

Resource Summary Report

Generated by [nidm-terms](#) on Jul 28, 2026

SURFACE: Surface Residues and Functions Annotated, Compared and Evaluated

RRID:SCR_007953

Type: Tool

Proper Citation

SURFACE: Surface Residues and Functions Annotated, Compared and Evaluated
(RRID:SCR_007953)

Resource Information

URL: <http://cbm.bio.uniroma2.it/surface>

Proper Citation: SURFACE: Surface Residues and Functions Annotated, Compared and Evaluated (RRID:SCR_007953)

Description: A database containing the results of a large-scale protein annotation and local structural comparison project. A non-redundant set of protein chains is used to build a database of protein surface patches, defined as putative surface functional sites. Each patch is annotated with sequence and structure-derived information about function or interaction abilities. Users can search the annotations and the results of the surface patches comparisons stored in the DB based on PDB code, PROSITE pattern, or ligand. A new procedure for structure comparison is used to exert an all-versus-all patches comparison. Selection of the results obtained with stringent parameters offers a similarity score that can be used to associate different patches and may allow reliable annotation by similarity. protein, protein structure, structural comparison, protein ligand, protein surface, protein morphology

Synonyms: SURFACE

Resource Type: database, data or information resource

Keywords: protein, protein ligand, protein morphology, protein structure, protein surface, structural comparison

Resource Name: SURFACE: Surface Residues and Functions Annotated, Compared and Evaluated

Resource ID: SCR_007953

Alternate IDs: nif-0000-03518

Record Creation Time: 20220129T080244+0000

Record Last Update: 20260725T191151+0000

Ratings and Alerts

No rating or validation information has been found for SURFACE: Surface Residues and Functions Annotated, Compared and Evaluated.

No alerts have been found for SURFACE: Surface Residues and Functions Annotated, Compared and Evaluated.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 21 mentions in open access literature.

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

Pereyra EES, et al. (2025) Morphology of the maxilla informs about the type of predation strategy in the evolution of Abelisauridae (Dinosauria: Theropoda). Scientific reports, 15(1), 7857.

Rubin JJ, et al. (2025) Strong bat predation and weak environmental constraints predict longer moth tails. Proceedings. Biological sciences, 292(2046), 20242824.

Dean LL, et al. (2023) On the Origins of Phenotypic Parallelism in Benthic and Limnetic Stickleback. Molecular biology and evolution, 40(9).

Smith EG, et al. (2023) Micro and macroevolution of sea anemone venom phenotype. Nature communications, 14(1), 249.

Church SH, et al. (2022) Phylotranscriptomics Reveals Discordance in the Phylogeny of Hawaiian Drosophila and Scaptomyza (Diptera: Drosophilidae). Molecular biology and evolution, 39(3).

Park T, et al. (2019) Convergent evolution in toothed whale cochleae. BMC evolutionary biology, 19(1), 195.

Godoy PL, et al. (2019) The multi-peak adaptive landscape of crocodylomorph body size evolution. BMC evolutionary biology, 19(1), 167.

García-Navas V, et al. (2018) Environmental determinism, and not interspecific competition, drives morphological variability in Australasian warblers (Acanthizidae). Ecology and evolution, 8(8), 3871.

Rubin JJ, et al. (2018) The evolution of anti-bat sensory illusions in moths. *Science advances*, 4(7), eaar7428.

Aguilar-Puntriano C, et al. (2018) The shadow of the past: Convergence of young and old South American desert lizards as measured by head shape traits. *Ecology and evolution*, 8(23), 11399.

Faria SC, et al. (2017) Phylogenetic patterns and the adaptive evolution of osmoregulation in fiddler crabs (*Brachyura*, *Uca*). *PloS one*, 12(2), e0171870.

Martin B, et al. (2017) A Bayesian Perspective on Accumulation in the Magnitude System. *Scientific reports*, 7(1), 630.

Romão CV, et al. (2016) Structure of *Escherichia coli* Flavodiiron Nitric Oxide Reductase. *Journal of molecular biology*, 428(23), 4686.

Szitenberg A, et al. (2016) Genetic Drift, Not Life History or RNAi, Determine Long-Term Evolution of Transposable Elements. *Genome biology and evolution*, 8(9), 2964.

Ma RY, et al. (2015) Convergent Evolution towards High Net Carbon Gain Efficiency Contributes to the Shade Tolerance of Palms (*Arecaceae*). *PloS one*, 10(10), e0140384.

Astudillo-Clavijo V, et al. (2015) Selection towards different adaptive optima drove the early diversification of locomotor phenotypes in the radiation of Neotropical geophagine cichlids. *BMC evolutionary biology*, 15, 77.

Chen Y, et al. (2009) Crystal structure of myeloid cell activating receptor leukocyte Ig-like receptor A2 (LILRA2/ILT1/LIR-7) domain swapped dimer: molecular basis for its non-binding to MHC complexes. *Journal of molecular biology*, 386(3), 841.

Velikovsky CA, et al. (2009) Structure of a lamprey variable lymphocyte receptor in complex with a protein antigen. *Nature structural & molecular biology*, 16(7), 725.

Merelli I, et al. (2005) High performance workflow implementation for protein surface characterization using grid technology. *BMC bioinformatics*, 6 Suppl 4(Suppl 4), S19.

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