Resource Summary Report

Generated by RRID on Apr 11, 2025

CTFFIND

RRID:SCR_016732
Type: Tool

Proper Citation

CTFFIND (RRID:SCR_016732)

Resource Information

URL: http://grigoriefflab.janelia.org/ctffind4

Proper Citation: CTFFIND (RRID:SCR_016732)

Description: Software tool for finding CTFs of electron micrographs. Program used for the estimation of objective lens defocus parameters from transmission electron micrographs. The program CTFFIND3 is an updated version of the program CTFFIND2. For micrographs collected on photographic film and scanned in use CTFFIND 3. For images from CCDs or direct detectors use CTFFIND 4.

Abbreviations: CTFFIND

Synonyms: CTFFinding, CTFFIND4, CTFFIND2, Contrast Transfer Function Finding, Contrast Transfer FunctionFinding, CTFFIND 3

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

Defining Citation: PMID:26278980

Funding: MRC

Resource Name: CTFFIND

Resource ID: SCR_016732

License: Janelia Research Campus Software Copyright 1.1.

Record Creation Time: 20220129T080332+0000

Record Last Update: 20250411T055920+0000

Ratings and Alerts

No rating or validation information has been found for CTFFIND.

No alerts have been found for CTFFIND.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 103 mentions in open access literature.

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

Dederer V, et al. (2024) A designed ankyrin-repeat protein that targets Parkinson's disease-associated LRRK2. The Journal of biological chemistry, 300(7), 107469.

Hernandez CM, et al. (2024) Development and Characterization of 50 nanometer diameter Genetically Encoded Multimeric Nanoparticles. bioRxiv : the preprint server for biology.

Frank HM, et al. (2024) Structural basis of ligand specificity and channel activation in an insect gustatory receptor. Cell reports, 43(4), 114035.

Cai SW, et al. (2024) POT1 recruits and regulates CST-Pol?/primase at human telomeres. Cell, 187(14), 3638.

Doran MH, et al. (2023) Myosin loop-4 is critical for optimal tropomyosin repositioning on actin during muscle activation and relaxation. The Journal of general physiology, 155(2).

Doran MH, et al. (2023) Conformational changes linked to ADP release from human cardiac myosin bound to actin-tropomyosin. The Journal of general physiology, 155(3).

Mauxion F, et al. (2023) The human CNOT1-CNOT10-CNOT11 complex forms a structural platform for protein-protein interactions. Cell reports, 42(1), 111902.

Agip AA, et al. (2023) Cryo-EM structures of mitochondrial respiratory complex I from Drosophila melanogaster. eLife, 12.

Trastoy B, et al. (2023) Mechanism of antibody-specific deglycosylation and immune evasion by Streptococcal IgG-specific endoglycosidases. Nature communications, 14(1), 1705.

De Gieter S, et al. (2023) Sterol derivative binding to the orthosteric site causes

conformational changes in an invertebrate Cys-loop receptor. eLife, 12.

Simonis A, et al. (2023) Discovery of highly neutralizing human antibodies targeting Pseudomonas aeruginosa. Cell, 186(23), 5098.

Jiang X, et al. (2023) The two-step cargo recognition mechanism of heterotrimeric kinesin. EMBO reports, 24(11), e56864.

Cui N, et al. (2023) Type IV-A CRISPR-Csf complex: Assembly, dsDNA targeting, and CasDinG recruitment. Molecular cell, 83(14), 2493.

Huang P, et al. (2022) Structural basis for catalyzed assembly of the Sonic hedgehog-Patched1 signaling complex. Developmental cell, 57(5), 670.

Fiedorczuk K, et al. (2022) Mechanism of CFTR correction by type I folding correctors. Cell, 185(1), 158.

Chen H, et al. (2022) Structures of oxysterol sensor EBI2/GPR183, a key regulator of the immune response. Structure (London, England : 1993), 30(7), 1016.

Zhang JT, et al. (2022) Structure and assembly pattern of a freshwater short-tailed cyanophage Pam1. Structure (London, England : 1993), 30(2), 240.

Juette MF, et al. (2022) Didemnin B and ternatin-4 differentially inhibit conformational changes in eEF1A required for aminoacyl-tRNA accommodation into mammalian ribosomes. eLife, 11.

Simões V, et al. (2022) Redox-sensitive E2 Rad6 controls cellular response to oxidative stress via K63-linked ubiquitination of ribosomes. Cell reports, 39(8), 110860.

Vahokoski J, et al. (2022) High-resolution structures of malaria parasite actomyosin and actin filaments. PLoS pathogens, 18(4), e1010408.