

Resource Summary Report

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Buccaneer

RRID:SCR_014221

Type: Tool

Proper Citation

Buccaneer (RRID:SCR_014221)

Resource Information

URL: <http://www.ccp4.ac.uk/html/cbuccaneer.html>

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Description: Software which performs statistical chain tracing by identifying connected alpha-carbon positions using a likelihood-based density target. The target distributions are generated by a simulation calculation using a known reference structure for which calculated phases are available. The success of the method is dependent on the features of the reference structure matching those of the unsolved work structure. For almost all cases, a single reference structure can be used, with modifications automatically applied to the reference structure to match its features to the work structure.

Synonyms: buccaneer - Statistical protein chain tracing

Resource Type: data analysis software, data processing software, sequence analysis software, software application, software resource

Defining Citation: [PMID:16929101](#)

Keywords: statistical chain tracing, alpha carbon position, sequence analysis software, bio.tools

Resource Name: Buccaneer

Resource ID: SCR_014221

Alternate IDs: biotools:buccaneer

Alternate URLs: <https://bio.tools/buccaneer>

Record Creation Time: 20220129T080319+0000

Record Last Update: 20260821T194014+0000

Ratings and Alerts

No rating or validation information has been found for Buccaneer.

No alerts have been found for Buccaneer.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 335 mentions in open access literature.

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

Vasireddy PCR, et al. (2026) Direct from the seed: an atomic resolution protein structure by ab initio MicroED. *Nature communications*, 17(1).

Krull J, et al. (2026) Sulfated mannan of diatoms selects host-specific microbiota in the sunlit ocean. *Microbiome*, 14(1).

Bista S, et al. (2026) Targeting of interaction between BB0323-BB0238 informs new paradigms in Lyme disease therapeutics. *PLoS pathogens*, 22(1), e1013805.

Chubb JJ, et al. (2025) De Novo Design of Parallel and Antiparallel A3B3 Heterohexameric α -Helical Barrels. *Biochemistry*, 64(9), 1973.

Zhang N, et al. (2025) Structural basis of SIRT2 pre-catalysis NAD⁺ binding dynamics and mechanism. *RSC chemical biology*, 6(11), 1749.

Xu X, et al. (2025) Dimerization of the BAR domain-containing protein FAM92A modulates lipid binding and interaction with CBY1. *The Journal of biological chemistry*, 301(7), 110346.

Huang LY, et al. (2025) NAL1 forms a molecular cage to regulate FZP phase separation. *Proceedings of the National Academy of Sciences of the United States of America*, 122(15), e2419961122.

Agbavor C, et al. (2025) Structural analysis of extracellular ATP-independent chaperones of streptococcal species and protein substrate interactions. *mSphere*, 10(2), e0107824.

Hestehave S, et al. (2025) Quinoline-Based Neuropilin² Antagonists Exhibit a Pure Antagonist Profile and Block Vascular Endothelial Growth Factor-Induced Pain. *ACS pharmacology & translational science*, 8(11), 3844.

Vasireddy PCR, et al. (2025) Direct from the Seed: An Atomic-Resolution Protein Structure by Ab Initio MicroED. *bioRxiv* : the preprint server for biology.

Brannigan JA, et al. (2025) Structure and activity of the essential UCH family deubiquitinase DUB16 from *Leishmania donovani*. *The Biochemical journal*, 482(14), 969.

Pramono H, et al. (2025) Crystal structure of a novel heterooligomeric aminotransferase from *Serratia* sp. ATCC 39006 provides insights into function. *FEBS letters*, 599(1), 74.

Brangulis K, et al. (2025) CspZ variant-specific interaction with factor H incorporates a metal site to support *Lyme borreliæ* complement evasion. *The Journal of biological chemistry*, 301(1), 108083.

Vickers CJ, et al. (2025) The complete κ -carrageenan depolymerization cascade from a marine *Pseudoalteromonad* revealed by structural analysis of the enzymes. *The Journal of biological chemistry*, 301(10), 110719.

Beckwith SL, et al. (2025) Probing the molecular determinants of Ty1 retrotransposon restriction specificity in yeast. *PLoS genetics*, 21(10), e1011898.

Monteiro R, et al. (2025) Molecular properties of the RmlT wall teichoic acid rhamnosyltransferase that modulates virulence in *Listeria monocytogenes*. *Nature communications*, 16(1), 24.

Mahana Y, et al. (2024) Structural evidence for protein-protein interaction between the non-canonical methyl-CpG-binding domain of SETDB proteins and C11orf46. *Structure* (London, England : 1993), 32(3), 304.

Fernandez-Ciruelos B, et al. (2024) Repurposing Hsp90 inhibitors as antimicrobials targeting two-component systems identifies compounds leading to loss of bacterial membrane integrity. *Microbiology spectrum*, 12(8), e0014624.

Ludzia P, et al. (2024) NMR study of the structure and dynamics of the BRCT domain from the kinetochore protein KKT4. *Biomolecular NMR assignments*, 18(1), 15.

Beck IN, et al. (2024) Toxin release by conditional remodelling of ParDE1 from *Mycobacterium tuberculosis* leads to gyrase inhibition. *Nucleic acids research*, 52(4), 1909.