

# Resource Summary Report

Generated by [NIF](#) on Aug 29, 2026

## ALTER

RRID:SCR\_015968

Type: Tool

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### Proper Citation

ALTER (RRID:SCR\_015968)

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### Resource Information

**URL:** <http://sing.ei.uvigo.es/ALTER/>

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**Description:** Web application to perform program-oriented conversion of DNA and protein alignments and transform between multiple sequence alignment formats. ALTER focuses on the specifications of mainstream alignment and analysis programs rather than on the conversion among more or less specific formats.

**Synonyms:** ALTER: ALignment Transformation EnviRonment, ALignment Transformation EnviRonment

**Resource Type:** alignment software, data analysis software, data processing software, image analysis software, sequence analysis software, software application, software resource, web application

**Defining Citation:** [PMID:20439312](#), [DOI:10.1093/nar/gkq321](#)

**Keywords:** Alignment conversion, genome, sequence, DNA, protein, format alignment, phylogenetics, bio.tools

**Funding:** European Research Council ERC-2007-Stg 203161-PHYGENOM to D.P.; INBIOMED initiative ; Spanish Ministry of Science and Education BFU2009-08611 to D.P.; University of Vigo 09VIB10 to F.F.-R.; Xunta de Galicia PGIDIT07PXIB310202PR to D.P.

**Availability:** Freely available, Free, Available for download

**Resource Name:** ALTER

**Resource ID:** SCR\_015968

**Alternate IDs:** OMICS\_19786, biotools:alter

**Alternate URLs:** <https://github.com/sing-group/ALTER>, <https://bio.tools/alter>, <https://sources.debian.org/src/alter-sequence-alignment/>

**License:** GNU Lesser General Public License v3.0

**Record Creation Time:** 20220129T080328+0000

**Record Last Update:** 20260821T194031+0000

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## Ratings and Alerts

No rating or validation information has been found for ALTER.

No alerts have been found for ALTER.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 125 mentions in open access literature.

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

Tian XG, et al. (2026) Taxonomic and phylogenetic analyses reveal two new *Comoclathris* taxa (Dothideomycetes, Pleosporaceae) from Inner Mongolia, China. *MycoKeys*, 129, 107.

Meng W, et al. (2026) Two new species of *Ceratostomella* and *Pararamichloridium* (Sordariomycetes) from Guangdong, China, based on morphological and phylogenetic evidence. *MycoKeys*, 133, 259.

Purohit D, et al. (2026) Impact of High-Dose Rifampicin on Linezolid Pharmacokinetics in Tuberculous Meningitis. *Open forum infectious diseases*, 13(4), ofag154.

Derouiche L, et al. (2026) Genetic evidence for the rediscovery in the wild of the critically endangered Sahara killifish *Apricaphanius saurensis* (Cyprinodontiformes: Aphaniidae). *Die Naturwissenschaften*, 113(1), 21.

Shen HW, et al. (2026) Morpho-phylogenetic evidence uncovers new taxa of lignicolous freshwater Sordariomycetes from Yunnan and Guizhou provinces, China. *MycoKeys*, 128, 97.

Yuan Q, et al. (2026) Morphological and molecular identification of three new bamboo-inhabiting species of *Nigrochaete* (Auriculariales, Basidiomycota) from China. *MycoKeys*, 132, 191.

Sooksawasdi Na Ayudhya S, et al. (2025) Attachment Patterns of Avian Influenza H5 Clade 2.3.4.4b Virus in Respiratory Tracts of Marine Mammals, North Atlantic Ocean. *Emerging infectious diseases*, 31(9), 1729.

Absalan S, et al. (2025) Morpho-Molecular Characterization of Hypocrealean Fungi Isolated from Rice in Northern Thailand. *Journal of fungi (Basel, Switzerland)*, 11(4).

Li Q, et al. (2025) A vetiver-specific terpene synthase VzTPS9 contributes to the high attractiveness of vetiver to rice stem borer. *Proceedings of the National Academy of Sciences of the United States of America*, 122(20), e2424863122.

Zhang GQ, et al. (2025) Fungi from *Malus* in Qujing, China: two new species, three new records, and insights into potential host jumping and lifestyle switching. *Frontiers in cellular and infection microbiology*, 15, 1517908.

De Elías-Escribano A, et al. (2025) Wide Variation of *Aedes albopictus* Genotypes First Introduced into Canary Islands Assessed by rDNA Internal Transcribed Spacer Region and mtDNA *cox1* Sequencing and Cloning. *Tropical medicine and infectious disease*, 10(2).

Wimalasena MK, et al. (2025) In-vitro evaluation of synthetic dye decolourisation by filamentous ascomycetous fungi isolated from freshwater environments in Sri Lanka and development of a prototype for addressing environmental pollution from synthetic dye contamination. *Frontiers in cellular and infection microbiology*, 15, 1650835.

Urriza M, et al. (2025) Comparative genomics of native plasmids from plant pathogenic Gammaproteobacteria. *DNA research : an international journal for rapid publication of reports on genes and genomes*, 32(3).

De Elías-Escribano A, et al. (2025) *Schistosoma mansoni* x *S. haematobium* hybrids frequently infecting sub-Saharan migrants in southeastern Europe: Egg DNA genotyping assessed by RD-PCR, sequencing and cloning. *PLoS neglected tropical diseases*, 19(3), e0012942.

Du TY, et al. (2025) ?New *Aquilariomyces* and *Mangifericomes* species (Pleosporales, Ascomycota) from *Aquilaria* spp. in China. *MycoKeys*, 112, 103.

Sun P, et al. (2025) CamITree: a streamlined software for phylogenetic analysis of viral and mitochondrial genomes. *BMC bioinformatics*, 26(1), 53.

Haÿ V, et al. (2025) Phylogeography of *Microphis retzii* (Bleeker, 1856) and *Microphis brachyurus* (Bleeker, 1854) in the Pacific. *Journal of fish biology*, 106(2), 602.

P?ikrylová I, et al. (2024) *Gyrodactylus serra* n. sp. (Gyrodactylidae), from the Near-Threatened *Clanwilliam* Sawfin, *Cheilobarbus serra* (Peters) (Cyprinidae, Smilogastrinae), in the Cape Fold Ecoregion, South Africa. *Systematic parasitology*, 101(6), 67.

Du TY, et al. (2024) ?*Melomastia* (Dothideomycetes, Ascomycota) species associated with Chinese *Aquilaria* spp. *MycoKeys*, 111, 65.

Wang WP, et al. (2024) New Species and Records of Pleurotheciaceae from Karst Landscapes in Yunnan Province, China. *Journal of fungi (Basel, Switzerland)*, 10(8).