Phobius
RRID:SCR_015643
Type: Tool

Proper Citation

Phobius (RRID:SCR_015643)

Resource Information

URL: http://phobius.sbc.su.se/

Proper Citation: Phobius (RRID:SCR_015643)

Description: Web application for combined transmembrane topology and signal peptide prediction. Used for whole genome annotation of signal peptides and transmembrane regions. Predictor is based on hidden Markov model (HMM) that models different sequence regions of signal peptide and different regions of transmembrane protein in series of interconnected states.

Synonyms: PHOBIUS

Resource Type: web service, data access protocol, analysis service resource, service resource, software resource, production service resource

Defining Citation: PMID:15111065, PMID:30976793

Keywords: Signal peptide prediction, whole genome annotation, transmembrane region, protein prediction, transmembrane topology, signal peptide, fasta, hidden markov model

Availability: Freely Available, Free, Available for download

Resource Name: Phobius

Resource ID: SCR_015643

Alternate IDs: SCR_018767

Alternate URLs: http://phobius.binf.ku.dk/, https://www.ebi.ac.uk/Tools/pfa/phobius/
Ratings and Alerts

No rating or validation information has been found for Phobius.

No alerts have been found for Phobius.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 350 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.


Tsunoda T, et al. (2022) ENTREP/FAM189A2 encodes a new ITCH ubiquitin ligase activator that is downregulated in breast cancer. EMBO reports, 23(2), e51182.

Ramdass AC, et al. (2022) Detection and diversity of the mannosylerythritol lipid (MEL) gene cluster and lipase A and B genes of Moesziomyces antarcticus isolated from terrestrial sites chronically contaminated with crude oil in Trinidad. BMC microbiology, 22(1), 43.


Wyka SA, et al. (2021) Whole genome comparisons of ergot fungi reveals the divergence and evolution of species within the genus Claviceps are the result of varying mechanisms driving genome evolution and host range expansion. Genome biology and evolution.


Tinti M, et al. (2021) Polysomal mRNA Association and Gene Expression in. Wellcome open research, 6, 36.
