

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, software application, software resource, sequence analysis software, data processing software

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: 20260801T190459+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 332 mentions in open access literature.

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

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.

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

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

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.

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.

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.

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

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

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.

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

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

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.

Öster L, et al. (2024) The structures of salt-inducible kinase 3 in complex with inhibitors reveal determinants for binding and selectivity. *The Journal of biological chemistry*, 300(5), 107201.

Sharma R, et al. (2024) Structural and biochemical analysis of highly similar HLA-B allotypes differentially associated with type 1 diabetes. *The Journal of biological chemistry*, 300(9), 107702.

Went SC, et al. (2024) Structure and rational engineering of the PglX methyltransferase and specificity factor for BREX phage defence. *Nature communications*, 15(1), 7236.

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.