

# Resource Summary Report

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## GCTF

RRID:SCR\_016500

Type: Tool

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### Proper Citation

GCTF (RRID:SCR\_016500)

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### Resource Information

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

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**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:** data analysis software, data processing software, software application, software resource

**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.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 101 mentions in open access literature.

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

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.

Xue J, et al. (2025) Structural mechanisms of PIP2 activation and SEA0400 inhibition in human cardiac sodium-calcium exchanger NCX1. *eLife*, 14.

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 Ca<sup>2+</sup> 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.

Shen J, et al. (2022) Extracellular domain of PepT1 interacts with TM1 to facilitate substrate transport. *Structure* (London, England : 1993), 30(7), 1035.

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.

Zhang K, et al. (2022) A step-by-step protocol for capturing conformational snapshots of ligand gated ion channels by single-particle cryo-EM. *STAR protocols*, 3(4), 101732.

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.