

Resource Summary Report

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DINO

RRID:SCR_013497

Type: Tool

Proper Citation

DINO (RRID:SCR_013497)

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: 20260903T235207+0000

Ratings and Alerts

No rating or validation information has been found for DINO.

No alerts have been found for DINO.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 164 mentions in open access literature.

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

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.

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.

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.

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

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.

Arya A, et al. (2025) Navigating single-cell RNA-sequencing: protocols, tools, databases, and applications. *Genomics & informatics*, 23(1), 13.

Han R, et al. (2025) Defect detection in EBSM components through selective box fusion of modern object detection. *Scientific reports*, 15(1), 11899.

Banov M, et al. (2025) Securing gait recognition with homomorphic encryption. *Scientific reports*, 15(1), 29528.

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.

Breen J, et al. (2025) A comprehensive evaluation of histopathology foundation models for ovarian cancer subtype classification. *NPJ precision oncology*, 9(1), 33.

Sukalskaia A, et al. (2025) Interactions between TTYH2 and APOE facilitate endosomal lipid transfer. *Nature*, 644(8075), 273.

Matsuura T, et al. (2025) Selective identification of polyploid hepatocellular carcinomas with poor prognosis by artificial intelligence-based pathological image recognition. *Communications medicine*, 5(1), 270.

Zhai H, et al. (2025) InteBOMB: Integrating generic object tracking and segmentation with pose estimation for animal behavior analysis. *Zoological research*, 46(2), 355.

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.