

Resource Summary Report

Generated by [RRID](#) on Sep 19, 2026

AMBER

RRID:SCR_016151

Type: Tool

Proper Citation

AMBER (RRID:SCR_016151)

Resource Information

URL: <https://github.com/CAMI-challenge/AMBER>

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Description: Software toolkit for the comparative assessment of genome reconstructions from metagenome benchmark datasets. It provides performance metrics, results rankings, and comparative visualizations for assessing multiple programs or parameter effects.

Abbreviations: AMBER

Synonyms: AMBER: Assessment of Metagenome BinnERs

Resource Type: data analysis software, data processing software, data visualization software, software application, software resource, software toolkit

Defining Citation: [DOI:10.1101/239582](https://doi.org/10.1101/239582)

Keywords: binning, metagenomics, benchmarking, biobox, evaluation, comparison, reconstruction, metric,

Availability: Free, Available for download

Resource Name: AMBER

Resource ID: SCR_016151

License: Apache 2.0

Record Creation Time: 20220129T080329+0000

Record Last Update: 20260912T195836+0000

Ratings and Alerts

No rating or validation information has been found for AMBER.

No alerts have been found for AMBER.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2205 mentions in open access literature.

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

?apc? AOB, et al. (2026) krepp: a k-mer-based maximum pseudo-likelihood method for estimating read distances and genome-wide phylogenetic placement. *Genome biology*, 27(1).

Klemm N, et al. (2025) The Prolonged Half-Life of the p53 Missense Variant R248Q Promotes Accumulation and Heterotetramer Formation with Wild-Type p53 to Exert the Dominant-Negative Effect. *Cancer research*, 85(11), 1978.

Mancini L, et al. (2025) A New Biphenol-bis(polyazacyclophane) Receptor with Unusual Photophysical Properties Towards Zn²⁺. *ChemPlusChem*, 90(1), e202400342.

Zhao W, et al. (2025) De novo design of protein condensation inhibitors by targeting an allosteric site of cGAS. *Nature communications*, 16(1), 5140.

Dehabadi MH, et al. (2025) Predicting Reduction Potentials of Blue Copper Proteins Using Quantum Mechanical Calculations. *Inorganic chemistry*, 64(8), 3917.

Majeed S, et al. (2025) Identification of candidate nsSNPs of the human FNDC5 gene and their structural and functional consequences using in silico analysis. *Scientific reports*, 15(1), 7681.

Fernandes AI, et al. (2025) Genetically Diverse Mycobacterium tuberculosis Isolates Manipulate Inflammasome and Interleukin 1 β Secretion Independently of Macrophage Metabolic Rewiring. *The Journal of infectious diseases*, 231(4), e671.

Zhu Y, et al. (2025) C7-Substituted Quinolines as Potent Inhibitors of AdeG Efflux Pumps in *Acinetobacter baumannii*. *ACS infectious diseases*, 11(3), 626.

Cooper GW, et al. (2025) SMARCB1 missense mutants disrupt SWI/SNF complex stability and remodeling activity. *Research square*.

Kakoulidis P, et al. (2025) Comparative structural insights and functional analysis for the distinct unbound states of Human AGO proteins. *Scientific reports*, 15(1), 9432.

Lewis R, et al. (2025) A bespoke rapid evidence review process engaging stakeholders for supporting evolving and time-sensitive policy and clinical decision-making: reflection and

lessons learned from the Wales COVID-19 Evidence Centre 2021-2023. Health research policy and systems, 23(1), 36.

Kliuchnikov E, et al. (2025) Improving the potency prediction for chemically modified siRNAs through insights from molecular modeling of individual sequence positions. Molecular therapy. Nucleic acids, 36(1), 102415.

Barrera EE, et al. (2025) Deciphering opening mechanisms of 14-3-3 proteins. Protein science : a publication of the Protein Society, 34(4), e70108.

Paloncýová M, et al. (2025) Computational Methods for Modeling Lipid-Mediated Active Pharmaceutical Ingredient Delivery. Molecular pharmaceutics, 22(3), 1110.

Soonthonsrima T, et al. (2025) A Promising Resveratrol Analogue Suppresses CSCs in Non-Small-Cell Lung Cancer via Inhibition of the ErbB2 Signaling Pathway. Chemical research in toxicology, 38(3), 415.

Gao YY, et al. (2025) High-Throughput Fluorescence Screening Enables Globally Consistent Identification of ABA Signaling Modulators. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 12(22), e2417212.

Bezpalaya E, et al. (2025) Conformational Dynamics of Mitochondrial Inorganic Pyrophosphatase hPPA2 and Its Changes Caused by Pathogenic Mutations. Life (Basel, Switzerland), 15(1).

Teskey G, et al. (2025) Lipid droplet targeting of the lipase coactivator ABHD5 and the fatty liver disease-causing variant PNPLA3 I148M is required to promote liver steatosis. The Journal of biological chemistry, 301(2), 108186.

Zhao Y, et al. (2025) Structural basis for human NKCC1 inhibition by loop diuretic drugs. The EMBO journal, 44(5), 1540.

Emanuelson C, et al. (2025) Rational Design of Stapled Covalent Peptide Modifiers of Oncoprotein E6 from Human Papillomavirus. ACS chemical biology, 20(3), 746.