

Resource Summary Report

Generated by [FDI Lab - SciCrunch.org](https://fdi-lab.sci-crunch.org) on Apr 11, 2025

SNPdbe

RRID:SCR_005190

Type: Tool

Proper Citation

SNPdbe (RRID:SCR_005190)

Resource Information

URL: <https://www.rostlab.org/services/snpdbe/>

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Description: A database to fill the annotation gap left by the high cost of experimental testing for functional significance of protein variants. It joins related bits of knowledge, currently distributed throughout various databases, into a consistent, easily accessible, and updatable resource. It currently covers over 155,000 protein sequences which come from more than 2,600 organisms. Overall more than one million single amino acid substitutions (SAASs) are referenced consisting of natural variants, SAASs from mutagenesis experiments and sequencing conflicts. SNPdbe offers the following pieces of information (if available) on each SAAS: * Experimentally derived functional and structural impact * Predicted functional effect * Associated disease * Average heterozygosity * Experimental evidence of the nsSNP * Evolutionary conservation of wildtype and mutant amino acid * Link-outs to external databases A convenient webinterface to query SAASs on the following levels is offered: * Protein and gene identifiers and keywords * Disease keywords * Protein sequence on different sequence identity thresholds * Variant identifier (dbSNP rs, SwissVar, PMD) or specific mutant like XposY and specified sequence They offer the possibility to submit protein sequences along with experimentally substantiated mutations in order to predict their functional effect and inclusion into our database.

Abbreviations: SNPdbe

Synonyms: SNPdbe - nsSNP database of functional effects, nsSNP database of functional effects

Resource Type: database, data or information resource, service resource, storage service resource, data repository

Defining Citation: [PMID:22210871](https://pubmed.ncbi.nlm.nih.gov/22210871/)

Keywords: single amino acid substitution, protein variant, protein, variant, protein sequence, natural variant, mutagenesis, sequencing, mutation

Funding:

Availability: Free for academic use, Non-commercial, Commercial use with permission, The community can contribute to this resource

Resource Name: SNPdbe

Resource ID: SCR_005190

Alternate IDs: OMICS_00185

Record Creation Time: 20220129T080228+0000

Record Last Update: 20250411T054954+0000

Ratings and Alerts

No rating or validation information has been found for SNPdbe.

No alerts have been found for SNPdbe.

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 [FDI Lab - SciCrunch.org](https://fdilab.org/).

Shanazarov N, et al. (2023) Association of Gene Polymorphisms with Breast Cancer Risk in the Kazakh Population. Asian Pacific journal of cancer prevention : APJCP, 24(12), 4195.

Vidal OM, et al. (2022) ADGRL3 genomic variation implicated in neurogenesis and ADHD links functional effects to the incretin polypeptide GIP. Scientific reports, 12(1), 15922.

Reeb J, et al. (2016) Predicted Molecular Effects of Sequence Variants Link to System Level of Disease. PLoS computational biology, 12(8), e1005047.

Uyar B, et al. (2014) Proteome-wide analysis of human disease mutations in short linear motifs: neglected players in cancer? *Molecular bioSystems*, 10(10), 2626.