Resource Summary Report

Generated by RRID on Apr 28, 2025

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

Defining Citation: PMID:16929101

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

Funding:

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: 20250428T053810+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 322 mentions in open access literature.

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

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 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.

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.

Ballmer D, et al. (2024) Kinetoplastid kinetochore proteins KKT14-KKT15 are divergent

Bub1/BubR1-Bub3 proteins. Open biology, 14(6), 240025.

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.

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.

Vasina DV, et al. (2024) Development of novel antimicrobials with engineered endolysin LysECD7-SMAP to combat Gram-negative bacterial infections. Journal of biomedical science, 31(1), 75.

Ariza A, et al. (2024) Evolutionary and molecular basis of ADP-ribosylation reversal by zinc-dependent macrodomains. The Journal of biological chemistry, 300(10), 107770.

Verschueren KHG, et al. (2024) The Structure of the LysR-type Transcriptional Regulator, CysB, Bound to the Inducer, N-acetylserine. European biophysics journal : EBJ, 53(5-6), 311.

Bulvas O, et al. (2024) Deciphering the allosteric regulation of mycobacterial inosine-5'-monophosphate dehydrogenase. Nature communications, 15(1), 6673.

Brangulis K, et al. (2024) Mechanistic insights into structure-based design of a Lyme disease subunit vaccine. bioRxiv : the preprint server for biology.

Li M, et al. (2024) Structural basis for C. elegans pairing center DNA binding specificity by the ZIM/HIM-8 family proteins. Nature communications, 15(1), 10355.

Thompson CMA, et al. (2023) Structural insights into the mechanism of adaptive ribosomal modification by Pseudomonas RimK. Proteins, 91(3), 300.

Wang S, et al. (2023) Structural insights into the recognition of telomeric variant repeat TTGGGG by broad-complex, tramtrack and bric-à-brac - zinc finger protein ZBTB10. The Journal of biological chemistry, 299(3), 102918.

Foor SD, et al. (2023) A unique borrelial protein facilitates microbial immune evasion. mBio, 14(5), e0213523.