

Resource Summary Report

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SINA

RRID:SCR_005067

Type: Tool

Proper Citation

SINA (RRID:SCR_005067)

Resource Information

URL: <http://www.arb-silva.de/aligner/>

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Description: Service to align and optionally taxonomically classify your rRNA gene sequences. The results can be combined with any other sequences aligned by SINA or taken from the SILVA databases by concatenation of FASTA files or using the ARB MERGE tool. Note: Submission is currently limited to at most 1000 sequences of at most 6000 bases each. If your requirements exceed this limitation, get Opens internal link in current windowSINA for local installation.

Abbreviations: SINA

Synonyms: SINA Alignment Service, SILVA Incremental Aligner

Resource Type: data analysis service, service resource, production service resource, software resource, analysis service resource

Defining Citation: [PMID:22556368](#)

Keywords: alignment, taxonomic classification, rrna, gene sequence, fasta, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: SINA

Resource ID: SCR_005067

Alternate IDs: OMICS_01438, biotools:sina

Alternate URLs: <https://bio.tools/sina>, <https://sources.debian.org/src/sina/>, <https://github.com/epruesse/SINA>

Record Creation Time: 20220129T080228+0000

Ratings and Alerts

No rating or validation information has been found for SINA.

No alerts have been found for SINA.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 369 mentions in open access literature.

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

Park J, et al. (2025) An experimental test of the influence of microbial manipulation on sugar kelp (*Saccharina latissima*) supports the core influences host function hypothesis. *Applied and environmental microbiology*, 91(6), e0030125.

Intze E, et al. (2025) The infant microbiota hopscotches between community states toward maturation-longitudinal stool parameters and microbiota development in a cohort of European toddlers. *ISME communications*, 5(1), ycaf016.

Böswald LF, et al. (2025) Fibre supplementation alters the gastrointestinal microbiome, the microbial metabolites and indicators of neurodegeneration in a mouse model of Alzheimer's disease. *Scientific reports*, 15(1), 32705.

Wolf S, et al. (2025) Microbial carbon oxidation in seawater below the hypoxic threshold. *Scientific reports*, 15(1), 2838.

Farrell AA, et al. (2025) Bacterial Growth Temperature as a Horizontally Acquired Polygenic Trait. *Genome biology and evolution*, 17(1).

Crull S, et al. (2025) Seasonal Host Shifts for *Legionella* Within an Industrial Water-Cooling System. *Environmental microbiology reports*, 17(4), e70132.

Fechtner S, et al. (2025) 3,3-Dimethyl-1-Butanol and its Metabolite 3,3-Dimethylbutyrate Ameliorate Collagen-induced Arthritis Independent of Choline Trimethylamine Lyase Activity. *Inflammation*, 48(3), 1350.

Viver T, et al. (2025) Comparative metagenomics indicates metabolic niche differentiation of benthic and planktonic Woeseiaceae. *Environmental microbiome*, 20(1), 74.

Liu Y, et al. (2025) Methane filtration and metabolic cooperation of microbial communities in cold seep water columns from South China Sea. *Communications biology*, 8(1), 1052.

de Sosa I, et al. (2025) No Mate, No Problem: Molecular Mechanisms Involved in Parthenogenesis in the Cosmopolitan Earthworm *Aporrectodea trapezoides* (Annelida, Clitellata). *Molecular ecology*, 34(16), e70010.

Shepherd RM, et al. (2025) The Biogeography of Apicomplexan Parasites in Tropical Soils. *Ecology and evolution*, 15(6), e71478.

Miralles-Lorenzo J, et al. (2025) Environmental Gradients and Conservation Status Determine the Structure and Carbon-Related Metabolic Potential of the Prokaryotic Communities of Mediterranean Inland Saline Shallow Lakes. *Ecology and evolution*, 15(5), e71286.

Kujala K, et al. (2025) Enrichment and characterization of steroid-degrading microbes for targeted removal of steroid hormone micropollutants in small-scale wastewater treatment solutions. *Microbiology spectrum*, 13(11), e0064925.

Dregni J, et al. (2025) Wolbachia-mediated parthenogenesis induction in the aphid hyperparasitoid *Alloxysta brevis* (Hymenoptera: Figitidae: Charipinae). *Applied and environmental microbiology*, 91(12), e0130825.

Wittlinger J-P, et al. (2025) *Shewanella* is a putative producer of polyunsaturated fatty acids in the gut soil of the composting earthworm *Eisenia fetida*. *Applied and environmental microbiology*, 91(2), e0206924.

Schalch-Schuler M, et al. (2025) The planktonic freshwater ciliate *Balanion planctonicum* (Ciliophora, Prostomatea): A cryptic species complex or a "complex species"? *The Journal of eukaryotic microbiology*, 72(1), e13084.

Arnesen H, et al. (2025) Comparison of naturalization mouse model setups uncover distinct effects on intestinal mucosa depending on microbial experience. *Discovery immunology*, 4(1), kyaf002.

Schagerl M, et al. (2025) Testing the Purity of *Limnospira fusiformis* Cultures After Axenicity Treatments. *Cells*, 14(2).

Turon M, et al. (2025) The archaeal class *Nitrososphaeria* is a key component of the reproductive microbiome in sponges during gametogenesis. *mBio*, 16(6), e0201924.

Vladar EK, et al. (2025) Transcriptomic and functional responses of the cystic fibrosis airway epithelium to CFTR modulator therapy. *JCI insight*, 10(21).