

Resource Summary Report

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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;
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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: 20260919T195814+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 [dkNET](#) .

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.

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.

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.

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.

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

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.

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 γ -tubulin helix 11' in heterodimer conformation and microtubule dynamics. *bioRxiv : the preprint server for biology*.

Chałupczyńska 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.

Peebles 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).