Resource Summary Report

Generated by NIF on Apr 19, 2025

Nomenclature Committee of IUBMB

RRID:SCR_003024
Type: Tool

Proper Citation

Nomenclature Committee of IUBMB (RRID:SCR_003024)

Resource Information

URL: https://iubmb.qmul.ac.uk/

Proper Citation: Nomenclature Committee of IUBMB (RRID:SCR_003024)

Description: Portal for Recommendations on Biochemical and Organic Nomenclature, Symbols and Terminology. NC IUBMB,established by IUPAC-IUBMB Joint Commission, publishes standards on biochemical nomenclature, including enzyme nomenclature, in some cases jointly with the International Union of Pure and Applied Chemistry (IUPAC).

Abbreviations: NC-IUBMB

Synonyms: Nomenclature Committee of the International Union of Biochemistry and Molecular Biology, IUBMB Nomenclature Committee

Resource Type: organization portal, data or information resource, portal

Keywords: Recommendations on Biochemical and Organic Nomenclature, Symbols and Terminology, biochemical nomenclature, IUPAC-IUBMB Joint Commission,

Funding:

Availability: Free, Freely available

Resource Name: Nomenclature Committee of IUBMB

Resource ID: SCR_003024

Alternate IDs: nif-0000-03054

Alternate URLs: https://iubmb.org/about/committees/biochemical-nomenclature-committees/

Old URLs: http://www.chem.qmul.ac.uk/iubmb/

Record Creation Time: 20220129T080216+0000

Record Last Update: 20250419T054909+0000

Ratings and Alerts

No rating or validation information has been found for Nomenclature Committee of IUBMB.

No alerts have been found for Nomenclature Committee of IUBMB.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 14 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Chen L, et al. (2024) PredictEFC: a fast and efficient multi-label classifier for predicting enzyme family classes. BMC bioinformatics, 25(1), 50.

Maia LB, et al. (2018) Putting xanthine oxidoreductase and aldehyde oxidase on the NO metabolism map: Nitrite reduction by molybdoenzymes. Redox biology, 19, 274.

Tronconi MA, et al. (2018) Chimeric Structure of Plant Malic Enzyme Family: Different Evolutionary Scenarios for NAD- and NADP-Dependent Isoforms. Frontiers in plant science, 9, 565.

Chang YC, et al. (2015) Differences between Cryptococcus neoformans and Cryptococcus gattii in the Molecular Mechanisms Governing Utilization of D-Amino Acids as the Sole Nitrogen Source. PloS one, 10(7), e0131865.

Rose PW, et al. (2013) The RCSB Protein Data Bank: new resources for research and education. Nucleic acids research, 41(Database issue), D475.

Alexander SP, et al. (2013) The Concise Guide to PHARMACOLOGY 2013/14: enzymes. British journal of pharmacology, 170(8), 1797.

Yagi T, et al. (2013) Studies on hydrogenase. Proceedings of the Japan Academy. Series B, Physical and biological sciences, 89(1), 16.

Stobbe MD, et al. (2013) Consensus and conflict cards for metabolic pathway databases. BMC systems biology, 7, 50.

Howe GT, et al. (2013) A SNP resource for Douglas-fir: de novo transcriptome assembly and SNP detection and validation. BMC genomics, 14, 137.

Szaw?owska U, et al. (2012) TsPAP1 encodes a novel plant prolyl aminopeptidase whose expression is induced in response to suboptimal growth conditions. Biochemical and biophysical research communications, 419(1), 104.

Madupu R, et al. (2012) CharProtDB: a database of experimentally characterized protein annotations. Nucleic acids research, 40(Database issue), D237.

Murphy C, et al. (2011) Curation of characterized glycoside hydrolases of fungal origin. Database : the journal of biological databases and curation, 2011, bar020.

Bjursell MK, et al. (2011) Adenosine kinase deficiency disrupts the methionine cycle and causes hypermethioninemia, encephalopathy, and abnormal liver function. American journal of human genetics, 89(4), 507.

Galperin MY, et al. (2005) The Molecular Biology Database Collection: 2005 update. Nucleic acids research, 33(Database issue), D5.