

Resource Summary Report

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SIMAP

RRID:SCR_007927

Type: Tool

Proper Citation

SIMAP (RRID:SCR_007927)

Resource Information

URL: <http://mips.gsf.de/simap/>

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Description: It provides a database based on a pre-computed similarity matrix covering the similarity space formed by >4 million amino acid sequences from public databases and completely sequenced genomes. The database is capable of handling very large datasets and is updated incrementally. For sequence similarity searches and pairwise alignments, we implemented a grid-enabled software system, which is based on FASTA heuristics and the Smith Waterman algorithm. SimpleSIMAP and AdvancedSIMAP retrieve homologs for given protein sequences that need to be contained in the SIMAP database. While SimpleSIMAP provides only selected parameters and preconfigured search spaces, the AdvancedSIMAP allows the user to specify search space, filtering and sorting parameters in a flexible manner. Both types of queries result in lists of homologs that are linked in turn to their homologs. So the web interfaces allow users to explore quickly and interactively the protein world by homology. Sponsors: SIMAP is supported by the Department of Genome Oriented Bioinformatics of the Technische Universitt Mnchen and the Institute for Bioinformatics of the GSF-National Research Center for Environment and Health.

Abbreviations: SIMAP

Synonyms: The Similarity Matrix of Proteins, Similarity Matrix of Proteins

Resource Type: data or information resource, database

Keywords: genome, alignment, amino acid, homolog, matrix, protein, protein domain and protein classification databases, sequence

Resource Name: SIMAP

Resource ID: SCR_007927

Record Creation Time: 20220129T080244+0000

Ratings and Alerts

No rating or validation information has been found for SIMAP.

No alerts have been found for SIMAP.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 14 mentions in open access literature.

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

La Paglia L, et al. (2025) Bioinformatics analyses of the proteome of *Holothuria tubulosa* coelomic fluid and the first evidence of primary cilium in coelomocyte cells. *Frontiers in immunology*, 16, 1539751.

Sarton-Lohéac G, et al. (2025) Reconstructing Evolutionary Histories with Hierarchical Orthologous Groups. *Journal of molecular evolution*, 93(6), 740.

Alejandro C, et al. (2024) Synergistic epistasis among cancer drivers can rescue early tumors from the accumulation of deleterious passengers. *PLoS computational biology*, 20(4), e1012081.

Dukes E, et al. (2023) Footprints in Action: How UVA Is Managing Its Sustainability Stewardship. *Sustainability and climate change*, 16(1), 48.

Doncheva NT, et al. (2023) Cytoscape stringApp 2.0: Analysis and Visualization of Heterogeneous Biological Networks. *Journal of proteome research*, 22(2), 637.

Kim W, et al. (2022) Transcriptional Divergence Underpinning Sexual Development in the Fungal Class Sordariomycetes. *mBio*, 13(3), e0110022.

Freitas LGA, et al. (2020) Time-resolved effective connectivity in task fMRI: Psychophysiological interactions of Co-Activation patterns. *NeuroImage*, 212, 116635.

Nicolopoulos S, et al. (2019) Novel TEM Microscopy and Electron Diffraction Techniques to Characterize Cultural Heritage Materials: From Ancient Greek Artefacts to Maya Mural Paintings. *Scanning*, 2019, 4870695.

Juárez OE, et al. (2018) Transcriptomic and metabolic response to chronic and acute thermal exposure of juvenile geoduck clams *Panopea globosa*. *Marine genomics*, 42, 1.

Galperin MY, et al. (2017) The 24th annual Nucleic Acids Research database issue: a look back and upcoming changes. *Nucleic acids research*, 45(D1), D1.

Pan ST, et al. (2016) Computational Identification of the Paralogs and Orthologs of Human Cytochrome P450 Superfamily and the Implication in Drug Discovery. *International journal of molecular sciences*, 17(7).

Esmailian P, et al. (2015) Community Detection in Signed Networks: the Role of Negative ties in Different Scales. *Scientific reports*, 5, 14339.

Ried CL, et al. (2012) Homotypic interaction and amino acid distribution of unilaterally conserved transmembrane helices. *Journal of molecular biology*, 420(3), 251.

Herrmann JR, et al. (2009) Complex patterns of histidine, hydroxylated amino acids and the GxxxG motif mediate high-affinity transmembrane domain interactions. *Journal of molecular biology*, 385(3), 912.