

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 [PRECISE-TBI](#) .

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.