

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

RASP

RRID:SCR_012062

Type: Tool

Proper Citation

RASP (RRID:SCR_012062)

Resource Information

URL: <http://sourceforge.net/projects/raspmr/>

Proper Citation: RASP (RRID:SCR_012062)

Description: Software that uses structure-based chemical shift predictions to solve the backbone resonance assignment problem in protein NMR spectroscopy.

Resource Type: software resource

Defining Citation: [PMID:24445369](https://pubmed.ncbi.nlm.nih.gov/24445369/)

Keywords: standalone software, python

Resource Name: RASP

Resource ID: SCR_012062

Alternate IDs: OMICS_03392

Record Creation Time: 20220129T080308+0000

Record Last Update: 20260905T132719+0000

Ratings and Alerts

No rating or validation information has been found for RASP.

No alerts have been found for RASP.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 347 mentions in open access literature.

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

Wan T, et al. (2026) Phylogeography and evolutionary history of *Prunus tomentosa* in China: guiding germplasm conservation and development. *BMC plant biology*, 26(1).

Chen Q, et al. (2026) Full spatio-temporal analyses of migration and colonization in evolution-dense 3D mapping of cancer metastases provides new insights. *Molecular biology and evolution*, 43(2).

Luo T, et al. (2026) Evolutionary history of Chinese cavefishes parallels paleogeoclimatic and river capture processes. *Communications biology*, 9(1).

Dissanayake D, et al. (2026) Predicting pyrazinamide resistance in *Mycobacterium tuberculosis* using a graph convolutional network. *BMC microbiology*, 26(1).

Almerekova S, et al. (2026) Phylogenomics, divergence time estimation, and biogeography of *Iris* species from Kazakhstan using plastome sequence analysis. *Frontiers in plant science*, 17, 1860819.

Ahn KJ, et al. (2026) Global diversification of coastal *Cafius* rove beetles (Coleoptera: Staphylinidae) driven by ocean currents since the early Miocene. *Cladistics : the international journal of the Willi Hennig Society*, 42(1), 79.

de Abreu J, et al. (2026) High-Throughput Sequencing Supports Strong Geographical Patterns in the *Cladia aggregata* Complex (Ascomycota, Lecanorales) and Identifies the Asian Clade as an Independent Species. *Journal of fungi (Basel, Switzerland)*, 12(2).

Douglas GM, et al. (2026) DEX: a consensus-based amino acid exchangeability measure for improved codon substitution modelling. *bioRxiv : the preprint server for biology*.

Sun X, et al. (2026) Comparative genomic and phylogenetic analyses of *Crataegus* chloroplast genomes: insights for evolution and identification. *Frontiers in plant science*, 17, 1767012.

Kim YG, et al. (2026) Plastome-based phylogeny and historical biogeography of *Erythronium* L. *BMC plant biology*, 26(1).

Xiao JM, et al. (2026) Worldwide phylogeny and integrative taxonomy of *Clematis*: Insights from phylogenomics. *Plant diversity*, 48(1), 16.

Starr AL, et al. (2026) Adaptive loss of function accelerated the evolution of ancient and modern human cognition. *bioRxiv : the preprint server for biology*.

Gaiddon T, et al. (2026) Behaviour-structure interplay drives acoustic signal divergence: emergence of multiple mechanisms in closely related crickets. *PeerJ*, 14, e21036.

Huang XP, et al. (2026) Phylogeography of *Cranoglanis* (Teleostei: Cranoglanididae) Reveals Discordance Between Nominal Species and Maternal Lineages: A Broadly

Distributed Clade Co-Occurring with a Cryptic Endemic in the Pearl River. *Animals* : an open access journal from MDPI, 16(11).

Setti A, et al. (2026) The role of low-complexity repeats in RNA-RNA interactions and a deep learning framework for duplex prediction. *Nature communications*, 17(1), 1637.

Li H, et al. (2026) Plastid phylogenomics illuminates backbone relationships, divergence times and character evolution in Caryophyllaceae. *BMC plant biology*, 26(1).

Ualiyeva D, et al. (2026) Mitochondrial genomic variations shed light on the phylogeny and biogeography of the *Phrynocephalus guttatus* species group (Reptilia: Agamidae) in arid Central Asia. *BMC genomics*, 27(1), 176.

Huang X, et al. (2026) The phylogeny and evolution of blow flies (Diptera: Calliphoridae) from the perspective of mitogenomics. *BMC genomics*, 27(1), 180.

Ranaivoson RM, et al. (2026) Plastid and nuclear phylogenomics of *Cyphostemma* (Vitaceae) provide new insights into genome size evolution across sub-Saharan Africa. *Journal of integrative plant biology*, 68(5), 1399.

Arnaudi M, et al. (2026) MAVISp: A modular structure-based framework for protein variant effects. *Protein science : a publication of the Protein Society*, 35(5), e70548.