HGV&TB: A comprehensive online resource on Human genes and genetic variants associated with Tuberculosis

Home Page:

The home page provides a brief overview to the content of the database. The users can query the database with multiple parameters that include GeneID, rsID, PMID, Technique, Template, Geographic Location, Phenotype and Concluded Pathogenecity. Three examples to access the database with each parameter have also been provided. Important characteristics of the data are shown in the figurative form under the highlights section.



Different types of queries available:

- **Gene:** The searching can be carried out based on gene HGNC symbol.
- * rsID: Searching can also be performed by using rsid. In case you don't remember the entire rsid, you can use a partial rsID as a search query as well.
- **PMID:** The searching can also be performed by using the PMID of the corresponding literature.
- Phenotype: The searching can be carried out based on the tuberculosis phenotype for example, Pulmonary Tuberculosis, Extrapulmonary Tuberculosis etc
- Template: Searching can also be performed by using the detection template like DNA, RNA etc
- **Technique:** Searching can also be performed by using the detection technique like PCR, MALDI-TOF etc.

- **Geographic Location:** Searching can also be performed by using the geographic location of the population studied.
- **Pathogenicity:** Searching can also be performed by the pathogenicity status of the variant.

Database can be accessed by:

Browsing Genes

Example: AKT1 | CCL1 | CCL5

Browsing PMID

Example: 16352737 | 19057661 | 20176143

Browsing Template
Example: DNA | RNA | mRNA
Browsing Phenotype

Example: Tuberculosis | Pulmonary Tuberculosis | Extrapulmonary Tuberculosis

Browsing RSID

Example: rs4586 | rs159290 | rs210837

Browsing Technique

Example: PCR | MALDI-TOF | Genotyping Browsing Geographic Location Example: China | India | Vietnam

Browsing Pathogenicity

Example: Pathogenic | Probably Pathogenic

Query Result:

The result is divided in four different sections namely Gene, Variant, Details and External Links.

Unique **HGVID** has been provided to all the entries within the database.

The **Gene** Section gives information regarding the gene that includes its name, associated haplotypes, location of the gene (Exonic, Intronic, 5' UTR, 3' UTR, Upstream or Downstream), the exon number on which the variant is present and the variation.

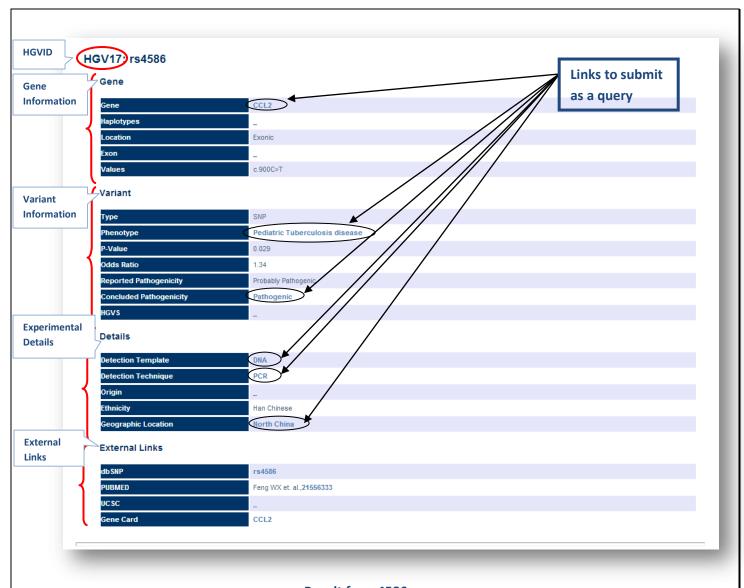
The **Variant** section details the variant information, quoting the type of variation reported in literature, the associated phenotype, the reported p-value and odds ratio corresponding to the variation, the reported and concluded pathogenecity and the HGVS notation for the query.

The **Details** section quotes the experimental details regarding the variant queried. It provides information on the type of detection technique and template used and the origin, ethnicity and geographic location of the sample in which the variation has been found.

The **External Links** section takes the user to dbSNP, PUBMED, UCSC and Gene Card with the variation into consideration.

Gene, Phenotype, Concluded Pathogenecity, Detection Technique, Detection Template and Geographic location in the query result have been linked to query the database as well.

In case of multiple results for a single query, all the sections for each associated result are reported one by one under their unique HGVID.



Result for rs4586 query