Variant Effect Predictor

New job Clear form

Species: Homo_sapiens X

Assembly: GRCh37.p13

VEP for non-human species is now only available on this site for Human (GRCh37). For other species, please visit our main site .

Name for this job (optional): My Ptof

Input data:

Either paste data:

Examples: Ensembl default, VCF, Variant identifiers, HGVS notations

Or upload file: Выберите файл snps_clean.vcf

Or provide file URL:

Transcript database to use:

- ○ Ensembl/GENCODE transcripts
- ○ Ensembl/GENCODE basic transcripts
- ◉ RefSeq transcripts
- ○ Ensembl/GENCODE and RefSeq transcripts

Additional configurations:

Identifiers *Additional identifiers for genes, transcripts and variants*

Identifiers

Gene symbol: ☑

Transcript version: ☐

Protein: ☑

UniProt: ☑

HGVS: ☐

Variants and frequency data *Co-located variants and frequency data*

Variants and frequency data

Find co-located known variants: Yes

Variant synonyms: ☐

Frequency data for co-located variants:

- ☐ 1000 Genomes global minor allele frequency
- ☐ 1000 Genomes continental allele frequencies
- ☑ gnomAD (exomes) allele frequencies
- ☐ gnomAD (genomes) allele frequencies

PubMed IDs for citations of co-located variants: ☑

Include flagged variants: ☐

Additional annotations *Addtional transcript, protein and regulatory annotations*

Transcript annotation

Transcript biotype: ☑

Exon and intron numbers: ☐

Upstream/Downstream distance (bp): 5000

miRNA structure: ☐

NMD: ☐

UTRAnnotator: ☐

Protein annotation

IntAct: ◉ Disabled ○ Enabled

Regulatory data

Get regulatory region consequences: Yes

Phenotype data and citations

Phenotypes: ☑

Gene Ontology: ☑

Mastermind: ☐

Predictions *Variant predictions, e.g. SIFT, PolyPhen*

Pathogenicity predictions

SIFT: Prediction and score

PolyPhen: Prediction and score

dbNSFP: ◉ Disabled ○ Enabled

CADD: ☐

MPC: ☐

LOEUF: ☐

Splicing predictions

dbscSNV: ☐

MaxEntScan: ☐

SpliceAI: ◉ Disabled ○ Enabled

Conservation

BLOSUM62: ☐

Ancestral allele: ☐

Filter by frequency:
- (●) No filtering
- ( ) Exclude common variants
- ( ) Advanced filtering

Return results for variants in coding regions only: [ ]

Restrict results: Show all results

NB: Restricting results may exclude biologically important data!

Advanced options | *Additional enhancements*

Advanced options

Buffer size: 5000

NB: When the **Regulatory data** option is selected then due to the large amount of regulatory data available, the **maximum buffer size** is automatically reduced from the default value of **5000** to **500**. This reduces the memory requirement but might increase the run time. If you find that your jobs are still failing due to memory limitations then you can select a value **lower than 500**.

Right align variants prior to consequence calculation: No

Run ›

Recent jobs

You have no jobs currently running or recently completed.