Resource Summary Report

Generated by NIF on Aug 12, 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: NIH T32 HG003284;
NSF IIS-0612231;
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NIGMS GM076275;
NIH P50 GM071508

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: 20260812T044314+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 NIF .

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.

Jurynec 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.

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).

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

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).

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).

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.

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

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.

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.

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.

Zhang Z, et al. (2026) Splicing mutation in DSPP causes dentinogenesis imperfecta and amelogenesis imperfecta. BMC oral health, 26(1).

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

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).