

# Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

## DINO

RRID:SCR\_013497

Type: Tool

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### Proper Citation

DINO (RRID:SCR\_013497)

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### Resource Information

**URL:** <http://www.dino3d.org/>

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**Description:** DINO is a realtime 3D visualization program for structural biology data. It runs under X-Windows and uses OpenGL. Supported architectures are Linux-i586 and Mac OSX. Versions for IRIX, OSF1 and SunOS are made available sporadically, usually upon request. DINO is distributed in binary form only, the current DINO version is 0.9.1. Structural Biology is a multidisciplinary research area, including x-ray crystallography, structural NMR, electron microscopy, atomic-force microscopy and bioinformatics (molecular dynamics, structure predictions, surface calculations etc). The data produced by these different research areas is very diverse: atomic coordinates (models and predictions), electron density maps, surface topographs, trajectories, molecular surfaces, electrostatic potentials, sequence alignments etc... DINO aims to visualize all this structural data in a single program and to allow the user to explore relationships between the data. There are five data-types supported: structure (atomic coordinates and trajectories), surface (molecular surfaces), scalar fields (electron densities and electrostatic potentials), topographs (surface topography scans) and geom (geometric primitives such as lines). The number and size of the data the program can handle is only limited by the amount of RAM present in the system. No artificial limits are set. Supported input file formats are PDB (coordinates), X-PLOR/CNS (coordinates, electron densities and trajectories), CHARMM (coordinates, trajectories and scalar fields), CCP4 (electron densities), UHBD (el, THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

**Synonyms:** DINO

**Resource Type:** d visualization software

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

**Resource Name:** DINO

**Resource ID:** SCR\_013497

**Alternate IDs:** nif-0000-30418

**Record Creation Time:** 20220129T080316+0000

**Record Last Update:** 20260905T132736+0000

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## Ratings and Alerts

No rating or validation information has been found for DINO.

No alerts have been found for DINO.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 164 mentions in open access literature.

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

Luan H, et al. (2025) Breast cancer homologous recombination deficiency prediction from pathological images with a sufficient and representative Transformer. NPJ precision oncology, 9(1), 160.

Bao QZ, et al. (2025) Zero-shot instance segmentation for plant phenotyping in vertical farming with foundation models and VC-NMS. Frontiers in plant science, 16, 1536226.

Liziczai M, et al. (2025) Structural basis for metal ion transport by the human SLC11 proteins DMT1 and NRAMP1. Nature communications, 16(1), 761.

Lee J, et al. (2025) A Study on Systematic Improvement of Transformer Models for Object Pose Estimation. Sensors (Basel, Switzerland), 25(4).

Kalweit G, et al. (2025) Leveraging a foundation model zoo for cell similarity search in oncological microscopy across devices. Frontiers in oncology, 15, 1480384.

Morelli FM, et al. (2025) uniDINO: Assay-independent feature extraction for fluorescence microscopy images. Computational and structural biotechnology journal, 27, 928.

McMahon J, et al. (2025) A novel framework for the automated characterization of Gram-stained blood culture slides using a large-scale vision transformer. Journal of clinical microbiology, 63(3), e0151424.

Zehnder P, et al. (2025) Diagnostic classification in toxicologic pathology using attention-guided weak supervision and whole slide image features: a pilot study in rat livers. Scientific reports, 15(1), 4202.

- Koga R, et al. (2025) Attention induction based on pathologist annotations for improving whole slide pathology image classifier. *Journal of pathology informatics*, 16, 100413.
- Panambur AB, et al. (2025) Attention-guided erasing for enhanced transfer learning in breast abnormality classification. *International journal of computer assisted radiology and surgery*, 20(3), 433.
- Hussien A, et al. (2025) Explainable self-supervised learning for medical image diagnosis based on DINO V2 model and semantic search. *Scientific reports*, 15(1), 32174.
- Han R, et al. (2025) Defect detection in EBSM components through selective box fusion of modern object detection. *Scientific reports*, 15(1), 11899.
- Breen J, et al. (2025) A comprehensive evaluation of histopathology foundation models for ovarian cancer subtype classification. *NPJ precision oncology*, 9(1), 33.
- Banov M, et al. (2025) Securing gait recognition with homomorphic encryption. *Scientific reports*, 15(1), 29528.
- Arya A, et al. (2025) Navigating single-cell RNA-sequencing: protocols, tools, databases, and applications. *Genomics & informatics*, 23(1), 13.
- Campanella G, et al. (2025) A clinical benchmark of public self-supervised pathology foundation models. *Nature communications*, 16(1), 3640.
- Wang Y, et al. (2025) Research on a traffic flow statistical algorithm based on YBOVDT and SAM2. *Scientific reports*, 15(1), 19024.
- Caldarelli P, et al. (2025) AI-based approach to dissect the variability of mouse stem cell-derived embryo models. *Nature communications*, 16(1), 1772.
- Zhai H, et al. (2025) InteBOMB: Integrating generic object tracking and segmentation with pose estimation for animal behavior analysis. *Zoological research*, 46(2), 355.
- Sukalskaia A, et al. (2025) Interactions between TTYH2 and APOE facilitate endosomal lipid transfer. *Nature*, 644(8075), 273.