Resource Summary Report

Generated by RRID on Aug 4, 2026

IDbases

RRID:SCR_002378
Type: Tool

Proper Citation

IDbases (RRID:SCR_002378)

Resource Information

URL: http://bioinf.uta.fi/base_root/

Proper Citation: IDbases (RRID:SCR_002378)

Description: IDbases are locus-specific databases for immunodeficiency-causing mutations. Our aim is to establish database for every immunodeficiency or provide links to those maintained elsewhere. IDbases contain in addition to gene mutation, also information about clinical presentation. Information has been collected from literature as well as received directly from researchers. It would be most glad if those analyzing mutations would send their information by using the interactive web submission available in each database. A number of articles have been published related to IDbases. IDbases are curated and distributed with proprietary MUTbase software suite.

Synonyms: IDbases

Resource Type: data repository, data or information resource, database, storage service resource, service resource

Defining Citation: PMID:17004234

Keywords: gene, clinical, database, immunodeficiency, immunological database, locus, mutation, presentation, specific

Resource Name: IDbases

Resource ID: SCR_002378

Alternate IDs: nif-0000-21214

Record Creation Time: 20220129T080213+0000

Record Last Update: 20260804T043148+0000

Ratings and Alerts

No rating or validation information has been found for IDbases.

No alerts have been found for IDbases.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 16 mentions in open access literature.

Listed below are recent publications. The full list is available at RRID .

Teku GN, et al. (2017) Simulation of the dynamics of primary immunodeficiencies in CD4+ T-cells. PloS one, 12(4), e0176500.

Benaglio P, et al. (2014) Mutational screening of splicing factor genes in cases with autosomal dominant retinitis pigmentosa. Molecular vision, 20, 843.

Nagy N, et al. (2014) CTSC and Papillon-Lefèvre syndrome: detection of recurrent mutations in Hungarian patients, a review of published variants and database update. Molecular genetics & genomic medicine, 2(3), 217.

Zhao W, et al. (2013) Functional comparison between genes dysregulated in ulcerative colitis and colorectal carcinoma. PloS one, 8(8), e71989.

Shihab HA, et al. (2013) Predicting the functional, molecular, and phenotypic consequences of amino acid substitutions using hidden Markov models. Human mutation, 34(1), 57.

De Lellis L, et al. (2013) Integrative analysis of hereditary nonpolyposis colorectal cancer: the contribution of allele-specific expression and other assays to diagnostic algorithms. PloS one, 8(11), e81194.

Izarzugaza JM, et al. (2012) Interpretation of the consequences of mutations in protein kinases: combined use of bioinformatics and text mining. Frontiers in physiology, 3, 323.

Laurila K, et al. (2011) PROlocalizer: integrated web service for protein subcellular localization prediction. Amino acids, 40(3), 975.

Dalgleish R, et al. (2010) Locus Reference Genomic sequences: an improved basis for describing human DNA variants. Genome medicine, 2(4), 24.

Küntzer J, et al. (2010) Human variation databases. Database : the journal of biological databases and curation, 2010, baq015.

Ortutay C, et al. (2008) PseudoGeneQuest - service for identification of different pseudogene types in the human genome. BMC bioinformatics, 9, 299.

Chun JK, et al. (2008) Analysis of clinical presentations of Bruton disease: a review of 20 years of accumulated data from pediatric patients at Severance Hospital. Yonsei medical journal, 49(1), 28.

Erdos M, et al. (2008) Molecular genetic analysis of Hungarian patients with the hyper-immunoglobulin M syndrome. Molecular immunology, 45(1), 278.

Ortutay C, et al. (2007) ImmTree: database of evolutionary relationships of genes and proteins in the human immune system. Immunome research, 3, 4.

Ortutay C, et al. (2006) Immunome: a reference set of genes and proteins for systems biology of the human immune system. Cellular immunology, 244(2), 87.

Väliaho J, et al. (2005) Distribution of immunodeficiency fact files with XML--from Web to WAP. BMC medical informatics and decision making, 5, 21.