# Resource Summary Report

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# DoG picker

RRID:SCR_016655
Type: Tool

## Proper Citation

DoG picker (RRID:SCR_016655)

## Resource Information

**URL:** https://omictools.com/dog-picker-tool

**Proper Citation:** DoG picker (RRID:SCR_016655)

**Description:** THIS RESOURCE IS NO LONGER IN SERVICE. Documented on July 18,2023. Software tool for general particle picking in the single-particle processing of unknown macromolecules. Reference free particle picker with ability to sort particles based on size or it can be used to bootstrap the creation of templates or training datasets for other particle pickers. Used to facilitate particle selection in single particle electron microscopy.

**Abbreviations:** DoG picker

**Synonyms:** Difference of Gaussians (DoG) picker, Difference of Gaussians Picker, Difference of Gaussians picker

**Resource Type:** data processing software, software application, software resource, image processing software

**Defining Citation:** PMID:19374019

**Keywords:** general, single, particle, picking, macromolecule, size, selection, electron, microscopy, image, transform

**Funding:** NCRR RR23093;
NCRR RR17573

**Availability:** THIS RESOURCE IS NO LONGER IN SERVICE

**Resource Name:** DoG picker

**Resource ID:** SCR_016655

**Alternate URLs:** http://emg.nysbc.org/redmine/projects/appion/wiki/Appion_Home

**Record Creation Time:** 20220129T080331+0000

**Record Last Update:** 20250331T061455+0000

## Ratings and Alerts

No rating or validation information has been found for DoG picker.

No alerts have been found for DoG picker.

## Data and Source Information

**Source:** SciCrunch Registry

## Usage and Citation Metrics

We found 21 mentions in open access literature.

**Listed below are recent publications.** The full list is available at FDI Lab - SciCrunch.org.

Zhang P, et al. (2024) Design of soluble HIV-1 envelope trimers free of covalent gp120-gp41 bonds with prevalent native-like conformation. Cell reports, 43(8), 114518.

Mostofian B, et al. (2022) Continuum dynamics and statistical correction of compositional heterogeneity in multivalent IDP oligomers resolved by single-particle EM. Journal of molecular biology, 434(9), 167520.

Clausen TM, et al. (2020) SARS-CoV-2 Infection Depends on Cellular Heparan Sulfate and ACE2. Cell, 183(4), 1043.

Zhou T, et al. (2020) Structure-Based Design with Tag-Based Purification and In-Process Biotinylation Enable Streamlined Development of SARS-CoV-2 Spike Molecular Probes. Cell reports, 33(4), 108322.

Hashimoto H, et al. (2020) Structural Basis of Protein Arginine Methyltransferase Activation by a Catalytically Dead Homolog (Prozyme). Journal of molecular biology, 432(2), 410.

Ringe RP, et al. (2020) Neutralizing Antibody Induction by HIV-1 Envelope Glycoprotein SOSIP Trimers on Iron Oxide Nanoparticles May Be Impaired by Mannose Binding Lectin. Journal of virology, 94(6).

Gorman J, et al. (2020) Structure of Super-Potent Antibody CAP256-VRC26.25 in Complex with HIV-1 Envelope Reveals a Combined Mode of Trimer-Apex Recognition. Cell reports, 31(1), 107488.

Yoder N, et al. (2020) The His-Gly motif of acid-sensing ion channels resides in a reentrant 'loop' implicated in gating and ion selectivity. eLife, 9.

Bepler T, et al. (2019) Positive-unlabeled convolutional neural networks for particle picking in cryo-electron micrographs. Nature methods, 16(11), 1153.

Wang N, et al. (2019) Structural Definition of a Neutralization-Sensitive Epitope on the MERS-CoV S1-NTD. Cell reports, 28(13), 3395.

Turner HL, et al. (2019) Potent anti-influenza H7 human monoclonal antibody induces separation of hemagglutinin receptor-binding head domains. PLoS biology, 17(2), e3000139.

Dubrovskaya V, et al. (2019) Vaccination with Glycan-Modified HIV NFL Envelope Trimer-Liposomes Elicits Broadly Neutralizing Antibodies to Multiple Sites of Vulnerability. Immunity, 51(5), 915.

Yuan M, et al. (2019) Conformational Plasticity in the HIV-1 Fusion Peptide Facilitates Recognition by Broadly Neutralizing Antibodies. Cell host & microbe, 25(6), 873.

Zhu X, et al. (2019) Structural Basis of Protection against H7N9 Influenza Virus by Human Anti-N9 Neuraminidase Antibodies. Cell host & microbe, 26(6), 729.

He L, et al. (2018) HIV-1 vaccine design through minimizing envelope metastability. Science advances, 4(11), eaau6769.

Noreng S, et al. (2018) Structure of the human epithelial sodium channel by cryo-electron microscopy. eLife, 7.

Dingens AS, et al. (2018) Complete functional mapping of infection- and vaccine-elicited antibodies against the fusion peptide of HIV. PLoS pathogens, 14(7), e1007159.

Borst AJ, et al. (2018) Germline VRC01 antibody recognition of a modified clade C HIV-1 envelope trimer and a glycosylated HIV-1 gp120 core. eLife, 7.

Koday MT, et al. (2016) A Computationally Designed Hemagglutinin Stem-Binding Protein Provides In Vivo Protection from Influenza Independent of a Host Immune Response. PLoS pathogens, 12(2), e1005409.

Fusco ML, et al. (2015) Protective mAbs and Cross-Reactive mAbs Raised by Immunization with Engineered Marburg Virus GPs. PLoS pathogens, 11(6), e1005016.