

Resource Summary Report

Generated by [SPARC SAWG](#) on Sep 16, 2026

Conservation

RRID:SCR_016064

Type: Tool

Proper Citation

Conservation (RRID:SCR_016064)

Resource Information

URL: <http://compbio.cs.princeton.edu/conservation/>

Proper Citation: Conservation (RRID:SCR_016064)

Description: Software for scoring protein sequence conservation using the Jensen-Shannon divergence. It can be used to predict catalytic sites and residues near bound ligands.

Synonyms: Conservation-code

Resource Type: software application, software resource, software toolkit

Defining Citation: [PMID:17519246](#)

Keywords: scoring, protein, sequence, conservation, Jensen-Shannon, divergence, predict, catalytic, site, bound, ligands, clustal, fasta, concave

Funding: NIGMS GM076275;
NIH P50 GM071508;
NIH T32 HG003284;
NSF IIS-0612231;
NSF PECASE MCB-0093399

Availability: Free, Available for download

Resource Name: Conservation

Resource ID: SCR_016064

License: GNU General Public License

Record Creation Time: 20220129T080328+0000

Record Last Update: 20260912T200253+0000

Ratings and Alerts

No rating or validation information has been found for Conservation.

No alerts have been found for Conservation.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1606 mentions in open access literature.

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

Gao C, et al. (2026) Enhance the annotation of long noncoding RNAs in the duck genome using multi-tissue transcriptome data. Poultry science, 105(2), 106239.

Jiang F, et al. (2026) Functional Screening of NDUFAF6 Variants in Knockout Cells and Complementary Computational Analysis. Journal of clinical laboratory analysis, 40(1), e70147.

Öner BM, et al. (2026) Genome-wide analysis of Phaseolus vulgaris L. miR172 gene family members under heavy metal stress. BMC genomics, 27(1), 135.

Jurynek MJ, et al. (2026) PIEZO1 variants that reduce open channel probability are associated with familial osteoarthritis. The Journal of biological chemistry, 302(5), 111426.

Roselli C, et al. (2026) Culture and anthropomorphism towards robots in middle school students: evidence from human-robot interaction. Scientific reports, 16(1).

Bowler AI, et al. (2026) Assessing Loggerhead Turtle Exposure to Fisheries in Northwest Africa: Predicted Risk and Management Gaps. Ecology and evolution, 16(6), e73729.

Kline BL, et al. (2026) RNA exosome component EXOSC10 variants identified in a patient with premature ovarian insufficiency†. Biology of reproduction, 114(4), 1416.

Cha?upczy?ska B, et al. (2026) Molecular Profiling of Polish Pediatric Patients with Epilepsy: A Single-Center Diagnostic Experience Using Next-Generation Sequencing. Genes, 17(2).

Hoff KJ, et al. (2026) Role of γ -tubulin helix 11' in heterodimer conformation and microtubule dynamics. bioRxiv : the preprint server for biology.

Barragán-Zúñiga J, et al. (2026) Hormone-Specific Reprogramming of the Phenylpropanoid Network in Juvenile Quercus sideroxyla Leaves Revealed by Targeted Metabolomics. Plants (Basel, Switzerland), 15(4).

Waqas M, et al. (2026) StabLyzeGraph: High-throughput screening of combinatorial mutations using graph neural networks. Protein science : a publication of the Protein

Society, 35(4), e70534.

Mouren JC, et al. (2026) Exonic enhancers are a widespread class of dual-function regulatory elements. *Nature communications*, 17(1).

Khadka S, et al. (2026) In silico design of a multiepitope vaccine against antibiotic drug-resistant *Acinetobacter baumannii*. *Scientific reports*, 16(1).

Su J, et al. (2026) Identification of a new frameshift homozygous variant of PEX3 gene in a preterm infant with profound global developmental delay and bilateral ptosis: a case report and updated literature review. *BMC pediatrics*, 26(1), 81.

Baldelli V, et al. (2026) The *Pseudomonas aeruginosa* sirB2 gene is a fitness determinant of anaerobic growth and its inactivation affects virulence and rugose small colony variants emergence. *Virulence*, 17(1), 2605800.

Islam N, et al. (2026) Single nucleotide polymorphisms affecting galantamine binding to acetylcholinesterase in Alzheimer's disease: a structural bioinformatics study. *Journal of computer-aided molecular design*, 40(1).

Micka M, et al. (2026) A Wnt-induced conformational phospho-switch in DVL3 controls association with Frizzled receptors and Wnt/ β -catenin signaling. *Science advances*, 12(20), eaed8899.

Peeples SM, et al. (2026) Asparaginyl-tRNA synthetase (NARS1) variants implicated in dominant neurological phenotypes display dominant-negative properties. *HGG advances*, 7(1), 100519.

Zhang H, et al. (2026) PON-Del predictor for sequence retaining protein deletions. *PLoS computational biology*, 22(2), e1014020.

Amaral EOS, et al. (2026) Mapping Patterns of G-Quadruplex-Forming Sequence Conservation in Primates. *Journal of molecular evolution*, 94(3), 455.