

# Resource Summary Report

Generated by PRECISE-TBI on Sep 8, 2026

## Protein Mutant Database

RRID:SCR\_007878

Type: Tool

### Proper Citation

Protein Mutant Database (RRID:SCR\_007878)

### Resource Information

**URL:** <http://pmd.ddbj.nig.ac.jp/>

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**Description:** It provides information on natural and artificial mutants, including random and site-directed ones, for all proteins except members of the globin and immunoglobulin families. The PMD is based on literature, and each entry in the database corresponds to one article which may describe one, several or a number of protein mutants. Each database entry is identified by a serial number and is defined as either natural or artificial, depending on the type of the mutation. For each entry the following are recorded : JOURNAL, TITLE, CROSS-REFERENCE, PROTEIN, N-TERMINAL, CHANGE, FUNCTION, STRUCTURE, STABILITY, etc. CROSS-REFERENCE indicates the code names of the protein given in other databases such as Protein Identification Resources (2). N-TERMINAL shows the N-terminal sequence of five amino acids which may help to show the unambiguous numbering of the sequence. CHANGE indicates the position and kind of mutations, such as amino acid substitution, insertion and deletion, denoted with a specific notation. Any functional or structural features (FUNCTION, STRUCTURE, STABILITY, etc) observed in the mutant are described immediately after "CHANGE". Relative differences in activity and/or stability, in comparison with the wild-type protein, are indicated with symbols (- -), (-), (=), (+) or (+ +). Complete loss of activity is denoted as (0). Data Submission A data submission system was newly prepared in the PMD. We welcome the authors of articles published in academic journals to submit their own mutant data to the PMD. After checking the contents, we will register the data with a unique accession number.

**Abbreviations:** PMD

**Synonyms:** Protein Mutant Database

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

**Keywords:** amino acid, artificial, deletion, insertion, mutant, natural, protein, sequence, substitution

**Resource Name:** Protein Mutant Database

**Resource ID:** SCR\_007878

**Record Creation Time:** 20220129T080244+0000

**Record Last Update:** 20260905T132615+0000

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## Ratings and Alerts

No rating or validation information has been found for Protein Mutant Database.

No alerts have been found for Protein Mutant Database.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 4 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [PRECISE-TBI](#) .

Verma R, et al. (2012) Computer-Aided Protein Directed Evolution: a Review of Web Servers, Databases and other Computational Tools for Protein Engineering. Computational and structural biotechnology journal, 2, e201209008.

Xi H, et al. (2009) SysPIMP: the web-based systematical platform for identifying human disease-related mutated sequences from mass spectrometry. Nucleic acids research, 37(Database issue), D913.

Guda P, et al. (2007) Conserved motifs in voltage-sensing and pore-forming modules of voltage-gated ion channel proteins. Biochemical and biophysical research communications, 352(2), 292.

Galperin MY, et al. (2005) The Molecular Biology Database Collection: 2005 update. Nucleic acids research, 33(Database issue), D5.