G, et al. (2023) Genetic risk variants in New Yorkers of Puerto Rican and Dominican Republic heritage with Parkinson's disease. *NPJ Parkinson's disease*, 9(1), 160.

Ishida O, et al. (2020) The Relationship Between Attentional Capture by Speech and Nonfluent Speech Under Delayed Auditory Feedback: A Pilot Examination of a Dual-Task Using Auditory or Tactile Stimulation. *Frontiers in human neuroscience*, 14, 51.

Furnham N, et al. (2016) Large-Scale Analysis Exploring Evolution of Catalytic Machineries and Mechanisms in Enzyme Superfamilies. *Journal of molecular biology*, 428(2 Pt A), 253.

Holliday GL, et al. (2015) Key challenges for the creation and maintenance of specialist protein resources. *Proteins*, 83(6), 1005.

Beattie KE, et al. (2015) Why do Sequence Signatures Predict Enzyme Mechanism? Homology versus Chemistry. *Evolutionary bioinformatics online*, 11, 267.

Holliday GL, et al. (2011) Characterizing the complexity of enzymes on the basis of their mechanisms and structures with a bio-computational analysis. *The FEBS journal*, 278(20), 3835.