Resource Summary Report

Generated by NIF on May 29, 2025

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eXtasy

RRID:SCR_008671
Type: Tool

Proper Citation

eXtasy (RRID:SCR_008671)

Resource Information

URL: http://homes.esat.kuleuven.be/~bioiuser/eXtasy/

Proper Citation: eXtasy (RRID:SCR_008671)

Description: A pipeline for ranking nonsynonymous single nucleotide variants given a specific phenotype.

Abbreviations: eXtasy

Resource Type: software resource

Funding:

Resource Name: eXtasy

Resource ID: SCR_008671

Alternate IDs: OMICS_00150

Record Creation Time: 20220129T080248+0000

Record Last Update: 20250525T031050+0000

Ratings and Alerts

No rating or validation information has been found for eXtasy.

No alerts have been found for eXtasy.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 4 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Wahid M, et al. (2022) Integrated Mechanisms of Polarity-Based Extracts of Cucumis melo L. Seed Kernels for Airway Smooth Muscle Relaxation via Key Signaling Pathways Based on WGCNA, In Vivo, and In Vitro Analyses. Pharmaceuticals (Basel, Switzerland), 15(12).

Boudellioua I, et al. (2017) Semantic prioritization of novel causative genomic variants. PLoS computational biology, 13(4), e1005500.

James RA, et al. (2016) A visual and curatorial approach to clinical variant prioritization and disease gene discovery in genome-wide diagnostics. Genome medicine, 8(1), 13.

Wang C, et al. (2015) Adverse Drug Events-based Tumor Stratification for Ovarian Cancer Patients Receiving Platinum Therapy. AMIA Joint Summits on Translational Science proceedings. AMIA Joint Summits on Translational Science, 2015, 51.