

Resource Summary Report

Generated by [RRID](#) on Sep 10, 2026

SNPeffect

RRID:SCR_005091

Type: Tool

Proper Citation

SNPeffect (RRID:SCR_005091)

Resource Information

URL: <http://snpeffect.vib.be/>

Proper Citation: SNPeffect (RRID:SCR_005091)

Description: A database for phenotyping human single nucleotide polymorphisms (SNPs) that primarily focuses on the molecular characterization and annotation of disease and polymorphism variants in the human proteome. They provide a detailed variant analysis using their tools such as: * TANGO to predict aggregation prone regions * WALTZ to predict amylogenic regions * LIMBO to predict hsp70 chaperone binding sites * FoldX to analyse the effect on structure stability. Further, SNPeffect holds per-variant annotations on functional sites, structural features and post-translational modification. The meta-analysis tool enables scientists to carry out a large scale mining of SNPeffect data and visualize the results in a graph. It is now possible to submit custom single protein variants for a detailed phenotypic analysis., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16, 2025.

Abbreviations: SNPeffect

Synonyms: SNPeffect 4 Phenotyping Human Mutations

Resource Type: analysis service resource, data analysis service, data or information resource, database, production service resource, service resource

Defining Citation: [PMID:22075996](#), [PMID:18086700](#), [PMID:16809394](#), [PMID:15608254](#)

Keywords: single nucleotide polymorphism, phenotyping, mutation, protein-coding variant, molecule, structure, phenotype, non-synonymous coding snp, allelic variation, gene, protein stability, functional site, protein phosphorylation, glycosylation, subcellular localization, protein turnover, protein aggregation, amyloidosis, chaperone interaction, protein variant, FASEB list

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: SNPeffect

Resource ID: SCR_005091

Alternate IDs: OMICS_00187, nif-0000-03480

Alternate URLs: <http://snpeffect.switchlab.org/>

Record Creation Time: 20220129T080228+0000

Record Last Update: 20260905T132958+0000

Ratings and Alerts

No rating or validation information has been found for SNPeffect.

No alerts have been found for SNPeffect.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 62 mentions in open access literature.

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

Wu C, et al. (2026) Molecular Mechanisms of CLCN5 Missense Mutations in Dent Disease Type 1: A Comprehensive Computational Analysis and Clinical Correlations in a Chinese Cohort. *Journal of cellular and molecular medicine*, 30(6), e71108.

De Guidi I, et al. (2024) QTL mapping reveals novel genes and mechanisms underlying variations in H₂S production during alcoholic fermentation in *Saccharomyces cerevisiae*. *FEMS yeast research*, 24.

Somerville V, et al. (2024) Genomic and phenotypic imprints of microbial domestication on cheese starter cultures. *Nature communications*, 15(1), 8642.

Brown AJ, et al. (2024) Host genetic variation guides hepatitis C clearance, chronicity, and liver fibrosis in mice. *Hepatology (Baltimore, Md.)*, 79(1), 183.

Chen J, et al. (2024) Identification of Pathogenic Missense Mutations of NF1 Using Computational Approaches. *Journal of molecular neuroscience : MN*, 74(4), 94.

Xu X, et al. (2023) Ultra-high static magnetic field induces a change in the spectrum but not frequency of DNA spontaneous mutations in *Arabidopsis thaliana*. *Frontiers in plant science*, 14, 1305069.

Correia C, et al. (2023) Relationship between BCL2 mutations and follicular lymphoma outcome in the chemoimmunotherapy era. *Blood cancer journal*, 13(1), 81.

Gupta YK, et al. (2023) Major proliferation of transposable elements shaped the genome of the soybean rust pathogen *Phakopsora pachyrhizi*. *Nature communications*, 14(1), 1835.

Vodicska B, et al. (2023) Real-world performance analysis of a novel computational method in the precision oncology of pediatric tumors. *World journal of pediatrics : WJP*, 19(10), 992.

Murakami K, et al. (2023) Association of SNPs in the PAI1 Gene with Disease Recurrence and Clinical Outcome in Bladder Cancer. *International journal of molecular sciences*, 24(5).

Jia Y, et al. (2022) In rice splice variants that restore the reading frame after frameshifting indel introduction are common, often induced by the indels and sometimes lead to organism-level rescue. *PLoS genetics*, 18(2), e1010071.

Taagen E, et al. (2022) If it ain't broke, don't fix it: evaluating the effect of increased recombination on response to selection for wheat breeding. *G3 (Bethesda, Md.)*, 12(12).

Somerville V, et al. (2022) Functional strain redundancy and persistent phage infection in Swiss hard cheese starter cultures. *The ISME journal*, 16(2), 388.

Mohkam M, et al. (2022) In Silico Evaluation of Nonsynonymous SNPs in Human ADAM33: The Most Common Form of Genetic Association to Asthma Susceptibility. *Computational and mathematical methods in medicine*, 2022, 1089722.

Bonet LFS, et al. (2021) Molecular dynamics and protein frustration analysis of human fused in Sarcoma protein variants in Amyotrophic Lateral Sclerosis type 6: An In Silico approach. *PloS one*, 16(9), e0258061.

Kajiya-Kanegae H, et al. (2021) *OryzaGenome2.1*: Database of Diverse Genotypes in Wild *Oryza* Species. *Rice (New York, N.Y.)*, 14(1), 24.

Nordin J, et al. (2021) Association of Protective HLA-A With HLA-B*27 Positive Ankylosing Spondylitis. *Frontiers in genetics*, 12, 659042.

Aftab A, et al. (2021) Computational analysis of Cyclin D1 gene SNPs and association with breast cancer. *Bioscience reports*, 41(1).

S UK, et al. (2020) Deciphering the Role of Filamin B Calponin-Homology Domain in Causing the Larsen Syndrome, Boomerang Dysplasia, and Atelosteogenesis Type I Spectrum Disorders via a Computational Approach. *Molecules (Basel, Switzerland)*, 25(23).

Karthikeyan V, et al. (2020) Estimation of varicocele associated human ARG2 and NOS1 proteins and computational analysis on the effect of its nsSNPs. *International journal of biological macromolecules*, 164, 735.