

Resource Summary Report

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ATGC: Montpellier bioinformatics platform

RRID:SCR_002917

Type: Tool

Proper Citation

ATGC: Montpellier bioinformatics platform (RRID:SCR_002917)

Resource Information

URL: <http://www.atgc-montpellier.fr/>

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Description: A bioinformatics platform that is a joint project of several South of France laboratories with available services based on their expertise, issued from their research activities which involve phylogenetics, population genetics, molecular evolution, genome dynamics, comparative and functional genomics, and transcriptome analysis. Most of the software and databases on ATGC are (co)authored by researchers from South of France teams. Some are widely used and highly cited. South of France laboratories: * CRBM (transcriptomes and stem cells). * IBC (computational biology). * MiVEGEC (evolution and phylogeny). * LGDP (plant genomics). * LIRMM (computer science). * South Green (plant genomics).

Abbreviations: ATGC

Synonyms: ATGC - South of France bioinformatics platform

Resource Type: database, catalog, topical portal, portal, data or information resource

Keywords: bioinformatics, genome, genetics, molecular evolution, comparative, functional, dynamics, transcriptome, analysis, database, data analysis service, software resource, data set, high-throughput sequencing, binary, phylogenetics, population genetics, genome dynamics, comparative genomics, functional genomics, transcriptome analysis, molecular, evolution, stem cell, computational biology, plant genomics, FASEB list

Resource Name: ATGC: Montpellier bioinformatics platform

Resource ID: SCR_002917

Alternate IDs: nif-0000-30044

Record Creation Time: 20220129T080216+0000

Record Last Update: 20260728T043137+0000

Ratings and Alerts

No rating or validation information has been found for ATGC: Montpellier bioinformatics platform.

No alerts have been found for ATGC: Montpellier bioinformatics platform.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 218 mentions in open access literature.

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

Smolander N, et al. (2025) Glyphosate and phosphate treatments in soil differentially affect crop microbiomes depending on species, tissue and growth stage. Scientific reports, 15(1), 25502.

Wu T, et al. (2025) Defensive Symbiont Genotype Distributions Are Linked to Parasitoid Attack Networks. Ecology letters, 28(2), e70082.

Woo JJ, et al. (2025) Uncovering Hidden Lineages in Korean Foliicolous Lichens (Strigulaceae, Strigulales): Discovery of a New Cryptic Genus and Species. Mycobiology, 53(4), 556.

Geraldini DB, et al. (2025) Identification of a putative new virus from the Jingmenvirus group in ticks from wild animals in Brazil. Virus evolution, 11(1), veaf045.

Mata-Marcano C, et al. (2025) Morphological and molecular assessment of muscle metacercariae infecting tench Tinca tinca from fish farms and wild populations in Germany. Scientific reports, 15(1), 23700.

Crespillo-Casado A, et al. (2024) Recognition of phylogenetically diverse pathogens through enzymatically amplified recruitment of RNF213. EMBO reports, 25(11), 4979.

Cote CK, et al. (2024) Virulence of Burkholderia pseudomallei ATS2021 Unintentionally Imported to United States in Aromatherapy Spray. Emerging infectious diseases, 30(10), 2056.

Dias HM, et al. (2024) TH11 Gene Evolutionary Trends: A Comprehensive Plant-Focused Assessment via Data Mining and Large-Scale Analysis. Genome biology and evolution, 16(10).

Maraganga JM, et al. (2024) Tegumental topography and molecular characterisation of two trematodes (Platyhelminthes: Digenea) from *Clarias gariepinus* (Burchell, 1822) in Kenya. *International journal for parasitology. Parasites and wildlife*, 23, 100897.

Becquart P, et al. (2024) Evidence for circulation of Rift Valley fever virus in wildlife and domestic animals in a forest environment in Gabon, Central Africa. *PLoS neglected tropical diseases*, 18(3), e0011756.

Quijano-Barraza JM, et al. (2023) Evolution and functional role prediction of the CYP6DE and CYP6DJ subfamilies in *Dendroctonus* (Curculionidae: Scolytinae) bark beetles. *Frontiers in molecular biosciences*, 10, 1274838.

Austin RM, et al. (2023) ?Complete mitochondrial genome of the Galápagos sea lion, *Zalophuswollebaeki* (Carnivora, Otariidae): paratype specimen confirms separate species status. *ZooKeys*, 1166, 307.

Lau ACC, et al. (2023) The dynamics of the microbiome in Ixodidae are shaped by tick ontogeny and pathogens in Sarawak, Malaysian Borneo. *Microbial genomics*, 9(2).

Andrews T, et al. (2023) A Transducing Bacteriophage Infecting *Staphylococcus epidermidis* Contributes to the Expansion of a Novel Siphovirus Genus and Implies the Genus Is Inappropriate for Phage Therapy. *mSphere*, 8(3), e0052422.

Rindoria NM, et al. (2023) Scanning Electron Microscopy and First Molecular Data of Two Species of *Lamproglana* (Copepoda: Lernaeidae) from *Labeo victorianus* (Cyprinidae) and *Clarias gariepinus* (Clariidae) in Kenya. *Pathogens (Basel, Switzerland)*, 12(8).

Dieme C, et al. (2022) Role of *Anopheles* Mosquitoes in Cache Valley Virus Lineage Displacement, New York, USA. *Emerging infectious diseases*, 28(2), 303.

Brooun M, et al. (2022) The Hippo pathway regulates axis formation and morphogenesis in *Hydra*. *Proceedings of the National Academy of Sciences of the United States of America*, 119(29), e2203257119.

Pardos-Blas JR, et al. (2022) Comparative Venomics of the Cryptic Cone Snail Species *Virroconus ebraeus* and *Virroconus judaeus*. *Marine drugs*, 20(2).

Yang Y, et al. (2022) Chromosome-level genome assembly of the shuttles hopppfish, *Periophthalmus modestus*. *GigaScience*, 11(1).

Pantoja C, et al. (2022) Digenean trematodes infecting the frigate tuna *Auxis thazard* (Scombriformes, Scombridae) off the Rio de Janeiro coast, Brazil, including molecular data. *Parasite (Paris, France)*, 29, 44.