Resource Summary Report

Generated by dkNET on May 20, 2025

FaBox

RRID:SCR_005350
Type: Tool

Proper Citation

FaBox (RRID:SCR_005350)

Resource Information

URL: http://users-birc.au.dk/biopv/php/fabox/

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Description: Tools for splitting, joining and otherwise manipulating FASTA format sequence files. The first tools in the toolbox is for manipulating fasta headers, cropping alignments and doing some sequence comparison allowing users to combine the description of data (often in excel spreadsheets) with the actual data (often DNA sequences). Also, producing correct input files for a range of programs seems to be problematic for the average user. Hence, some converters in some of the services have been included as well as some stand-alone converters. The converters are not necessarily meant to provide the final input file, but you''ll get a valid input file for Arlequin, MrBayes etc. - that you may further edit so it suit your needs. This means that you may need to combine several of the tools to finish your handling - but it keeps it relatively simple to use. Please note that FaBox is written in PHP and ONLY RUNS ON A WEBSERVER.

Abbreviations: FaBox

Synonyms: FaBox - an online fasta sequence toolbox

Resource Type: software resource

Keywords: fasta, dna, protein sequence, dna sequence, protein, sequence, php

Funding:

Availability: Acknowledgement requested

Resource Name: FaBox

Resource ID: SCR_005350

Alternate IDs: OMICS_01165

Record Creation Time: 20220129T080229+0000

Record Last Update: 20250519T203356+0000

Ratings and Alerts

No rating or validation information has been found for FaBox.

No alerts have been found for FaBox.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 110 mentions in open access literature.

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

Bernard AM, et al. (2025) Connections Across Open Water: A Bi-Organelle, Genomics-Scale Assessment of Atlantic-Wide Population Dynamics in a Pelagic, Endangered Apex Predator Shark (Isurus oxyrinchus). Evolutionary applications, 18(1), e70071.

Coello Peralta RD, et al. (2025) Identification of Ancylostoma caninum in Domestic Dogs from Ecuador via Various Techniques. Medical science monitor : international medical journal of experimental and clinical research, 31, e947069.

Prakas P, et al. (2024) Low Genetic Variability of the Tundra Vole in Lithuania. Animals : an open access journal from MDPI, 14(2).

Hilário S, et al. (2024) Comparative genomics reveals insights into the potential of Lysinibacillus irui as a plant growth promoter. Applied microbiology and biotechnology, 108(1), 370.

Nehemia A, et al. (2024) Anthropogenic activities along the Lake Nyasa catchments alter the habitat and genetic diversity of a Lake Salmon, Opsaridium microlepis. Heliyon, 10(20), e39051.

Prakas P, et al. (2024) First report of Sarcocystis halieti (Apicomplexa) in bearded vulture (Gypaetus barbatus). Veterinary research communications, 48(1), 541.

Cunha-Ferreira IC, et al. (2024) Impact of Paenibacillus elgii supernatant on screening bacterial strains with potential for biotechnological applications. Engineering microbiology, 4(3), 100163.

Takamura K, et al. (2024) Common Food Sources for Macrobenthic Communities in Different Bottom Covers: Submerged Macrophytes and Benthic Cyanobacteria in a Japanese Temperate Lake. Ecology and evolution, 14(11), e70359.

Huervana JJC, et al. (2023) Preliminary assessment of genetic variation in the Japanese endemic freshwater crab, Geothelphusadehaani, based on mitochondrial DNA sequences. Biodiversity data journal, 11, e97438.

Rane R, et al. (2023) Complex multiple introductions drive fall armyworm invasions into Asia and Australia. Scientific reports, 13(1), 660.

Lozano-Sardaneta YN, et al. (2023) Phylogenetic relations among Mexican phlebotomine sand flies (Diptera: Psychodidae) and their divergence time estimation. PloS one, 18(6), e0287853.

Hlebec D, et al. (2023) Molecular analyses of pseudoscorpions in a subterranean biodiversity hotspot reveal cryptic diversity and microendemism. Scientific reports, 13(1), 430.

Shapoval NA, et al. (2023) Phylogeography of Two Enigmatic Sulphur Butterflies, Colias mongola Alphéraky, 1897 and Colias tamerlana Staudinger, 1897 (Lepidoptera, Pieridae), with Relations to Wolbachia Infection. Insects, 14(12).

Koziatek-Sad?owska S, et al. (2022) Genetic Characterization of the Poultry Red Mite (Dermanyssus gallinae) in Poland and a Comparison with European and Asian Isolates. Pathogens (Basel, Switzerland), 11(11).

Ekanayaka AH, et al. (2022) A Review of the Fungi That Degrade Plastic. Journal of fungi (Basel, Switzerland), 8(8).

Jamdade R, et al. (2022) Multilocus marker-based delimitation of Salicornia persica and its population discrimination assisted by supervised machine learning approach. PloS one, 17(7), e0270463.

Guo R, et al. (2022) Molecular phylogeography and species distribution modelling evidence of 'oceanic' adaptation for Actinidia eriantha with a refugium along the oceanic-continental gradient in a biodiversity hotspot. BMC plant biology, 22(1), 89.

Tay WT, et al. (2022) Global population genomic signature of Spodoptera frugiperda (fall armyworm) supports complex introduction events across the Old World. Communications biology, 5(1), 297.

Bolotov IN, et al. (2022) Cryptic taxonomic diversity and high-latitude melanism in the glossiphoniid leech assemblage from the Eurasian Arctic. Scientific reports, 12(1), 20630.

Mabasa VV, et al. (2022) Multiple Novel Human Norovirus Recombinants Identified in

Wastewater in Pretoria, South Africa by Next-Generation Sequencing. Viruses, 14(12).