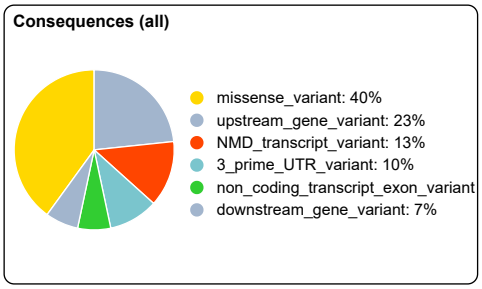
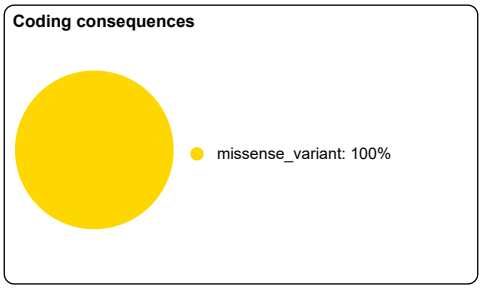
Variant Effect Predictor results

Job details

Summary statistics

Category	Count
Variants processed	1
Variants filtered out	0
Novel / existing variants	0 (0.0) / 1 (100.0)
Overlapped genes	2
Overlapped transcripts	26
Overlapped regulatory features	0





Results preview

Navigation (per variant)

Page: 1 of 1 | **Show:** 1 All variants

Filters

Uploaded variant | is | defined | Add

Download

All: VCF VEP TXT

BioMart: Variants Genes

New job

Show/hide columns (28 hidden)

Uploaded variant	Location	Allele	Consequence	Symbol	Gene	Feature type	Feature	Biotype	Exon
.	X:71121046-71121046	T	missense_variant	MED12	ENSG00000184634	Transcript	ENST00000333646.11	protein_coding	5/45
.	X:71121046-71121046	T	missense_variant	MED12	ENSG00000184634	Transcript	ENST00000374080.8	protein_coding	5/45
.	X:71121046-71121046	T	missense_variant	MED12	ENSG00000184634	Transcript	ENST00000374102.6	protein_coding	5/45
.	X:71121046-71121046	T	downstream_gene_variant	MED12	ENSG00000184634	Transcript	ENST00000429213.3	nonsense_mediated_decay	-
.	X:71121046-71121046	T	upstream_gene_variant	MED12	ENSG00000184634	Transcript	ENST00000462984.2	retained_intron	-
.	X:71121046-71121046	T	3_prime_UTR_variant, NMD_transcript_variant	MED12	ENSG00000184634	Transcript	ENST00000686548.1	nonsense_mediated_decay	5/45
.	X:71121046-71121046	T	missense_variant	MED12	ENSG00000184634	Transcript	ENST00000687382.1	protein_coding	5/46
.	X:71121046-71121046	T	upstream_gene_variant	MED12	ENSG00000184634	Transcript	ENST00000688079.1	retained_intron	-
.	X:71121046-71121046	T	missense_variant, NMD_transcript_variant	MED12	ENSG00000184634	Transcript	ENST00000688663.1	nonsense_mediated_decay	5/42
.	X:71121046-71121046	T	non_coding_transcript_exon_variant	MED12	ENSG00000184634	Transcript	ENST00000688718.1	retained_intron	5/9
.	X:71121046-71121046	T	3_prime_UTR_variant, NMD_transcript_variant	MED12	ENSG00000184634	Transcript	ENST00000689008.1	nonsense_mediated_decay	5/17
.	X:71121046-71121046	T	upstream_gene_variant	MED12	ENSG00000184634	Transcript	ENST00000689768.1	retained_intron	-
.	X:71121046-71121046	T	missense_variant	MED12	ENSG00000184634	Transcript	ENST00000690145.1	protein_coding	5/45
.	X:71121046-71121046	T	missense_variant	MED12	ENSG00000184634	Transcript	ENST00000690242.1	protein_coding	5/46
.	X:71121046-71121046	T	non_coding_transcript_exon_variant	MED12	ENSG00000184634	Transcript	ENST00000690828.1	retained_intron	5/40
.	X:71121046-71121046	T	upstream_gene_variant	MED12	ENSG00000184634	Transcript	ENST00000691113.1	nonsense_mediated_decay	-
.	X:71121046-71121046	T	upstream_gene_variant	MED12	ENSG00000184634	Transcript	ENST00000691385.1	retained_intron	-
.	X:71121046-71121046	T	upstream_gene_variant	MED12	ENSG00000184634	Transcript	ENST00000691426.1	retained_intron	-
.	X:71121046-71121046	T	missense_variant	MED12	ENSG00000184634	Transcript	ENST00000691468.1	protein_coding	5/38
.	X:71121046-71121046	T	missense_variant	MED12	ENSG00000184634	Transcript	ENST00000692304.1	protein_coding	5/45
.	X:71121046-71121046	T	3_prime_UTR_variant, NMD_transcript_variant	MED12	ENSG00000184634	Transcript	ENST00000692864.1	nonsense_mediated_decay	5/12
.	X:71121046-71121046	T	missense_variant	MED12	ENSG00000184634	Transcript	ENST00000693324.1	protein_coding	5/38

Uploaded variant	Location	Allele	Consequence	Symbol	Gene	Feature type	Feature	Biotype	Exon
.	X:71121046-71121046	T	upstream_gene_variant	MED12	ENSG00000184634	Transcript	ENST00000693391.1	protein_coding	-
.	X:71121046-71121046	T	downstream_gene_variant	-	ENSG00000228427	Transcript	ENST00000740246.1	lncRNA	-
.	X:71121046-71121046	T	missense_variant	MED12	ENSG00000184634	Transcript	ENST00000938012.1	protein_coding	5/45
.	X:71121046-71121046	T	missense_variant	MED12	ENSG00000184634	Transcript	ENST00000938013.1	protein_coding	5/45

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New job