

Resource Summary Report

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GCTF

RRID:SCR_016500

Type: Tool

Proper Citation

GCTF (RRID:SCR_016500)

Resource Information

URL: <https://www.mrc-lmb.cam.ac.uk/kzhang/Gctf/>

Proper Citation: GCTF (RRID:SCR_016500)

Description: Software tool as a Graphics Processing Units (GPU) accelerated computer program for real-time contrast transfer function (CTF) determination and correction. Used for a near-atomic resolution cryo electron microscopy (cryoEM) reconstruction to maximize the cross-correlation of a simulated CTF with the logarithmic amplitude spectra (LAS) of observed micrographs after background subtraction., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: GCTF

Synonyms: GContrast Transfer Function

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

Defining Citation: [PMID:26592709](#)

Keywords: accurate, real, time, constrast, transfer, function, determination, correction, atomic, resolution, cryo, electron, microscopy, reconstruction, micrograph

Funding: the Medical Research Council ;
United Kingdom MC_UP_A025_1011;
Wellcome Trust New Investigator Award

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: GCTF

Resource ID: SCR_016500

Record Creation Time: 20220129T080331+0000

Ratings and Alerts

No rating or validation information has been found for GCTF.

No alerts have been found for GCTF.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 101 mentions in open access literature.

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

Pinto CS, et al. (2026) Actin arginylation alters myosin engagement and F-actin patterning despite structural conservation. *The Journal of cell biology*, 225(1).

Afonso AC, et al. (2026) Ultrastructure Analysis by Cryo-Electron Tomography Revealed Mesosomes in the Gram-negative Delftia Acidovorans. *Microbial ecology*, 89(1), 48.

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Dam KA, et al. (2025) Mapping essential somatic hypermutations in a CD4-binding site bNAb informs HIV-1 vaccine design. *Cell reports*, 44(5), 115713.

Segura-Covarrubias G, et al. (2025) Structural basis of GluK2 kainate receptor activation by a partial agonist. *Nature structural & molecular biology*, 32(8), 1456.

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

Shen J, et al. (2023) Mechanism of Ca²⁺ transport by ferroportin. *eLife*, 12.

Subramanian A, et al. (2023) A Legionella toxin exhibits tRNA mimicry and glycosyl transferase activity to target the translation machinery and trigger a ribotoxic stress response. *Nature cell biology*, 25(11), 1600.

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

Louro JA, et al. (2023) Nucleosome dyad determines the H1 C-terminus collapse on distinct DNA arms. *Structure (London, England : 1993)*, 31(2), 201.

Yu X, et al. (2023) The evolution and determinants of neutralization of potent head-binding antibodies against Ebola virus. *Cell reports*, 42(11), 113366.

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Zhang M, et al. (2022) Structural basis for the catalytic activity of filamentous human serine beta-lactamase-like protein LACTB. *Structure* (London, England : 1993), 30(5), 685.

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Cheung CS, et al. (2022) Structure of an influenza group 2-neutralizing antibody targeting the hemagglutinin stem supersite. *Structure* (London, England : 1993), 30(7), 993.

Wang L, et al. (2022) Conserved structural elements specialize ATAD1 as a membrane protein extraction machine. *eLife*, 11.

Noviello CM, et al. (2022) Structural mechanisms of GABAA receptor autoimmune encephalitis. *Cell*, 185(14), 2469.

Cai S, et al. (2022) In situ architecture of the lipid transport protein VPS13C at ER-lysosome membrane contacts. *Proceedings of the National Academy of Sciences of the United States of America*, 119(29), e2203769119.

Puno MR, et al. (2022) Structural basis for RNA surveillance by the human nuclear exosome targeting (NEXT) complex. *Cell*, 185(12), 2132.

Rong Y, et al. (2021) TMEM120A contains a specific coenzyme A-binding site and might not mediate poking- or stretch-induced channel activities in cells. *eLife*, 10.