

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 toolkit, software resource, software application

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: 20260731T042959+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 1564 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

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

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.

Hagemann N, et al. (2025) Arterial specification precedes microvascular restitution in the peri-infarct cortex that is driven by small microvessels. Journal of cerebral blood flow and metabolism : official journal of the International Society of Cerebral Blood Flow and Metabolism, 45(1), 171.

Takasaki Y, et al. (2025) Pervasive Indigenous and local knowledge of tropical wild species. Ambio, 54(4), 680.

Chaiya C, et al. (2025) Empowering climate resilience: A people-centered exploration of Thailand's greenhouse gas emissions trading and sustainable environmental development through climate risk management in community forests. Heliyon, 11(2), e41844.

Anderson EC, et al. (2025) gscramble: Simulation of Admixed Individuals Without Reuse of Genetic Material. Molecular ecology resources, 25(4), e14069.

Mangione RM, et al. (2025) DNA lesions can frequently precede DNA:RNA hybrid accumulation. Nature communications, 16(1), 2401.

Smenderovac E, et al. (2025) Mixed Model Approaches Can Leverage Database Information to Improve the Estimation of Size-Adjusted Contaminant Concentrations in Fish Populations. Environmental science & technology, 59(10), 4797.

Kjeldsen CMN, et al. (2025) The Proteinase PAPP-A has Deep Evolutionary Roots Outside of the IGF System. Genome biology and evolution, 17(3).

Wang Y, et al. (2025) Three novel heterozygous ANK1 loss-of-function variants cause hereditary spherocytosis in Chinese families. *Annals of hematology*, 104(8), 4045.

Agarwal M, et al. (2025) "In silico analysis of human TLR3 missense single nucleotide polymorphisms and their potential association with cancer". *Scientific reports*, 15(1), 30837.

Erberich JM, et al. (2025) SPEECHLESS duplication in grasses expands potential for environmental regulation of stomatal development. *bioRxiv : the preprint server for biology*.

Boneh-Shitrit T, et al. (2025) A segment-based framework for explainability in animal affective computing. *Scientific reports*, 15(1), 13670.

Kleist AB, et al. (2025) Encoding and decoding selectivity and promiscuity in the human chemokine-GPCR interaction network. *Cell*, 188(13), 3603.

Cui X, et al. (2025) CREATE: cell-type-specific cis-regulatory element identification via discrete embedding. *Nature communications*, 16(1), 4607.

Luo D, et al. (2025) Exploiting functional regions in the viral RNA genome as druggable entities. *eLife*, 13.

Wei R, et al. (2025) Clinical characteristics and genetic mutation analysis in 18 pediatric patients with Shwachman-Diamond syndrome. *Frontiers in genetics*, 16, 1603782.

Tassinari M, et al. (2025) Molecular mechanism of thyroxine transport by monocarboxylate transporters. *Nature communications*, 16(1), 4493.

Abuagla HA, et al. (2025) Impact of nonsynonymous single nucleotide polymorphisms in PROCR gene on protein stability and thrombotic risk: a molecular dynamic approach. *Frontiers in genetics*, 16, 1580993.

Kilpinen S, et al. (2025) Gene regulatory mechanisms guiding bifurcation of inhibitory and excitatory neuron lineages in the mouse anterior brainstem. *eLife*, 14.