Resource Summary Report

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Assisted Model Building with Energy Refinement (AMBER)

RRID:SCR_014230
Type: Tool

Proper Citation

Assisted Model Building with Energy Refinement (AMBER) (RRID:SCR_014230)

Resource Information

URL: http://ambermd.org/

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Description: Software package of molecular simulation programs. It is distributed into AmberTools15 and Amber14. AmberTools15 is a software package which can carry out complete molecular dynamics simulations with either explicit water or generalized Born solvent models. It is distributed in source code format and must be compiled in order to be used. Amber14 builds on AmberTools15 by adding the pmemd program, which provides better performance on multiple CPUs and dramatic speed improvements on GPUs compared to sander (molecular dynamics). GPU info, manuals, and tutorials are available on the website.

Abbreviations: AMBER

Synonyms: Assisted Model Building with Energy Refinement

Resource Type: software application, simulation software, standalone software, software resource

Keywords: molecular simulation, simulation software, software package, molecular dynamics, pmemed, sander, bio.tools

Availability: Acknowledgement requested

Resource Name: Assisted Model Building with Energy Refinement (AMBER)

Resource ID: SCR_014230

Alternate IDs: biotools:amber

Alternate URLs: https://bio.tools/amber

License: Licenses vary depending on the type of user purchasing the AMBER license

Record Creation Time: 20220129T080319+0000

Record Last Update: 20260729T044346+0000

Ratings and Alerts

No rating or validation information has been found for Assisted Model Building with Energy Refinement (AMBER).

No alerts have been found for Assisted Model Building with Energy Refinement (AMBER).

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 4032 mentions in open access literature.

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

Huang J, et al. (2026) Cryo-EM structures of antibodies elicited by germline-targeting HIV MPER epitope scaffolds. Cell reports, 45(1), 116818.

Yang M, et al. (2026) Dihydroalterperylenol from endophytic fungus Alternaria semiverrucosa and its antitumour activity uncovered by transcriptome analysis, molecular docking and molecular dynamics simulations. Molecular medicine reports, 33(1).

Li Z, et al. (2025) Phased high-quality genome of the gymnosperm Himalayan Yew assists in paclitaxel pathway exploration. GigaScience, 14.

Bangaru S, et al. (2025) Structural serology of polyclonal antibody responses to mRNA-1273 and NVX-CoV2373 COVID-19 vaccines. Cell reports, 44(7), 115986.

Tao E, et al. (2025) Drugs exhibit diverse binding modes and access routes in the Nav1.5 cardiac sodium channel pore. The Journal of general physiology, 157(2).

Jaumotte JD, et al. (2025) Physiologic and structural characterization of desisobutyryl-ciclesonide, a selective glucocorticoid receptor modulator in newborn rats. PNAS nexus, 4(1), pgae573.

Liang Q, et al. (2025) Rational design yields RNA-binding zinc finger domains with altered sequence specificity. RNA (New York, N.Y.), 31(2), 150.

Saadabadi A, et al. (2025) Insights into Molecular Interactions and Biological Effect of Natural Stilbenoids at the TRPA1 Ion Channel. ChemMedChem, 20(3), e202400501.

Alqahtani SM, et al. (2025) Discovering broad-spectrum inhibitors for SARS-CoV-2 variants: a cheminformatics and biophysical approach targeting the main protease. Frontiers in pharmacology, 16, 1459581.

Benslama O, et al. (2025) Silymarin as a Therapeutic Agent for Hepatocellular Carcinoma: A Multi-Approach Computational Study. Metabolites, 15(1).

Bourgeois B, et al. (2025) The disordered p53 transactivation domain is the target of FOXO4 and the senolytic compound FOXO4-DRI. Nature communications, 16(1), 5672.

Ned?lníková A, et al. (2025) Atomistic Insights Into Interaction of Doxorubicin With DNA: From Duplex to Nucleosome. Journal of computational chemistry, 46(3), e70035.

Basmenj ER, et al. (2025) Computational epitope-based vaccine design with bioinformatics approach; a review. Heliyon, 11(1), e41714.

Nguyen A, et al. (2025) Structural and functional characterization of integrin ?5-targeting antibodies for anti-angiogenic therapy. bioRxiv : the preprint server for biology.

Cheng Z, et al. (2025) Vitamin A family suppresses periodontitis by restoring mitochondrial metabolic reprogramming in macrophages through JAK-STAT pathway. Frontiers in genetics, 16, 1505933.

Zhao G, et al. (2025) Nucleus-translocated glucokinase functions as a protein kinase to phosphorylate TAZ and promote tumour growth. Nature communications, 16(1), 7156.

Jendrusch MA, et al. (2025) AlphaDesign: a de novo protein design framework based on AlphaFold. Molecular systems biology, 21(9), 1166.

Gil-Salvador M, et al. (2025) Postzygotic mosaicism in SMC1A and the first reported case of a female with Cornelia de Lange syndrome. Scientific reports, 15(1), 20772.

Fujii W, et al. (2025) Gene-environment interaction modifies the association between hyperinsulinemia and serum urate levels through SLC22A12. The Journal of clinical investigation, 135(10).

Adeleke MA, et al. (2025) Computational Development of Transmission-Blocking Vaccine Candidates Based on Fused Antigens of Pre- and Post-fertilization Gametocytes Against Plasmodium falciparum. Bioinformatics and biology insights, 19, 11779322241306215.