## **Resource Summary Report**

Generated by dkNET on Apr 30, 2025

# **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:** 20250420T014433+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 dkNET.

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.