

Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 19, 2026

Orphelia

RRID:SCR_000119

Type: Tool

Proper Citation

Orphelia (RRID:SCR_000119)

Resource Information

URL: <http://orphelia.gobics.de/>

Proper Citation: Orphelia (RRID:SCR_000119)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on August 23, 2022. A metagenomic open reading frame (ORF) finding tool for the prediction of protein coding genes in short, environmental DNA sequences with unknown phylogenetic origin. The resource is based on a two-stage machine learning approach that uses linear discriminants to extract features from the ORFs. An artificial neural network then combines the features and computes a gene probability for each ORF fragment.

Resource Type: simulation software, software application, software resource

Defining Citation: [PMID:19429689](#)

Keywords: metagenomic open reading frame, tool, resource, protein, genes, DNA, phylogenetic origin, machine learning, linear discriminates, artificial neural network, computation, scientific computing, fragment

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Orphelia

Resource ID: SCR_000119

Alternate IDs: OMICS_01492

Record Creation Time: 20220129T080159+0000

Record Last Update: 20260912T195503+0000

Ratings and Alerts

No rating or validation information has been found for Orphelia.

No alerts have been found for Orphelia.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Sharpton TJ, et al. (2014) An introduction to the analysis of shotgun metagenomic data. Frontiers in plant science, 5, 209.

Wang X, et al. (2011) The draft genome of the carcinogenic human liver fluke Clonorchis sinensis. Genome biology, 12(10), R107.