Variant Effect Predictor

New job		Clear form
Species:	Assembly: GRCh37.p13 VEP for non-human species is now only available on this site visit our main site	for Human (GRCh37). For other species, please
Name for this job (optional):	My Ptof	
	Examples: Ensembl default, VCF, Variant identifiers, HGVS notations Or upload file: Выберите файл snps_cl 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	ots and variants
	Identifiers	
	Gene symbol:	
	Transcript version:	
	Protein:	
	UniProt:	☑
	HGVS:	
	Variants and frequency data	and frequency data
Variants and frequency data		
	Find co-located known variants:	Yes
	Variant synonyms:	
	Frequency data for co-located variants: PubMed IDs for citations of co-located variants:	□ 1000 Genomes global minor allele frequency □ 1000 Genomes continental allele frequencies □ gnomAD (exomes) allele frequencies □ gnomAD (genomes) allele frequencies

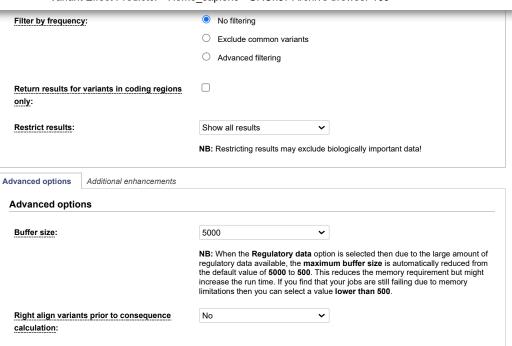
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Include flagged variants:			
Additional annotations	in and regulatory annotations		
Transcript annotation			
Transcript biotype:			
Exon and intron numbers:			
Upstream/Downstream distance (bp):	5000		
miRNA structure:			
NMD:			
UTRAnnotator:			
Protein 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		
	O Enabled		
CADD:			
MPC:			
LOEUF:			
Splicing predictions			
dbscSNV:			
MaxEntScan:			
SpliceAl:	Disabled		
Conservation	O Enabled		
BLOSUM62:			
Ancestral allele:			
Alluestial allele.	J		

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