Resource Summary Report

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Ensembl Variation

RRID:SCR_001630
Type: Tool

Proper Citation

Ensembl Variation (RRID:SCR_001630)

Resource Information

URL: http://uswest.ensembl.org/info/docs/variation/index.html

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Description: Public database that stores areas of genome that differ between individual genomes (variants) and, where available, associated disease and phenotype information. Different types of variants for several species: single nucleotide polymorphisms (SNPs), short nucleotide insertions and/or deletions, and longer variants classified as structural variants (including CNVs). Effects of variants on the Ensembl transcripts and regulatory features for each species are predicted. You can run same analysis on your own data using Variant Effect Predictor. These data are integrated with other data sources in Ensembl, and can be accessed using the API or website. For several different species in Ensembl, they import variation data (SNPs, CNVs, allele frequencies, genotypes, etc) from a variety of sources (e.g. dbSNP). Imported variants and alleles are subjected to quality control process to flag suspect data. In human, they calculate linkage disequilibrium for each variant, by population.

Abbreviations: Ensembl Variation

Synonyms: ensembl variation

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

Defining Citation: PMID:23203987, PMID:20562413, PMID:20459810, PMID:20459805

Keywords: genome, disease, phenotype, genomic variant, single nucleotide polymorphism nucleotide, insertion, deletion, structural variant, copy number variation, inversion, translocation, somatic variant, allele frequency, genotype, disease phenotype, inherited

disease

Funding:

Availability: Free, Freely available

Resource Name: Ensembl Variation

Resource ID: SCR_001630

Alternate IDs: nlx_153897

Record Creation Time: 20220129T080208+0000

Record Last Update: 20250528T060433+0000

Ratings and Alerts

No rating or validation information has been found for Ensembl Variation.

No alerts have been found for Ensembl Variation.

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.

Alatwi E, et al. (2024) The role of genetic polymorphisms in the sulfation of pregnenolone by human cytosolic sulfotransferase SULT2B1a. Scientific reports, 14(1), 8050.

Alatwi E, et al. (2023) The role of genetic polymorphisms in the sulfation of pregnenolone by human cytosolic sulfotransferase SULT2B1a. Research square.

Srivastava M, et al. (2021) Transcriptome-wide high-throughput mapping of protein-RNA occupancy profiles using POP-seq. Scientific reports, 11(1), 1175.

Pua CJ, et al. (2016) Development of a Comprehensive Sequencing Assay for Inherited Cardiac Condition Genes. Journal of cardiovascular translational research, 9(1), 3.