

Resource Summary Report

Generated by [nidm-terms](#) on Jul 28, 2026

ALTER

RRID:SCR_015968

Type: Tool

Proper Citation

ALTER (RRID:SCR_015968)

Resource Information

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

Proper Citation: ALTER (RRID:SCR_015968)

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: sequence analysis software, data analysis software, image analysis software, software resource, software application, alignment software, data processing software, 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.; Spanish Ministry of Science and Education BFU2009-08611 to D.P.; Xunta de Galicia PGIDIT07PXIB310202PR to D.P.; INBIOMED initiative ; 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

Record Last Update: 20260728T043507+0000

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 112 mentions in open access literature.

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

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).

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.

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.

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).

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.

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

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.

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).

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

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.

Jiang C, et al. (2024) DNA barcode reference library of the fish larvae and eggs of the South China Sea: taxonomic effectiveness and geographic structure. *BMC ecology and evolution*, 24(1), 132.

Aravamuthan S, et al. (2024) DairyCoPilot-Automated data compilation and analysis tools for DairyComp data assets. *PloS one*, 19(4), e0297827.

Jung H, et al. (2024) The identification of small molecule inhibitors with anthelmintic activities that target conserved proteins among ruminant gastrointestinal nematodes. *mBio*, 15(3), e0009524.

Valki?nas G, et al. (2024) Unexpected absence of exo-erythrocytic merogony during high gametocytaemia in two species of *Haemoproteus* (Haemosporida: Haemoproteidae), including description of *Haemoproteus angustus* n. sp. (lineage hCWT7) and a report of previously unknown residual bodies during in vitro gametogenesis. *International journal for parasitology. Parasites and wildlife*, 23, 100905.

Li YL, et al. (2024) Characterization of *Firmiana danxiaensis* plastomes and comparative analysis of *Firmiana*: insight into its phylogeny and evolution. *BMC genomics*, 25(1), 203.

Lee DAB, et al. (2024) First report of unusual case of parasitism by *Amblyomma nodosum* (Neumann, 1889) in a yellow cururu toad (*Rhinella icterica*) in the Northeastern Brazilian Caatinga. *Revista brasileira de parasitologia veterinaria = Brazilian journal of veterinary parasitology : Orgao Oficial do Colegio Brasileiro de Parasitologia Veterinaria*, 33(2), e005324.

Bargues MD, et al. (2024) Human fascioliasis emergence in southern Asia: Complete nuclear rDNA spacer and mtDNA gene sequences prove Indian patient infection related to fluke hybridization in northeastern India and Bangladesh. *One health* (Amsterdam, Netherlands), 18, 100675.