

Resource Summary Report

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Phymm and PhymmBL

RRID:SCR_004751

Type: Tool

Proper Citation

Phymm and PhymmBL (RRID:SCR_004751)

Resource Information

URL: <http://www.cbcb.umd.edu/software/phymm/>

Proper Citation: Phymm and PhymmBL (RRID:SCR_004751)

Description: Software for Phylogenetic Classification of Metagenomic Data with Interpolated Markov Models to taxonomically classify DNA sequences and accurately classify reads as short as 100 bp. PhymmBL, the hybrid classifier included in this distribution which combines analysis from both Phymm and BLAST, produces even higher accuracy.

Abbreviations: Phymm, PhymmBL

Resource Type: software resource

Defining Citation: [PMID:19648916](#), [PMID:21527926](#)

Keywords: metagenome, sequence, taxonomy, classification, phylogenetic classification, genome, short read

Funding: NLM R01-LM006845

Availability: Open-source license

Resource Name: Phymm and PhymmBL

Resource ID: SCR_004751

Alternate IDs: OMICS_01461

Record Creation Time: 20220129T080226+0000

Record Last Update: 20260905T132523+0000

Ratings and Alerts

No rating or validation information has been found for Phymm and PhymmBL.

No alerts have been found for Phymm and PhymmBL.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 12 mentions in open access literature.

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

Smith G, et al. (2022) Human follicular mites: Ectoparasites becoming symbionts. *Molecular biology and evolution*, 39(6).

Lewin GR, et al. (2022) Long-Term Cellulose Enrichment Selects for Highly Cellulolytic Consortia and Competition for Public Goods. *mSystems*, 7(2), e0151921.

Xu C, et al. (2021) LightCUD: a program for diagnosing IBD based on human gut microbiome data. *BioData mining*, 14(1), 2.

Kvist S, et al. (2020) Draft genome of the European medicinal leech *Hirudo medicinalis* (Annelida, Clitellata, Hirudiniformes) with emphasis on anticoagulants. *Scientific reports*, 10(1), 9885.

Manzano-Marín A, et al. (2016) Reinventing the Wheel and Making It Round Again: Evolutionary Convergence in *Buchnera-Serratia* Symbiotic Consortia between the Distantly Related Lachninae Aphids *Tuberolachnus salignus* and *Cinara cedri*. *Genome biology and evolution*, 8(5), 1440.

Oceguera-Figueroa A, et al. (2016) Comparative Mitogenomics of Leeches (Annelida: Clitellata): Genome Conservation and *Placobdella*-Specific *trnD* Gene Duplication. *PLoS one*, 11(5), e0155441.

Kumar S, et al. (2015) Metagenomics: Retrospect and Prospects in High Throughput Age. *Biotechnology research international*, 2015, 121735.

Manzano-Marín A, et al. (2015) Solving a Bloody Mess: B-Vitamin Independent Metabolic Convergence among Gammaproteobacterial Obligate Endosymbionts from Blood-Feeding Arthropods and the Leech *Haementeria officinalis*. *Genome biology and evolution*, 7(10), 2871.

Mandal RS, et al. (2015) Metagenomic surveys of gut microbiota. *Genomics, proteomics & bioinformatics*, 13(3), 148.

Hou T, et al. (2015) Classification of metagenomics data at lower taxonomic level using a robust supervised classifier. *Evolutionary bioinformatics online*, 11, 3.

Manzano-Marín A, et al. (2014) Settling down: the genome of *Serratia symbiotica* from the aphid *Cinara tujaefilina* zooms in on the process of accommodation to a cooperative intracellular life. *Genome biology and evolution*, 6(7), 1683.

Wood DE, et al. (2014) Kraken: ultrafast metagenomic sequence classification using exact alignments. *Genome biology*, 15(3), R46.