

# Resource Summary Report

Generated by [NIF](#) on Aug 30, 2026

## SNPdryad

RRID:SCR\_006414

Type: Tool

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### Proper Citation

SNPdryad (RRID:SCR\_006414)

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### 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

**Resource Name:** SNPdryad

**Resource ID:** SCR\_006414

**Alternate IDs:** OMICS\_02198

**Record Creation Time:** 20220129T080236+0000

**Record Last Update:** 20260829T182236+0000

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### Ratings and Alerts

No rating or validation information has been found for SNPdryad.

No alerts have been found for SNPdryad.

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### Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 3 mentions in open access literature.

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

Castellana S, et al. (2021) Mitlmpact 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.