Resource Summary Report

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SNPeffect

RRID:SCR_005091
Type: Tool

Proper Citation

SNPeffect (RRID:SCR_005091)

Resource Information

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

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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.

Abbreviations: SNPeffect

Synonyms: SNPeffect 4 Phenotyping Human Mutations

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

Funding:

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: 20250430T055333+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 59 mentions in open access literature.

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

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.

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

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

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.

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.

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.

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.

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.

Pereira GRC, et al. (2020) In silico analysis of the tryptophan hydroxylase 2 (TPH2) protein

variants related to psychiatric disorders. PloS one, 15(3), e0229730.

Mohamadian M, et al. (2020) A novel homozygous variant in an Iranian pedigree with cerebellar ataxia, mental retardation, and dysequilibrium syndrome type 4. Journal of clinical laboratory analysis, 34(11), e23484.

Jin H, et al. (2020) Identification of potential causal variants for premature ovarian failure by whole exome sequencing. BMC medical genomics, 13(1), 159.