

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

Consequences (all)

missense\_variant: 40%

upstream\_gene\_variant: 23%

NMD\_transcript\_variant: 13%

3\_prime\_UTR\_variant: 10%

non\_coding\_transcript\_exon\_variant

downstream\_gene\_variant: 7%

Coding consequences

missense\_variant: 100%

Results preview

Navigation (per variant)

Filters

Download

Page: 1 of 1 | Show: 1 variant

Uploaded variant is defined

Add

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
.	<a href="#">X:71121046-71121046</a>	T	missense_variant	MED12	<a href="#">ENSG00000184634</a>	Transcript	<a href="#">ENST00000333646.11</a>	protein_coding	5/45
.	<a href="#">X:71121046-71121046</a>	T	missense_variant	MED12	<a href="#">ENSG00000184634</a>	Transcript	<a href="#">ENST00000374080.8</a>	protein_coding	5/45
.	<a href="#">X:71121046-71121046</a>	T	missense_variant	MED12	<a href="#">ENSG00000184634</a>	Transcript	<a href="#">ENST00000374102.6</a>	protein_coding	5/45
.	<a href="#">X:71121046-71121046</a>	T	downstream gene variant	MED12	<a href="#">ENSG00000184634</a>	Transcript	<a href="#">ENST00000429213.3</a>	nonsense_mediated_decay	-
.	<a href="#">X:71121046-71121046</a>	T	upstream gene variant	MED12	<a href="#">ENSG00000184634</a>	Transcript	<a href="#">ENST00000462984.2</a>	retained_intron	-
.	<a href="#">X:71121046-71121046</a>	T	3 prime UTR variant, NMD transcript variant	MED12	<a href="#">ENSG00000184634</a>	Transcript	<a href="#">ENST00000686548.1</a>	nonsense_mediated_decay	5/45
.	<a href="#">X:71121046-71121046</a>	T	missense_variant	MED12	<a href="#">ENSG00000184634</a>	Transcript	<a href="#">ENST00000687382.1</a>	protein_coding	5/46
.	<a href="#">X:71121046-71121046</a>	T	upstream gene variant	MED12	<a href="#">ENSG00000184634</a>	Transcript	<a href="#">ENST00000688079.1</a>	retained_intron	-
.	<a href="#">X:71121046-71121046</a>	T	missense_variant, NMD transcript variant	MED12	<a href="#">ENSG00000184634</a>	Transcript	<a href="#">ENST00000688663.1</a>	nonsense_mediated_decay	5/42
.	<a href="#">X:71121046-71121046</a>	T	non coding transcript exon variant	MED12	<a href="#">ENSG00000184634</a>	Transcript	<a href="#">ENST00000688718.1</a>	retained_intron	5/9
.	<a href="#">X:71121046-71121046</a>	T	3 prime UTR variant, NMD transcript variant	MED12	<a href="#">ENSG00000184634</a>	Transcript	<a href="#">ENST00000689008.1</a>	nonsense_mediated_decay	5/17
.	<a href="#">X:71121046-71121046</a>	T	upstream gene variant	MED12	<a href="#">ENSG00000184634</a>	Transcript	<a href="#">ENST00000689768.1</a>	retained_intron	-
.	<a href="#">X:71121046-71121046</a>	T	missense_variant	MED12	<a href="#">ENSG00000184634</a>	Transcript	<a href="#">ENST00000690145.1</a>	protein_coding	5/45
.	<a href="#">X:71121046-71121046</a>	T	missense_variant	MED12	<a href="#">ENSG00000184634</a>	Transcript	<a href="#">ENST00000690242.1</a>	protein_coding	5/46
.	<a href="#">X:71121046-71121046</a>	T	non coding transcript exon variant	MED12	<a href="#">ENSG00000184634</a>	Transcript	<a href="#">ENST00000690828.1</a>	retained_intron	5/40
.	<a href="#">X:71121046-71121046</a>	T	upstream gene variant	MED12	<a href="#">ENSG00000184634</a>	Transcript	<a href="#">ENST00000691113.1</a>	nonsense_mediated_decay	-
.	<a href="#">X:71121046-71121046</a>	T	upstream gene variant	MED12	<a href="#">ENSG00000184634</a>	Transcript	<a href="#">ENST00000691385.1</a>	retained_intron	-
.	<a href="#">X:71121046-71121046</a>	T	upstream gene variant	MED12	<a href="#">ENSG00000184634</a>	Transcript	<a href="#">ENST00000691426.1</a>	retained_intron	-
.	<a href="#">X:71121046-71121046</a>	T	missense_variant	MED12	<a href="#">ENSG00000184634</a>	Transcript	<a href="#">ENST00000691468.1</a>	protein_coding	5/38
.	<a href="#">X:71121046-71121046</a>	T	missense_variant	MED12	<a href="#">ENSG00000184634</a>	Transcript	<a href="#">ENST00000692304.1</a>	protein_coding	5/45
.	<a href="#">X:71121046-71121046</a>	T	3 prime UTR variant, NMD transcript variant	MED12	<a href="#">ENSG00000184634</a>	Transcript	<a href="#">ENST00000692864.1</a>	nonsense_mediated_decay	5/12
.	<a href="#">X:71121046-71121046</a>	T	missense_variant	MED12	<a href="#">ENSG00000184634</a>	Transcript	<a href="#">ENST00000693324.1</a>	protein_coding	5/38

Uploaded variant	Location	Allele	Consequence	Symbol	Gene	Feature type	Feature	Biotype	Exon
.	<a href="#">X:71121046-71121046</a>	T	upstream gene variant	MED12	<a href="#">ENSG00000184634</a>	Transcript	<a href="#">ENST00000693391.1</a>	protein_coding	-
.	<a href="#">X:71121046-71121046</a>	T	downstream gene variant	-	<a href="#">ENSG00000228427</a>	Transcript	<a href="#">ENST00000740246.1</a>	lncRNA	-
.	<a href="#">X:71121046-71121046</a>	T	missense variant	MED12	<a href="#">ENSG00000184634</a>	Transcript	<a href="#">ENST00000938012.1</a>	protein_coding	5/45
.	<a href="#">X:71121046-71121046</a>	T	missense variant	MED12	<a href="#">ENSG00000184634</a>	Transcript	<a href="#">ENST00000938013.1</a>	protein_coding	5/45

Page: 1 of 1 | Show: 1 All variants

[New job](#)

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