

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 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 [NIF](#) .

?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.

Tan H, et al. (2025) Identification of naturally occurring drug-resistant mutations of SARS-CoV-2 papain-like protease. *Nature communications*, 16(1), 4548.

Li Z, et al. (2025) Perfluorinated compounds exposure and atherogenic risk characteristics in a high-fat diet condition: In vitro/in vivo models and population panel study. *PNAS nexus*, 4(5), pgaf153.

Baweja L, et al. (2025) Mechanistic basis for the opposing effects of H2A and H2B ubiquitination on nucleosome stability and dynamics. *bioRxiv : the preprint server for biology*.

Dutta A, et al. (2025) Coordinated subdomain movements of MlaC regulate ligand binding and transport. *Computational and structural biotechnology journal*, 27, 2074.

Ullah S, et al. (2025) In Silico Designed Multi-Epitope Vaccine Based on the Conserved Fragments in Viral Proteins for Broad-Spectrum Protection Against Porcine Reproductive and Respiratory Syndrome Virus. *Veterinary sciences*, 12(6).

Ayyildiz M, et al. (2025) Evaluation of Physics-Based Protein Design Methods for Predicting Single Residue Effects on Peptide Binding Specificities. *Journal of computational chemistry*, 46(17), e70160.

Nenadovi? M, et al. (2025) Efficient Degradation of Consumer-Grade PLA by Commercial Savinase: Optimized Conditions and Molecular Dynamics Insights. *ACS sustainable chemistry & engineering*, 13(24), 9269.

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

Ma X, et al. (2025) Improvement of Catalytic Activity and Thermostability of Alginate Lyase VxAlly7B-CM via Rational Computational Design Strategies. *Marine drugs*, 23(5).

Bejcek LP, et al. (2025) Deconstruction of Desacetamidocolchicine's B Ring Reveals a Class 3 Atropisomeric AC Ring with Tubulin Binding Properties. *The Journal of organic chemistry*, 90(22), 7246.

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.

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.

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.

Yang W, et al. (2025) Insights into anti-tuberculosis drug design on the scaffold of nitroimidazole derivatives using structure-based computer-aided approaches. *RSC advances*, 15(28), 22745.

Wińska P, et al. (2025) Pro-Apoptotic Activity of 1-(4,5,6,7-Tetrabromo-1H-benzimidazol-1-yl)propan-2-one, an Intracellular Inhibitor of PIM-1 Kinase in Acute Lymphoblastic Leukemia and Breast Cancer Cells. *International journal of molecular sciences*, 26(12).

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

Ma J, et al. (2025) Qimai Feiluoping Decoction Inhibits EndMT to Alleviate Pulmonary Fibrosis by Reducing PI3K/AKT/mTOR Pathway-Mediated the Restoration of Autophagy. *Journal of inflammation research*, 18, 8447.