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

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 103 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

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

P?ikrylová I, et al. (2024) Gyrodactylus serrai 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).

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.

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.

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

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.

Lv P, et al. (2024) Genome-wide profiles of H3K9me3, H3K27me3 modifications, and DNA methylation during diapause of Asian corn borer (Ostrinia furnacalis). Genome research, 34(5), 725.

Brahmachari R, et al. (2024) Leveraging the social networks of informal healthcare providers for universal health coverage: insights from the Indian Sundarbans. Health policy and planning, 39(Supplement_2), i105.

Bundhun D, et al. (2024) ?Taxonomic novelty in Pleomonodictydaceae and new reports for Ampelomycesquisqualis (Phaeosphaeriaceae), Melomastiamaolanensis and M.oleae (Pleurotremataceae). MycoKeys, 111, 147.

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.

Zhu Q, et al. (2023) Cost-effectiveness analysis of anlotinib as a third-line or further treatment for advanced non-small cell lung cancer in China. Translational lung cancer research, 12(8), 1782.

Yang EF, et al. (2023) Taxonomic and Phylogenetic Studies of Saprobic Fungi Associated with Mangifera indica in Yunnan, China. Journal of fungi (Basel, Switzerland), 9(6).

Shen HW, et al. (2023) Lignicolous Freshwater Fungi from Plateau Lakes in China (I):

Morphological and Phylogenetic Analyses Reveal Eight Species of Lentitheciaceae, Including New Genus, New Species and New Records. Journal of fungi (Basel, Switzerland), 9(10).

Shrader CH, et al. (2023) Network-level HIV risk norms are associated with individual-level HIV risk and harm reduction behaviors among people who inject drugs: a latent profile analysis. AIDS and behavior, 27(2), 484.

Luo D, et al. (2023) Identification and Phylogenetic Analysis of the R2R3-MYB Subfamily in Brassica napus. Plants (Basel, Switzerland), 12(4).

Romon-Ochoa P, et al. (2023) Cryphonectria parasitica Detections in England, Jersey, and Guernsey during 2020-2023 Reveal Newly Affected Areas and Infections by the CHV1 Mycovirus. Journal of fungi (Basel, Switzerland), 9(10).