Resource Summary Report

Generated by ASWG on Sep 19, 2026

Mobyle@Pasteur

RRID:SCR_013089
Type: Tool

Proper Citation

Mobyle@Pasteur (RRID:SCR_013089)

Resource Information

URL: http://mobyle.pasteur.fr/

Proper Citation: Mobyle@Pasteur (RRID:SCR_013089)

Description: A portal for bioinformatics analyses, including the following: alignment assembly database display genetics hmm information nucleic phylogeny protein sequence structure

Synonyms: Mobyle@Pasteur

Resource Type: analysis service resource, data analysis service, data or information resource, database, production service resource, service resource

Keywords: FASEB list

Resource Name: Mobyle@Pasteur

Resource ID: SCR_013089

Alternate IDs: nlx_156919

Record Creation Time: 20220129T080314+0000

Record Last Update: 20260912T195758+0000

Ratings and Alerts

No rating or validation information has been found for Mobyle@Pasteur.

No alerts have been found for Mobyle@Pasteur.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 203 mentions in open access literature.

Listed below are recent publications. The full list is available at ASWG .

Markina-Iñarrairaegui A, et al. (2020) Tolerance to alkaline ambient pH in Aspergillus nidulans depends on the activity of ENA proteins. Scientific reports, 10(1), 14325.

Boukadida C, et al. (2018) NS2 proteases from hepatitis C virus and related hepaciviruses share composite active sites and previously unrecognized intrinsic proteolytic activities. PLoS pathogens, 14(2), e1006863.

Zhu J, et al. (2017) Identification and characterization of a ?-defensin gene involved in the immune defense response of channel catfish, Ictalurus punctatus. Molecular immunology, 85, 256.

Gelormini G, et al. (2017) Infectious keratoconjunctivitis in wild Caprinae: merging field observations and molecular analyses sheds light on factors shaping outbreak dynamics. BMC veterinary research, 13(1), 67.

Pyle JD, et al. (2017) Amalga-like virus infecting Antonospora locustae, a microsporidian pathogen of grasshoppers, plus related viruses associated with other arthropods. Virus research, 233, 95.

Antsotegi-Uskola M, et al. (2017) Copper Resistance in Aspergillus nidulans Relies on the PI-Type ATPase CrpA, Regulated by the Transcription Factor AceA. Frontiers in microbiology, 8, 912.

Neeb ZT, et al. (2017) Preferential expression of scores of functionally and evolutionarily diverse DNA and RNA-binding proteins during Oxytricha trifallax macronuclear development. PloS one, 12(2), e0170870.

Castella C, et al. (2017) Post-translational modifications of Medicago truncatula glutathione peroxidase 1 induced by nitric oxide. Nitric oxide : biology and chemistry, 68, 125.

Mehlferber EC, et al. (2017) Duplication and Sub/Neofunctionalization of Malvolio, an Insect Homolog of Nramp, in the Subsocial Beetle Nicrophorus vespilloides. G3 (Bethesda, Md.), 7(10), 3393.

Da Cunha V, et al. (2017) Lokiarchaea are close relatives of Euryarchaeota, not bridging the gap between prokaryotes and eukaryotes. PLoS genetics, 13(6), e1006810.

Baker RH, et al. (2016) Spermatogenesis Drives Rapid Gene Creation and Masculinization of the X Chromosome in Stalk-Eyed Flies (Diopsidae). Genome biology and evolution, 8(3), 896.

Urlacher E, et al. (2016) Honey Bee Allatostatins Target Galanin/Somatostatin-Like Receptors and Modulate Learning: A Conserved Function? PloS one, 11(1), e0146248.

Trus I, et al. (2016) Immunity raised by recent European subtype 1 PRRSV strains allows better replication of East European subtype 3 PRRSV strain Lena than that raised by an older strain. Veterinary research, 47, 15.

Ruge H, et al. (2016) The calmodulin-like proteins AtCML4 and AtCML5 are single-pass membrane proteins targeted to the endomembrane system by an N-terminal signal anchor sequence. Journal of experimental botany, 67(13), 3985.

D?u?ewska J, et al. (2016) Tocopherol Cyclases-Substrate Specificity and Phylogenetic Relations. PloS one, 11(7), e0159629.

Ison J, et al. (2016) Tools and data services registry: a community effort to document bioinformatics resources. Nucleic acids research, 44(D1), D38.

Lebrigand K, et al. (2016) Comparative Genomic Analysis of Drechmeria coniospora Reveals Core and Specific Genetic Requirements for Fungal Endoparasitism of Nematodes. PLoS genetics, 12(5), e1006017.

Zhang Y, et al. (2015) The selective post-translational processing of transcription factor Nrf1 yields distinct isoforms that dictate its ability to differentially regulate gene expression. Scientific reports, 5, 12983.

Bajda S, et al. (2015) Transcriptome profiling of a spirodiclofen susceptible and resistant strain of the European red mite Panonychus ulmi using strand-specific RNA-seq. BMC genomics, 16, 974.

Penuliar GM, et al. (2015) Phenotypic and transcriptional profiling in Entamoeba histolytica reveal costs to fitness and adaptive responses associated with metronidazole resistance. Frontiers in microbiology, 6, 354.