

Resource Summary Report

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ALTER

RRID:SCR_015968

Type: Tool

Proper Citation

ALTER (RRID:SCR_015968)

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

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

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

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University of Vigo 09VIB10 to F.F.-R.

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

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Ratings and Alerts

No rating or validation information has been found for ALTER.

No alerts have been found for ALTER.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 125 mentions in open access literature.

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

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 saourensis* (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.

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

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.

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 *Aquilaromyces* 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.

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).

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