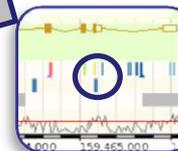


- The **genome** is shown as a blue bar, labeled with contig names
- **Configure this page** to turn on variation tracks
- **Variations** are coloured according to their consequence type

- **Conserved sequences**
- **Transcripts** for the TAGAP gene are aligned to the genome



- **Gene** and transcript locations
- **Allele frequencies** for populations
- **Associated phenotypes**

Location: 6:159,455,500-159,466,184 Gene: TAGAP Variation: rs1738074

Variation class: SNP (rs1738074 source dbSNP_132 - Variants (including SNPs and indels) imported from dbSNP)
 ENSEMBL_ENSNP6836092_ENSNP13172251
 Illumina_HumanE60W-quad rs1738074
 Illumina_CytoSNP12v1 rs1738074
 dbSNP rs58921506
 Illumina_Human1M-duoV3 rs1738074

Present in: Phenotype-associated variations (NHGRI_GWAS_catalog, OMIM), HapMap (HapMap Phase II, HapMap Phase III), Clinical/LSDb variations from dbSNP, ENSEMBL_Ventur, ENSEMBL_Watson, 1000 genomes - Low coverage (1000 genomes - Low coverage - CEU, 1000 genomes - Low coverage - CHB+JPT, 1000 genomes - Low coverage - YRI), 1000 genomes - High coverage - Trios (1000 genomes - High coverage - Trios - CEU, 1000 genomes - High coverage - Trios - YRI)

Alleles: TIC (Ambiguity code: Y)
Ancestral allele: T

Location: This feature maps to 6:159465977 (forward strand) [View in location tab](#)

Phenotype Data

Disease/Trait	Source	Study	Associated Gene(s)	Associated variant	Most associated allele	P value
DIABETES MELLITUS, INSULIN-DEPENDENT, 21 [View on Karyotype]	[OMIM]	MIM:612521	IDDM21	rs1738074		
Celiac disease [View on Karyotype]	[NHGRI_GWAS_catalog]	pubmed/20190752	TAGAP	rs1738074	rs1738074-A	3e-15
CELIAC DISEASE, SUSCEPTIBILITY TO, 12 [View on Karyotype]	[OMIM]	MIM:612910	CELIAC12	rs1738074		
DIABETES MELLITUS, INSULIN-DEPENDENT [View on Karyotype]	[OMIM]	MIM:222100	OAS1, HNF1A, PTPN22, IL6, IDDM1, ITPR3, FOXP3	rs1738074		

▪ **Jump to the location tab**

Follow the blue link to open the variation tab

Click a variation for a detailed pop-up

Variation: rs1738074

rs1738074 properties

bp 6:159465977

Status -

Class SNP

Ambiguity Y

code

Mapweight 1

Alleles T/C

Source ENSEMBL, Illumina_CytoSNP12v1, Illumina_HumanE60W-quad, dbSNP, Illumina_Human1M-duoV3

Type 5PRIME_UTR



- Contextual navigation for a **gene**
- View variations in the genomic **sequence**
- The **variation table** shows variations for a gene
- Use the **variant effect predictor**

Location: 6:159,455,500-159,466,184 **Gene: TAGAP** Variation: rs1738074

Gene: TAGAP (ENSG00000164691)

Description: T-cell activation RhoGTPase activating protein [Source:HGNC Symbol;Acc:15669]

Location: [Chromosome 6: 159,455,500-159,466,184 reverse strand.](#)

Transcripts: There are 4 transcripts in this gene

Name	Transcript ID	Length (bp)	Protein ID	Length (aa)	Biotype	CCDS
TAGAP-001	ENST00000367066	3897	ENSP00000356023	731	Protein coding	CCDS5261
TAGAP-002	ENST00000326365	3051	ENSP00000322650	553	Protein coding	CCDS5262
TAGAP-003	ENST00000338313	1183	ENSP00000340217	266	Protein coding	CCDS5263
TAGAP-201	ENST00000367061	3358	ENSP00000356028	553	Protein coding	CCDS5262

Variation Table [help](#)

Summary of variations in ENSG00000164691 by consequence type

Number of variants	Type	Description
0	Essential splice site	In the first 2 or the last 2 basepairs of an intron
0	Stop gained	In coding sequence, resulting in the gain of a stop codon
0	Stop lost	In coding sequence, resulting in the loss of a stop codon
0	Complex in/del	Insertion or deletion that spans an exon/intron or coding sequence/UTR border
6	Frameshift coding	In coding sequence, resulting in a frameshift
19	Non-synonymous coding	In coding sequence and results in an amino acid change in the encoded peptide sequence
4	Splice site	1-3 bps into an exon or 3-8 bps into an intron
0	Partial codon	Located within the final, incomplete codon of a transcript whose end coordinate is unknown
8	Silent synonymous coding	In coding sequence, not resulting in an amino acid change (silent mutation)

The **transcript table** lists splice variants and has **sortable columns**

Page-specific **help** is available

Click 'Tools' for the **Variant Effect Predictor**

1	881907	881906	-/C	+
5	140532	140532	T/C	+
12	1017956	1017956	T/A	+
2	946507	946507	G/C	+
14	19584687	19584687	C/T	-

Show a table for one **variation type**

0 - Complex in/del

6 [Show](#) Frameshift coding

19 [Show](#) Non-synonymous coding

View variations on the cDNA sequence in the **transcript tab**

```

      R M
1351 CTGGCTTGGATAGCGCGGGCCCACAGGATG
1019 CTGGCTTGGATAGCGCGGGCCACAGGATG
 340 A--G--L--D--S--A--G==P--Q--D--

1381 CCCGAGAGGTCAGCCAGAGCCCATTGTGA
1049 CCCGAGAGGTCAGCCAGAGCCCATTGTGA
 350 A--R--E--V--S--P--E--P--I--V--
    
```

Non-synonymous coding variants

ID	Chr: bp	Alleles	Source	Amino Acid	AA co-ordinate	Transcript
rs13106561	4:123301312	A/C	dbSNP	T/P	30 (1)	ENST00000458011
rs13106730	4:123301310	C/G	dbSNP	A/G	29 (2)	ENST00000458011
rs13106366	4:123301235	A/C	dbSNP	N/T	4 (2)	ENST00000458011
rs13106561	4:123301312	A/C	dbSNP	T/P	30 (1)	ENST00000446706
rs13106730	4:123301310	C/G	dbSNP	A/G	29 (2)	ENST00000446706
rs13106366	4:123301235	A/C	dbSNP	N/T	4 (2)	ENST00000446706
rs13106561	4:123301312	A/C	dbSNP	T/P	30 (1)	ENST00000439307
rs13106730	4:123301310	C/G	dbSNP	A/G	29 (2)	ENST00000439307
rs13106366	4:123301235	A/C	dbSNP	N/T	4 (2)	ENST00000439307
rs13106561	4:123301312	A/C	dbSNP	T/P	12 (1)	ENST00000388725
rs13106730	4:123301310	C/G	dbSNP	A/G	11 (2)	ENST00000388725
rs13106561	4:123301312	A/C	dbSNP	T/P	30 (1)	ENST00000388724
rs13106730	4:123301310	C/G	dbSNP	A/G	29 (2)	ENST00000388724
rs13106561	4:123301235	A/C	dbSNP	N/T	4 (2)	ENST00000388724

Ensembl **transcripts** (splice variants) are listed

Click a **variation ID** to open the variation tab

Possible **amino acids** at a position