

# Resource Summary Report

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## 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, data processing software, software application, 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:** 20260912T195844+0000

### Ratings and Alerts

No rating or validation information has been found for CTFFIND.

No alerts have been found for CTFFIND.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 114 mentions in open access literature.

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

Perry TN, et al. (2026) Structural basis of Cas8-independent Cas3 recruitment in Type I-F2 CRISPR-Cas. *Nucleic acids research*, 54(5).

Yan L, et al. (2026) The Erlin1/2 complex is a dynamic scaffold for membrane microdomain assembly on the endoplasmic reticulum. *Molecular cell*, 86(7), 1362.

Lupton CJ, et al. (2026) Structure of the lysosomal KICSTOR-GATOR1-SAMTOR nutrient-sensing supercomplex. *Cell*.

Do TT, et al. (2026) A correlative workflow for synaptic imaging by cryo-electron tomography. *Structure (London, England : 1993)*, 34(5), 839.

Yang K, et al. (2026) Double-ring assembly of mpox virus I3L reveals an unconventional mechanism for ssDNA engagement. *Cell reports*, 45(7), 117659.

Xiao W, et al. (2026) Metabolite-gated vascular contractility switch: OXGR1 activation mechanism enables agonist therapy for rosacea erythema. *Cell*, 189(7), 1990.

Hu S, et al. (2025) Structural and functional analysis of the Nipah virus polymerase complex. *Cell*, 188(3), 688.

Bergheim BG, et al. (2025) Molecular dynamics of the matrisome across sea anemone life history. *eLife*, 14.

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

Xiao X, et al. (2025) Structural insights into the biotechnologically relevant reversible NADPH-oxidizing NiFe-hydrogenase from *P.furiosus*. *Structure (London, England : 1993)*, 33(9), 1470.

Yu Z, et al. (2025) Mechanisms of HSV-1 helicase-primase inhibition and replication fork complex assembly. *Cell*.

Smith AM, et al. (2025) The HIV-1 nuclear export complex reveals the role of RNA in CRM1 cargo recognition. *Molecular cell*, 85(16), 3108.

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*.

Sokratian A, et al. (2024) Mouse  $\alpha$ -synuclein fibrils are structurally and functionally distinct from human fibrils associated with Lewy body diseases. *Science advances*, 10(44), eadq3539.

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 $\gamma$ /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.