

Resource Summary Report

Generated by [Kravitz](#) on Sep 15, 2026

Django

RRID:SCR_012855

Type: Tool

Proper Citation

Django (RRID:SCR_012855)

Resource Information

URL: <http://www.djangoproject.com/>

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Description: Django is a high-level Python Web framework that encourages rapid development and clean, pragmatic design. Developed four years ago by a fast-moving online-news operation, Django was designed to handle two challenges: the intensive deadlines of a newsroom and the stringent requirements of the experienced Web developers who wrote it. It lets you build high-performing, elegant Web applications quickly. Django focuses on automating as much as possible and adhering to the DRY principle.

Synonyms: Django

Resource Type: software resource

Resource Name: Django

Resource ID: SCR_012855

Alternate IDs: nif-0000-30460

Record Creation Time: 20220129T080312+0000

Record Last Update: 20260912T195754+0000

Ratings and Alerts

No rating or validation information has been found for Django.

No alerts have been found for Django.

Data and Source Information

Usage and Citation Metrics

We found 644 mentions in open access literature.

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

Hwang J, et al. (2026) Development of K-CORE: a web-based platform for integrated clinico-genomic analysis. Life science alliance, 9(8).

Peltonen JI, et al. (2026) Comparison of observed image quality and technical image quality parameters in 3D-FLAIR images. Magma (New York, N.Y.), 39(1), 37.

Hu X, et al. (2026) Spatial2GWAS: a database for linking spatial transcriptomic regions with GWAS traits. Nucleic acids research, 54(D1), D1309.

Yang M, et al. (2026) KnockRBP: an integrated multi-omics database of functional perturbation profiles for RNA-binding proteins. Nucleic acids research, 54(D1), D1174.

Kazakov A, et al. (2026) GenomeDepot: data management system for microbial comparative genomics. Bioinformatics advances, 6(1), vbag027.

Hadarovich A, et al. (2026) PICNIC web server for predicting proteins involved in biomolecular condensates. Bioinformatics (Oxford, England), 42(1).

Bundza P, et al. (2026) MCADS: Simultaneous Detection and Analysis of 18 Chest Radiographic Abnormalities Using Multi-Label Deep Learning. Diagnostics (Basel, Switzerland), 16(4).

Horecka I, et al. (2026) Expanding TheCellMap.org to visualize a genome-scale genetic interaction network for a human cell line. bioRxiv : the preprint server for biology.

Aalaei S, et al. (2026) Design and evaluation of a gamified mobile application for teaching cardiac rhythm interpretation to nursing students: a quasi-experimental pre-post study. BMC medical education, 26(1).

Rawal O, et al. (2026) ClusterChirp: A GPU-accelerated Web Server for Natural Language-Guided Interactive Visualization and Analysis of Large Omics Data. ArXiv.

Niedermaier F, et al. (2026) Navigating the lipid universe with LipidLibrarian: a cross-linked database for lipidomics data integration. Journal of lipid research, 67(7), 101049.

Boulay A, et al. (2026) PhaLP 2.0: extending the community-oriented phage lysis database with a SUBLYME pipeline for metagenomic discovery. Database : the journal of biological databases and curation, 2026.

Kimi J, et al. (2026) Systematic mapping of O-GlcNAc transferase and O-GlcNAcase defines disease-associated variants. The Journal of biological chemistry, 302(6), 113134.

Guo Y, et al. (2026) BRPtools: An AutoML-Powered web platform for multiclass disease prediction from bulk blood RNA-seq data. *Molecular therapy. Nucleic acids*, 37(2), 102956.

Zhang Y, et al. (2026) TEITbase: a database for transposable element (TE)-initiated transcripts in human cancers. *Database : the journal of biological databases and curation*, 2026.

Zhu S, et al. (2026) MetabFlow: a comprehensive metabolic map for exogenous natural products. *Nucleic acids research*, 54(D1), D607.

Jalili A, et al. (2026) A comprehensive web-based platform for calculation of abiotic stress tolerance indices in plant breeding. *Scientific reports*, 16(1).

Yang Q, et al. (2026) A centralized database for the genus *Monascus*: biology, metabolites, and metabolic regulation strategies. *Fungal biology and biotechnology*, 13(1).

Sipos-Szabó L, et al. (2026) Benchmarking pKa Prediction Algorithms against an Extensive, Public Data Set. *Journal of chemical information and modeling*, 66(8), 4607.

Kang W, et al. (2026) Introducing iCatalog as a clinical decision support tool for collaborative pediatric precision oncology studies. *Communications medicine*, 6(1), 88.