

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

PhyloFacts

RRID:SCR_007849

Type: Tool

Proper Citation

PhyloFacts (RRID:SCR_007849)

Resource Information

URL: <http://phylogenomics.berkeley.edu/phylofacts/>

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Description: It contains pre-calculated structural and phylogenomic analyses of over 57,000 protein families and domains. The PhyloFacts resource includes "books" for protein families across the Tree of Life. Each book includes a multiple sequence alignment, one or more phylogenetic trees, predicted subfamilies, predicted 3D protein structures, active sites and other key residues, cellular localization, and Gene Ontology (GO) annotations and evidence codes. PhyloFacts includes hidden Markov models for classification of user-submitted (DNA or protein) sequences to protein families and subfamilies across the tree of life. Our primary current focus is on covering all the gene families represented in the human genome and all structural domains, but plan to expand the resource to include all proteins in all species. The protein families in this resource typically contain homologs from many species. The phylogenetic distribution of a protein family can vary from highly restricted (e.g., to hominidae or mammals) to throughout the tree of life. Gathering homologs from many divergent species enables us to take advantage of experimental investigations in different systems, and allows powerful inferences of function and structure that might not otherwise be possible.

Synonyms: PhyloFacts

Resource Type: data or information resource, database

Resource Name: PhyloFacts

Resource ID: SCR_007849

Alternate IDs: nif-0000-03280

Record Creation Time: 20220129T080244+0000

Record Last Update: 20260905T133146+0000

Ratings and Alerts

No rating or validation information has been found for PhyloFacts.

No alerts have been found for PhyloFacts.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 4 mentions in open access literature.

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

Friesen ML, et al. (2014) The ecological genomic basis of salinity adaptation in Tunisian *Medicago truncatula*. BMC genomics, 15(1), 1160.

Pieper U, et al. (2011) ModBase, a database of annotated comparative protein structure models, and associated resources. Nucleic acids research, 39(Database issue), D465.

Kordis D, et al. (2009) Phylogenomic analysis of the cystatin superfamily in eukaryotes and prokaryotes. BMC evolutionary biology, 9, 266.

Krishnamurthy N, et al. (2006) PhyloFacts: an online structural phylogenomic encyclopedia for protein functional and structural classification. Genome biology, 7(9), R83.