

Resource Summary Report

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Philius

RRID:SCR_004625

Type: Tool

Proper Citation

Philius (RRID:SCR_004625)

Resource Information

URL: <http://noble.gs.washington.edu/proj/philius/>

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Description: Web server that predicts protein transmembrane topology and signal peptides. Hidden Markov models (HMM) have been successfully applied to the tasks of transmembrane protein topology prediction and signal peptide prediction. They expand upon this work by making use of the more powerful class of dynamic Bayesian networks (DBN). Their model, Philius, is inspired by a previously published HMM, Phobius, and combines a signal peptide sub-model with a transmembrane sub-model. They introduce a two-stage DBN decoder which combines the power of posterior decoding with the grammar constraints of Viterbi-style decoding. Philius also provides protein type, segment, and topology confidence metrics to aid in the interpretation of the predictions.

Abbreviations: Philius

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

Defining Citation: [PMID:18989393](#)

Keywords: hidden markov model, protein type, segment, topology, confidence metric, prediction, protein, transmembrane, signal peptide, peptide, bio.tools

Resource Name: Philius

Resource ID: SCR_004625

Alternate IDs: nlx_62426, biotools:philius

Alternate URLs: <https://bio.tools/philius>

Record Creation Time: 20220129T080225+0000

Record Last Update: 20260806T054405+0000

Ratings and Alerts

No rating or validation information has been found for Philius.

No alerts have been found for Philius.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We have not found any literature mentions for this resource.