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
Transcript biotype:	Enabled
Transcript database to use:	Ensembl transcripts
Transcript support level:	Enabled
Transcript version:	Enabled
UniProt:	Enabled
Upstream/Downstream distance (bp):	5000

(p) = functionality from VEP plugin

VEP and data version

1000genomes	phase3
Assembly	GRCh38.p14
Cache	111_GRCh38
ClinVar	202306
COSMIC	98
Database	homo_sapiens_core_111_38
dbSNP	156

GENCODE	GENCODE 45
Genebuild	2014-07
gnomADe	r2.1.1
gnomADg	v3.1.2
HGMD-PUBLIC	20204
Polyphen	2.2.3
Regbuild	1.0
SIFT	6.2.1
Time	2024-03-13 15:54:17
VEP	v111

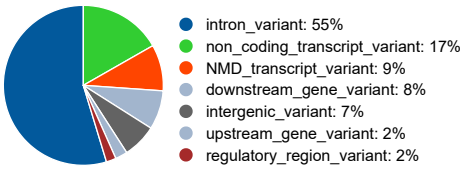
Command line equivalent

```
./vep --af --af_1kg --af_gnomade --appris --biotype --buffer_size 500 --check_existing --distance 5000 --
```

Summary statistics

Category	Count
Variants processed	35
Variants filtered out	0
Novel / existing variants	22 (62.9) / 13 (37.1)
Overlapped genes	12
Overlapped transcripts	60
Overlapped regulatory features	1

Consequences (all)



Results preview

Navigation (per variant) **Show:** 1 5 10 All variants

Filters Uploaded variant | is | defined | Add

Download New job
All: VCF VEP TXT
BioMart: Variants Genes

Show/hide columns (42 hidden)

Uploaded variant	Location	Allele	Consequence	Symbol	Gene	Feature type	Feature	Biotype
.	15:19564270-19564270	C	intergenic_variant	-	-	-	-	-
.	15:19564271-19564271	C	intergenic_variant	-	-	-	-	-
.	15:19564277-19564277	T	intergenic_variant	-	-	-	-	-
.	15:19564285-19564285	T	intergenic_variant	-	-	-	-	-
.	15:19564293-19564293	C	intergenic_variant	-	-	-	-	-
.	15:20301175-20301175	G	upstream_gene_variant	-	ENSG00000287122	Transcript	ENST00000656782.1	lncRNA
.	15:20301176-20301176	T	upstream_gene_variant	-	ENSG00000287122	Transcript	ENST00000656782.1	lncRNA
.	15:23549774-23549774	T	intergenic_variant	-	-	-	-	-
.	15:23549777-23549777	A	intergenic_variant	-	-	-	-	-
.	15:23549778-23549778	C	intergenic_variant	-	-	-	-	-
.	15:27037763-27037763	T	intron_variant	GABRG3	ENSG00000182256	Transcript	ENST00000555083.5	protein_coding
.	15:27037763-27037763	T	intron_variant	GABRG3	ENSG00000182256	Transcript	ENST00000615808.5	protein_coding
.	15:27037763-27037763	T	downstream_gene_variant	GABRG3-AS1	ENSG00000228740	Transcript	ENST00000660679.1	lncRNA
.	15:27037773-27037773	A	intron_variant	GABRG3	ENSG00000182256	Transcript	ENST00000555083.5	protein_coding
.	15:27037773-27037773	A	intron_variant	GABRG3	ENSG00000182256	Transcript	ENST00000615808.5	protein_coding
.	15:27037773-	A	downstream_gene_variant	GABRG3-	ENSG00000228740	Transcript	ENST00000660679.1	lncRNA

Uploaded variant	Location	Allele	Consequence	Symbol	Gene	Feature type	Feature	Biotype
	27037773			AS1				
.	15:27037781-27037781	T	intron_variant	GABRG3	ENSG00000182256	Transcript	ENST00000555083.5	protein_coding
.	15:27037781-27037781	T	intron_variant	GABRG3	ENSG00000182256	Transcript	ENST00000615808.5	protein_coding
.	15:27037781-27037781	T	downstream_gene_variant	GABRG3-AS1	ENSG00000228740	Transcript	ENST00000660679.1	lncRNA
.	15:27037784-27037784	T	intron_variant	GABRG3	ENSG00000182256	Transcript	ENST00000555083.5	protein_coding
.	15:27037784-27037784	T	intron_variant	GABRG3	ENSG00000182256	Transcript	ENST00000615808.5	protein_coding
.	15:27037784-27037784	T	downstream_gene_variant	GABRG3-AS1	ENSG00000228740	Transcript	ENST00000660679.1	lncRNA
.	15:40130004-40130004	G	downstream_gene_variant	-	ENSG00000259239	Transcript	ENST00000559747.1	processed_pseudogene
.	15:40130007-40130007	A	downstream_gene_variant	-	ENSG00000259239	Transcript	ENST00000559747.1	processed_pseudogene
.	15:43139690-43139690	T	intron_variant	TMEM62	ENSG00000137842	Transcript	ENST00000260403.7	protein_coding
.	15:43139690-43139690	T	intron_variant	TMEM62	ENSG00000137842	Transcript	ENST00000564494.1	protein_coding
.	15:43139690-43139690	T	intron_variant	TMEM62	ENSG00000137842	Transcript	ENST00000564698.5	protein_coding
.	15:43139690-43139690	T	intron_variant	TMEM62	ENSG00000137842	Transcript	ENST00000565291.5	protein_coding
.	15:43139690-43139690	T	intron_variant, NMD_transcript_variant	TMEM62	ENSG00000137842	Transcript	ENST00000567441.5	nonsense_mediated_decay
.	15:43139690-43139690	T	intron_variant, NMD_transcript_variant	TMEM62	ENSG00000137842	Transcript	ENST00000568182.5	nonsense_mediated_decay
.	15:43139690-43139690	T	intron_variant, NMD_transcript_variant	TMEM62	ENSG00000137842	Transcript	ENST00000568197.1	nonsense_mediated_decay
.	15:43139690-43139690	T	intron_variant, NMD_transcript_variant	TMEM62	ENSG00000137842	Transcript	ENST00000569535.5	nonsense_mediated_decay
.	15:43139690-43139690	T	intron_variant, NMD_transcript_variant	TMEM62	ENSG00000137842	Transcript	ENST00000569926.5	nonsense_mediated_decay
.	15:43139690-43139690	T	downstream_gene_variant	TMEM62	ENSG00000137842	Transcript	ENST00000570109.1	retained_intron
.	15:43139690-43139690	T	intron_variant, non_coding_transcript_variant	-	ENSG00000285080	Transcript	ENST00000570199.2	lncRNA
.	15:43139691-43139691	T	intron_variant	TMEM62	ENSG00000137842	Transcript	ENST00000260403.7	protein_coding
.	15:43139691-43139691	T	intron_variant	TMEM62	ENSG00000137842	Transcript	ENST00000564494.1	protein_coding
.	15:43139691-43139691	T	intron_variant	TMEM62	ENSG00000137842	Transcript	ENST00000564698.5	protein_coding
.	15:43139691-43139691	T	intron_variant	TMEM62	ENSG00000137842	Transcript	ENST00000565291.5	protein_coding
.	15:43139691-43139691	T	intron_variant, NMD_transcript_variant	TMEM62	ENSG00000137842	Transcript	ENST00000567441.5	nonsense_mediated_decay
.	15:43139691-43139691	T	intron_variant, NMD_transcript_variant	TMEM62	ENSG00000137842	Transcript	ENST00000568182.5	nonsense_mediated_decay
.	15:43139691-43139691	T	intron_variant, NMD_transcript_variant	TMEM62	ENSG00000137842	Transcript	ENST00000568197.1	nonsense_mediated_decay
.	15:43139691-43139691	T	intron_variant, NMD_transcript_variant	TMEM62	ENSG00000137842	Transcript	ENST00000569535.5	nonsense_mediated_decay
.	15:43139691-43139691	T	intron_variant, NMD_transcript_variant	TMEM62	ENSG00000137842	Transcript	ENST00000569926.5	nonsense_mediated_decay
.	15:43139691-43139691	T	downstream_gene_variant	TMEM62	ENSG00000137842	Transcript	ENST00000570109.1	retained_intron
.	15:43139691-43139691	T	intron_variant, non_coding_transcript_variant	-	ENSG00000285080	Transcript	ENST00000570199.2	lncRNA
.	15:44864405-44864405	G	upstream_gene_variant	SORD2P	ENSG00000259479	Transcript	ENST00000558556.5	transcribed_unprocessed_pseudogen
.	15:44864405-44864405	G	intron_variant, non_coding_transcript_variant	SORD2P	ENSG00000290387	Transcript	ENST00000561384.3	lncRNA

Uploaded variant	Location	Allele	Consequence	Symbol	Gene	Feature type	Feature	Biotype
.	15:49501756-49501756	A	intron_variant	FAM227B	ENSG00000166262	Transcript	ENST00000299338.11	protein_coding
.	15:49501756-49501756	A	intron_variant, non_coding_transcript_variant	FAM227B	ENSG00000166262	Transcript	ENST00000559351.1	protein_coding_CDS_not_defined
.	15:49501756-49501756	A	intron_variant	FAM227B	ENSG00000166262	Transcript	ENST00000561064.5	protein_coding
.	15:49501758-49501758	G	intron_variant	FAM227B	ENSG00000166262	Transcript	ENST00000299338.11	protein_coding
.	15:49501758-49501758	G	intron_variant, non_coding_transcript_variant	FAM227B	ENSG00000166262	Transcript	ENST00000559351.1	protein_coding_CDS_not_defined
.	15:49501758-49501758	G	intron_variant	FAM227B	ENSG00000166262	Transcript	ENST00000561064.5	protein_coding
.	15:49501767-49501767	C	intron_variant	FAM227B	ENSG00000166262	Transcript	ENST00000299338.11	protein_coding
.	15:49501767-49501767	C	intron_variant, non_coding_transcript_variant	FAM227B	ENSG00000166262	Transcript	ENST00000559351.1	protein_coding_CDS_not_defined
.	15:49501767-49501767	C	intron_variant	FAM227B	ENSG00000166262	Transcript	ENST00000561064.5	protein_coding
.	15:52426523-52426523	C	intron_variant	MYO5A	ENSG00000197535	Transcript	ENST00000356338.11	protein_coding
.	15:52426523-52426523	C	intron_variant	MYO5A	ENSG00000197535	Transcript	ENST00000399231.8	protein_coding
.	15:52426523-52426523	C	intron_variant	MYO5A	ENSG00000197535	Transcript	ENST00000399233.7	protein_coding
.	15:52426523-52426523	C	intron_variant	MYO5A	ENSG00000197535	Transcript	ENST00000553916.6	protein_coding
.	15:52426523-52426523	C	intron_variant, NMD_transcript_variant	MYO5A	ENSG00000197535	Transcript	ENST00000556196.6	nonsense_mediated_decay
.	15:52426523-52426523	C	upstream_gene_variant	MYO5A	ENSG00000197535	Transcript	ENST00000561810.1	retained_intron
.	15:52426523-52426523	C	intron_variant	MYO5A	ENSG00000197535	Transcript	ENST00000685053.1	protein_coding

Uploaded variant	Location	Allele	Consequence	Symbol	Gene	Feature type	Feature	Biotype
.	15:52426523-52426523	C	intron_variant	MYO5A	ENSG00000197535	Transcript	ENST00000685760.1	protein_coding
.	15:52426523-52426523	C	intron_variant	MYO5A	ENSG00000197535	Transcript	ENST00000687574.1	protein_coding
.	15:52426523-52426523	C	intron_variant	MYO5A	ENSG00000197535	Transcript	ENST00000687728.1	protein_coding
.	15:52426523-52426523	C	intron_variant, NMD_transcript_variant	MYO5A	ENSG00000197535	Transcript	ENST00000687748.1	nonsense_mediated_decay
.	15:52426523-52426523	C	intron_variant, NMD_transcript_variant	MYO5A	ENSG00000197535	Transcript	ENST00000687968.1	nonsense_mediated_decay
.	15:52426523-52426523	C	intron_variant	MYO5A	ENSG00000197535	Transcript	ENST00000689526.1	protein_coding
.	15:52426523-52426523	C	intron_variant	MYO5A	ENSG00000197535	Transcript	ENST00000690693.1	protein_coding
.	15:52426523-52426523	C	intron_variant	MYO5A	ENSG00000197535	Transcript	ENST00000691028.1	protein_coding

Uploaded variant	Location	Allele	Consequence	Symbol	Gene	Feature type	Feature	Biotype
.	15:52426523-52426523	C	intron_variant	MYO5A	ENSG00000197535	Transcript	ENST00000692556.1	protein_coding
.	15:52426523-52426523	C	intron_variant, NMD_transcript_variant	MYO5A	ENSG00000197535	Transcript	ENST00000693471.1	nonsense_mediated_decay
.	15:52426526-52426526	A	intron_variant	MYO5A	ENSG00000197535	Transcript	ENST00000356338.11	protein_coding
.	15:52426526-52426526	A	intron_variant	MYO5A	ENSG00000197535	Transcript	ENST00000399231.8	protein_coding
.	15:52426526-52426526	A	intron_variant	MYO5A	ENSG00000197535	Transcript	ENST00000399233.7	protein_coding
.	15:52426526-52426526	A	intron_variant	MYO5A	ENSG00000197535	Transcript	ENST00000553916.6	protein_coding
.	15:52426526-52426526	A	intron_variant, NMD_transcript_variant	MYO5A	ENSG00000197535	Transcript	ENST00000556196.6	nonsense_mediated_decay
.	15:52426526-52426526	A	upstream_gene_variant	MYO5A	ENSG00000197535	Transcript	ENST00000561810.1	retained_intron

Uploaded variant	Location	Allele	Consequence	Symbol	Gene	Feature type	Feature	Biotype
.	15:52426526-52426526	A	intron_variant	MYO5A	ENSG00000197535	Transcript	ENST00000685053.1	protein_coding
.	15:52426526-52426526	A	intron_variant	MYO5A	ENSG00000197535	Transcript	ENST00000685760.1	protein_coding
.	15:52426526-52426526	A	intron_variant	MYO5A	ENSG00000197535	Transcript	ENST00000687574.1	protein_coding
.	15:52426526-52426526	A	intron_variant	MYO5A	ENSG00000197535	Transcript	ENST00000687728.1	protein_coding
.	15:52426526-52426526	A	intron_variant, NMD_transcript_variant	MYO5A	ENSG00000197535	Transcript	ENST00000687748.1	nonsense_mediated_decay
.	15:52426526-52426526	A	intron_variant, NMD_transcript_variant	MYO5A	ENSG00000197535	Transcript	ENST00000687968.1	nonsense_mediated_decay
.	15:52426526-52426526	A	intron_variant	MYO5A	ENSG00000197535	Transcript	ENST00000689526.1	protein_coding
.	15:52426526-52426526	A	intron_variant	MYO5A	ENSG00000197535	Transcript	ENST00000690693.1	protein_coding

Uploaded variant	Location	Allele	Consequence	Symbol	Gene	Feature type	Feature	Biotype
.	15:52426526-52426526	A	intron_variant	MYO5A	ENSG00000197535	Transcript	ENST00000691028.1	protein_coding
.	15:52426526-52426526	A	intron_variant	MYO5A	ENSG00000197535	Transcript	ENST00000692556.1	protein_coding
.	15:52426526-52426526	A	intron_variant, NMD_transcript_variant	MYO5A	ENSG00000197535	Transcript	ENST00000693471.1	nonsense_mediated_decay
.	15:64199216-64199216	A	intron_variant	CSNK1G1	ENSG00000169118	Transcript	ENST00000303052.13	protein_coding
.	15:64199216-64199216	A	intron_variant	CSNK1G1	ENSG00000169118	Transcript	ENST00000561349.6	protein_coding
.	15:64199216-64199216	A	intron_variant, NMD_transcript_variant	CSNK1G1	ENSG00000169118	Transcript	ENST00000606225.1	nonsense_mediated_decay
.	15:64199216-64199216	A	intron_variant	CSNK1G1	ENSG00000169118	Transcript	ENST00000606793.3	protein_coding
.	15:64199216-64199216	A	intron_variant	CSNK1G1	ENSG00000169118	Transcript	ENST00000607537.6	protein_coding
.	15:64199216-64199216	A	intron_variant	CSNK1G1	ENSG00000169118	Transcript	ENST00000634302.1	protein_coding
.	15:64199216-64199216	A	intron_variant	CSNK1G1	ENSG00000169118	Transcript	ENST00000634654.1	protein_coding
.	15:64199216-64199216	A	intron_variant	CSNK1G1	ENSG00000169118	Transcript	ENST00000634722.1	protein_coding
.	15:64199216-64199216	A	intron_variant	CSNK1G1	ENSG00000169118	Transcript	ENST00000634811.1	protein_coding
.	15:64199216-64199216	A	intron_variant	CSNK1G1	ENSG00000169118	Transcript	ENST00000634909.1	protein_coding
.	15:64199216-64199216	A	intron_variant	CSNK1G1	ENSG00000169118	Transcript	ENST00000635142.1	protein_coding
.	15:64199216-64199216	A	intron_variant	CSNK1G1	ENSG00000169118	Transcript	ENST00000635230.1	protein_coding

Uploaded variant	Location	Allele	Consequence	Symbol	Gene	Feature type	Feature	Biotype
.	15:64199216-64199216	A	intron_variant	CSNK1G1	ENSG00000169118	Transcript	ENST00000635414.1	protein_coding
.	15:81414413-81414413	G	downstream_gene_variant	TMC3-AS1	ENSG00000259343	Transcript	ENST00000558086.1	lncRNA
.	15:81414413-81414413	G	intron_variant, non_coding_transcript_variant	TMC3-AS1	ENSG00000259343	Transcript	ENST00000559781.6	lncRNA
.	15:81414413-81414413	G	intron_variant, non_coding_transcript_variant	TMC3-AS1	ENSG00000259343	Transcript	ENST00000560851.2	lncRNA
.	15:81414413-81414413	G	intron_variant, non_coding_transcript_variant	TMC3-AS1	ENSG00000259343	Transcript	ENST00000642113.1	lncRNA
.	15:81414413-81414413	G	intron_variant, non_coding_transcript_variant	TMC3-AS1	ENSG00000259343	Transcript	ENST00000654210.1	lncRNA
.	15:81414413-81414413	G	intron_variant, non_coding_transcript_variant	TMC3-AS1	ENSG00000259343	Transcript	ENST00000662589.1	lncRNA
.	15:81414413-81414413	G	intron_variant, non_coding_transcript_variant	TMC3-AS1	ENSG00000259343	Transcript	ENST00000665273.1	lncRNA
.	15:81414413-81414413	G	intron_variant, non_coding_transcript_variant	TMC3-AS1	ENSG00000259343	Transcript	ENST00000667509.1	lncRNA
.	15:81414413-81414413	G	downstream_gene_variant	TMC3-AS1	ENSG00000259343	Transcript	ENST00000669758.1	lncRNA
.	15:81414413-81414413	G	regulatory_region_variant	-	-	RegulatoryFeature	ENSR00000995919	enhancer
.	15:81414418-81414418	A	downstream_gene_variant	TMC3-AS1	ENSG00000259343	Transcript	ENST00000558086.1	lncRNA
.	15:81414418-81414418	A	intron_variant, non_coding_transcript_variant	TMC3-AS1	ENSG00000259343	Transcript	ENST00000559781.6	lncRNA
.	15:81414418-81414418	A	intron_variant, non_coding_transcript_variant	TMC3-AS1	ENSG00000259343	Transcript	ENST00000560851.2	lncRNA
.	15:81414418-81414418	A	intron_variant, non_coding_transcript_variant	TMC3-AS1	ENSG00000259343	Transcript	ENST00000642113.1	lncRNA
.	15:81414418-81414418	A	intron_variant, non_coding_transcript_variant	TMC3-AS1	ENSG00000259343	Transcript	ENST00000654210.1	lncRNA
.	15:81414418-81414418	A	intron_variant, non_coding_transcript_variant	TMC3-AS1	ENSG00000259343	Transcript	ENST00000662589.1	lncRNA
.	15:81414418-81414418	A	intron_variant, non_coding_transcript_variant	TMC3-AS1	ENSG00000259343	Transcript	ENST00000665273.1	lncRNA
.	15:81414418-81414418	A	intron_variant, non_coding_transcript_variant	TMC3-AS1	ENSG00000259343	Transcript	ENST00000667509.1	lncRNA
.	15:81414418-81414418	A	downstream_gene_variant	TMC3-AS1	ENSG00000259343	Transcript	ENST00000669758.1	lncRNA
.	15:81414418-81414418	A	regulatory_region_variant	-	-	RegulatoryFeature	ENSR00000995919	enhancer
.	15:81414424-81414424	G	downstream_gene_variant	TMC3-AS1	ENSG00000259343	Transcript	ENST00000558086.1	lncRNA
.	15:81414424-81414424	G	intron_variant, non_coding_transcript_variant	TMC3-AS1	ENSG00000259343	Transcript	ENST00000559781.6	lncRNA
.	15:81414424-81414424	G	intron_variant, non_coding_transcript_variant	TMC3-AS1	ENSG00000259343	Transcript	ENST00000560851.2	lncRNA
.	15:81414424-81414424	G	intron_variant, non_coding_transcript_variant	TMC3-AS1	ENSG00000259343	Transcript	ENST00000642113.1	lncRNA
.	15:81414424-81414424	G	intron_variant, non_coding_transcript_variant	TMC3-AS1	ENSG00000259343	Transcript	ENST00000654210.1	lncRNA
.	15:81414424-81414424	G	intron_variant, non_coding_transcript_variant	TMC3-AS1	ENSG00000259343	Transcript	ENST00000662589.1	lncRNA
.	15:81414424-81414424	G	intron_variant, non_coding_transcript_variant	TMC3-AS1	ENSG00000259343	Transcript	ENST00000665273.1	lncRNA
.	15:81414424-81414424	G	intron_variant, non_coding_transcript_variant	TMC3-AS1	ENSG00000259343	Transcript	ENST00000667509.1	lncRNA
.	15:81414424-81414424	G	downstream_gene_variant	TMC3-AS1	ENSG00000259343	Transcript	ENST00000669758.1	lncRNA
.	15:81414424-81414424	G	regulatory_region_variant	-	-	RegulatoryFeature	ENSR00000995919	enhancer
.	15:81414438-81414438	C	downstream_gene_variant	TMC3-AS1	ENSG00000259343	Transcript	ENST00000558086.1	lncRNA
.	15:81414438-81414438	C	intron_variant, non_coding_transcript_variant	TMC3-AS1	ENSG00000259343	Transcript	ENST00000559781.6	lncRNA
.	15:81414438-81414438	C	intron_variant, non_coding_transcript_variant	TMC3-AS1	ENSG00000259343	Transcript	ENST00000560851.2	lncRNA
.	15:81414438-81414438	C	intron_variant, non_coding_transcript_variant	TMC3-AS1	ENSG00000259343	Transcript	ENST00000642113.1	lncRNA

Uploaded variant	Location	Allele	Consequence	Symbol	Gene	Feature type	Feature	Biotype
.	15:81414438-81414438	C	intron_variant, non_coding_transcript_variant	TMC3-AS1	ENSG00000259343	Transcript	ENST00000654210.1	lncRNA
.	15:81414438-81414438	C	intron_variant, non_coding_transcript_variant	TMC3-AS1	ENSG00000259343	Transcript	ENST00000662589.1	lncRNA
.	15:81414438-81414438	C	intron_variant, non_coding_transcript_variant	TMC3-AS1	ENSG00000259343	Transcript	ENST00000665273.1	lncRNA
.	15:81414438-81414438	C	intron_variant, non_coding_transcript_variant	TMC3-AS1	ENSG00000259343	Transcript	ENST00000667509.1	lncRNA
.	15:81414438-81414438	C	downstream_gene_variant	TMC3-AS1	ENSG00000259343	Transcript	ENST00000669758.1	lncRNA
.	15:81414438-81414438	C	regulatory_region_variant	-	-	RegulatoryFeature	ENSR00000995919	enhancer
.	15:87147870-87147870	C	intergenic_variant	-	-	-	-	-
.	15:87147871-87147871	A	intergenic_variant	-	-	-	-	-
.	15:87147874-87147874	G	intergenic_variant	-	-	-	-	-
.	15:87147878-87147878	C	intergenic_variant	-	-	-	-	-
.	15:87147884-87147884	G	intergenic_variant	-	-	-	-	-
.	15:87147888-87147888	C	intergenic_variant	-	-	-	-	-

Show: 1 5 10 All variants

New job