

Resource Summary Report

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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 processing software, software toolkit, data analysis software, data visualization software, software resource, software application

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: 20260731T042954+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 2204 mentions in open access literature.

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

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.

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

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.

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

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.

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

Xie W, et al. (2025) Accelerating discovery of bioactive ligands with pharmacophore-informed generative models. *Nature communications*, 16(1), 2391.

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.

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.
- Paloncýová M, et al. (2025) Computational Methods for Modeling Lipid-Mediated Active Pharmaceutical Ingredient Delivery. *Molecular pharmaceutics*, 22(3), 1110.
- Bezpalaya E, et al. (2025) Conformational Dynamics of Mitochondrial Inorganic Pyrophosphatase hPPA2 and Its Changes Caused by Pathogenic Mutations. *Life (Basel, Switzerland)*, 15(1).
- Cooper GW, et al. (2025) SMARCB1 missense mutants disrupt SWI/SNF complex stability and remodeling activity. *Research square*.
- 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.
- Zhu Y, et al. (2025) C7-Substituted Quinolines as Potent Inhibitors of AdeG Efflux Pumps in *Acinetobacter baumannii*. *ACS infectious diseases*, 11(3), 626.
- 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.
- 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.
- Mancini L, et al. (2025) A New Biphenol-bis(polyazacyclophane) Receptor with Unusual Photophysical Properties Towards Zn²⁺. *ChemPlusChem*, 90(1), e202400342.
- Al Khzem AH, et al. (2025) Integrative computational approaches identify haptoglobin inhibitors to modulate erythrocyte sedimentation rate in trauma-linked inflammatory and haematological malignancies. *Frontiers in chemistry*, 13, 1611972.