Resource Summary Report

Generated by RRID on May 8, 2025

SNPdryad

RRID:SCR_006414
Type: Tool

Proper Citation

SNPdryad (RRID:SCR_006414)

Resource Information

URL: http://snps.ccbr.utoronto.ca:8080/SNPdryad/

Proper Citation: SNPdryad (RRID:SCR_006414)

Description: Service to predict deleterious non-synonymous human Single Nucleotide Polymorphisms (SNPs) using only orthologous protein sequences.

Abbreviations: SNPdryad

Synonyms: SNPdryad - Deleterious Non-Synonymous SNP Predictions for Human

Resource Type: service resource

Defining Citation: PMID:24389653

Keywords: non-synonymous, single nucleotide polymorphism, ortholog, protein sequence

Funding:

Resource Name: SNPdryad

Resource ID: SCR_006414

Alternate IDs: OMICS_02198

Record Creation Time: 20220129T080236+0000

Record Last Update: 20250420T014326+0000

Ratings and Alerts

No rating or validation information has been found for SNPdryad.

No alerts have been found for SNPdryad.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 3 mentions in open access literature.

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

Castellana S, et al. (2021) MitImpact 3: modeling the residue interaction network of the Respiratory Chain subunits. Nucleic acids research, 49(D1), D1282.

Donato L, et al. (2020) Possible A2E Mutagenic Effects on RPE Mitochondrial DNA from Innovative RNA-Seq Bioinformatics Pipeline. Antioxidants (Basel, Switzerland), 9(11).

Wong KC, et al. (2016) A Novel Approach to Predict Core Residues on Cancer-Related DNA-Binding Domains. Cancer informatics, 15(Suppl 2), 1.