Resource Summary Report

Generated by NIF on Aug 9, 2026

Variant Effect Predictor

RRID:SCR_007931
Type: Tool

Proper Citation

Variant Effect Predictor (RRID:SCR_007931)

Resource Information

URL: http://www.ensembl.org/info/docs/tools/vep/index.html

Proper Citation: Variant Effect Predictor (RRID:SCR_007931)

Description: Data analysis service to predict the functional consequences of known and unknown variants.

Abbreviations: VEP

Synonyms: Ve!P

Resource Type: production service resource, software resource, data analysis service, analysis service resource, service resource

Keywords: perl, bio.tools

Resource Name: Variant Effect Predictor

Resource ID: SCR_007931

Alternate IDs: biotools:ensembl_variant_effect_predictor

Alternate URLs: https://bio.tools/ensembl_variant_effect_predictor

Record Creation Time: 20220129T080244+0000

Record Last Update: 20260808T185910+0000

Ratings and Alerts

No rating or validation information has been found for Variant Effect Predictor.

No alerts have been found for Variant Effect Predictor.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 2073 mentions in open access literature.

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

Valentín López JC, et al. (2026) Evolution of AR and Non-AR Alterations in ctDNA of Patients with Metastatic Prostate Cancer Treated in the Phase III Alliance A031201 Trial. Clinical cancer research : an official journal of the American Association for Cancer Research, 32(12), 2413.

Huang K, et al. (2026) Exploring a genetic basis for the metabolic perturbations in ME/CFS using UK biobank. iScience, 29(1), 114316.

Hang JF, et al. (2026) Out-of-frame CBX3::ALK fusion drives ALK activation and therapy response. Cell reports. Medicine, 7(4), 102697.

Mortazavi M, et al. (2026) Long-read genome sequencing improves detection and functional interpretation of structural and repeat variants in autism. Cell genomics, 6(5), 101186.

Ahmed S, et al. (2026) Identification of the ACTB p.Ser348Leu de novo variant in individuals with syndromic neonatal diabetes. EBioMedicine, 128, 106286.

Yun KH, et al. (2026) Phase IB/II Trial with Correlative Analyses of Doxorubicin plus Durvalumab Combination in Patients with Advanced Soft Tissue Sarcoma. Clinical cancer research : an official journal of the American Association for Cancer Research, 32(9), 1686.

Howard CJ, et al. (2026) Deep mutational scanning reveals pharmacologically relevant insights into TYK2 signaling and disease. eLife, 15.

Cappadona C, et al. (2026) Multi-omics identifies oxidative stress, prothrombotic pathways, and lactoperoxidase variants as key factors in COVID-19 severity. EBioMedicine, 123, 106111.

Radulovich N, et al. (2026) Preclinical Combination Targeting VEGF and PI3K in a Rare, Aggressive Mixed Endometrial Carcinoma: An Applied Case Report. Cancer research communications, 6(4), 832.

Gromadzi?ski L, et al. (2026) Unveiling the molecular impact of pulmonary embolism on the right ventricle: a multi-layer transcriptomic study in a porcine model. Molecular and cellular biochemistry, 481(1), 509.

Yang P, et al. (2026) SeekPCMdb: knowledge on disease-associated protein-coding mutations. Nucleic acids research, 54(D1), D1646.

Gumpert N, et al. (2026) Recurrent Immunogenic Neoantigens and Their Cognate T-cell Receptors in Treatment-Resistant Metastatic Prostate Cancer. Cancer discovery, 16(2), 250.

Lazare S, et al. (2026) Postoperative Lymph Is a Proximal Source of ctDNA for Detection of Recurrence in HPV-Independent Head and Neck Cancer. Clinical cancer research : an official journal of the American Association for Cancer Research, 32(1), 135.

Higasa K, et al. (2026) Whole-genome sequencing of 3135 individuals representing the genetic diversity of the Japanese population. Journal of human genetics, 71(4), 223.

Burkart S, et al. (2026) Expansion of the Phenotypic and Genotypic Spectrum for PRKAR1B -Related Marbach-Schaaf Neurodevelopmental Syndrome: A Case Series. Clinical genetics, 109(4), 679.

da Rosa LM, et al. (2026) Chronic Granulomatous Disease: Clinical and Molecular Characterization of Brazilian Patients. The journal of gene medicine, 28(2), e70086.

Lawless D, et al. (2026) Application of qualifying variants for genomic analysis. Bioinformatics (Oxford, England), 42(2).

Nicholas JC, et al. (2026) Cross-ancestry comparison of aptamer and antibody protein measures. Nature communications, 17(1), 1054.

Li R, et al. (2026) Mechanistic Insights Into Immune Cell Dysregulation Mediated by Novel Heterozygous Variants in CARD11 and MALT1. Journal of clinical immunology, 46(1).

Boudry A, et al. (2026) Assessment of measurable residual disease in ovarian tissue collected for fertility preservation in patients in remission from acute myeloid leukaemia: A pilot study. British journal of haematology, 208(3), 897.