

Resource Summary Report

Generated by T1D on Aug 1, 2026

Cube-DB

RRID:SCR_013233

Type: Tool

Proper Citation

Cube-DB (RRID:SCR_013233)

Resource Information

URL: <http://epsf.bmad.bii.a-star.edu.sg/cube/db/html/home.html>

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Description: Cube-DB is a database of pre-evaluated conservation and specialization scores for residues in paralogous proteins belonging to multi-member families of human proteins. Protein family classification follows (largely) the classification suggested by HUGO Gene Nomenclature Committee. Sets of orthologous protein sequences were generated by mutual-best-hit strategy using full vertebrate genomes available in Ensembl. The scores, described on documentation page, are assigned to each individual residue in a protein, and presented in the form of a table (html or downloadable xls formats) and mapped, when appropriate, onto the related structure (Jmol, Pymol, Chimera).

Abbreviations: Cube-DB

Synonyms: Cube-DB: Detection of Functional Divergence in Human Protein Families

Resource Type: data or information resource, database

Defining Citation: [PMID:22139934](#)

Keywords: protein, functional divergence, vertebrate, genome, ortholog, protein sequence, data set, bio.tools

Resource Name: Cube-DB

Resource ID: SCR_013233

Alternate IDs: nlx_149432, biotools:cube-db

Alternate URLs: <https://bio.tools/cube-db>

Record Creation Time: 20220129T080315+0000

Record Last Update: 20260801T191021+0000

Ratings and Alerts

No rating or validation information has been found for Cube-DB.

No alerts have been found for Cube-DB.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 3 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#) .

Nemoto W, et al. (2013) Recent advances in functional region prediction by using structural and evolutionary information - Remaining problems and future extensions. Computational and structural biotechnology journal, 8, e201308007.

Zhang ZH, et al. (2012) Cube-DB: detection of functional divergence in human protein families. Nucleic acids research, 40(Database issue), D490.

Galperin MY, et al. (2012) The 2012 Nucleic Acids Research Database Issue and the online Molecular Biology Database Collection. Nucleic acids research, 40(Database issue), D1.