

Variant Effect Predictor results

Job details

Job summary VEP analysis of group5_ngs_zain_chr15 in Homo_sapiens

Species  Human (Homo sapiens)

Assembly GRCh38

Options summary	1000 Genomes continental allele frequencies:	Enabled
	1000 Genomes global minor allele frequency:	Enabled
	Ancestral allele^(p):	Enabled
	APPRIS:	Enabled
	BLOSUM62^(p):	Enabled
	Buffer size:	5000
	DisGeNET^(p):	Enabled
	Filter by frequency:	Disabled
	Find co-located known variants:	Enabled
	Gene Ontology^(p):	Enabled
	Gene symbol:	Enabled
	gnomAD (exomes) allele frequencies:	Enabled
	MANE:	Enabled
	Phenotypes^(p):	Enabled
	PolyPhen:	Prediction and score
	Protein:	Enabled
	Protein matches:	Enabled
	PubMed IDs for citations of co-located variants:	Enabled
	Get regulatory region consequences:	Yes
	Restrict results:	Disabled
	Right align variants prior to consequence calculation:	Disabled
	SIFT:	Prediction and score

Loading component

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