

Resource Summary Report

Generated by [SPARC SAWG](#) on Sep 16, 2026

FACIL

RRID:SCR_004375

Type: Tool

Proper Citation

FACIL (RRID:SCR_004375)

Resource Information

URL: <http://facil-host.cmbi.umcn.nl/facil>

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Description: Genetic code prediction tool that infers the genetic code directly from any set of nucleic acid sequences and assigns a Random Forest-based reliability score to its predictions.

Abbreviations: FACIL

Synonyms: FACIL genetic code prediction tool, Genetic code prediction tool FACIL: Fast and Accurate genetic Code Inference and Logo

Resource Type: analysis service resource, data analysis service, production service resource, service resource, software resource

Defining Citation: [PMID:21653513](#)

Keywords: unix/linux

Availability: Commercial license, Free

Resource Name: FACIL

Resource ID: SCR_004375

Alternate IDs: OMICS_00299

Record Creation Time: 20220129T080224+0000

Record Last Update: 20260912T200010+0000

Ratings and Alerts

No rating or validation information has been found for FACIL.

No alerts have been found for FACIL.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 9 mentions in open access literature.

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

Richtá? M, et al. (2026) Charting the landscape of organellar genome evolution in eustigmatophyte algae. bioRxiv : the preprint server for biology.

Barcyt? D, et al. (2025) Expanded diversity of pedinophytes provides a window into the evolution of the genetic code in organelles. PLoS genetics, 21(10), e1011901.

Cedrola F, et al. (2024) Giants' cooperation: a draft genome of the giant ciliate Muniziella cunhai suggests its ecological role in the capybara's digestive metabolism. Microbial genomics, 10(7).

Mikhailov KV, et al. (2022) Genomic analysis reveals cryptic diversity in aphelids and sheds light on the emergence of Fungi. Current biology : CB, 32(21), 4607.

Schultz DT, et al. (2020) Conserved novel ORFs in the mitochondrial genome of the ctenophore Beroë forskalii. PeerJ, 8, e8356.

Mikhailov KV, et al. (2019) Coding palindromes in mitochondrial genes of Nematomorpha. Nucleic acids research, 47(13), 6858.

Bachvaroff TR, et al. (2019) Aprecedented nuclear genetic code with all three termination codons reassigned as sense codons in the syndinean Amoeboophrya sp. ex Karlodinium veneficum. PloS one, 14(2), e0212912.

Popova OV, et al. (2016) Mitochondrial Genomes of Kinorhyncha: trnM Duplication and New Gene Orders within Animals. PloS one, 11(10), e0165072.

Speth DR, et al. (2016) Genome-based microbial ecology of anammox granules in a full-scale wastewater treatment system. Nature communications, 7, 11172.