

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

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: 20260821T193652+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 230 mentions in open access literature.

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

Du X, et al. (2026) *Impatiens leshanensis* (Balsaminaceae), a new species from Sichuan, China. *PhytoKeys*, 274, 145.

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.

Ol?drzy?ska N, et al. (2025) A Multi-Evidence Approach to the Systematics of the Genus *Satyrrium* Sw. Based on Time-Calibrated Phylogeny, Morphology, and Biogeography. *International journal of molecular sciences*, 27(1).

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

Chen G, et al. (2025) The G311E Mutant Gene of MATE Family Protein DTX6 Confers Diquat and Paraquat Resistance in Rice Without Yield or Nutritional Penalties. *International journal of molecular sciences*, 26(13).

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.

Burzacka-Hinz A, et al. (2025) Evolution of morphological traits of *Dendrobium sensu lato* (Orchidaceae)-an attempt to resolve phylogenetic relationships in nominal and morphologically convergent sections. *BMC plant biology*, 25(1), 239.

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.

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).

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

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.

Kudlai O, et al. (2024) Helminth Parasites of Invasive Freshwater Fish in Lithuania. *Animals : an open access journal from MDPI*, 14(22).

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.

Zhang X, et al. (2023) Unveiling the functional diversity of ionotropic glutamate receptors in the Pacific oyster (*Crassostrea gigas*) by systematic studies. *Frontiers in physiology*, 14, 1280553.

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

Lipińska MM, et al. (2023) Characters evolution of *Encyclia* (Laeliinae-Orchidaceae) reveals a complex pattern not phylogenetically determined: insights from macro- and micromorphology. *BMC plant biology*, 23(1), 661.

Nowak S, et al. (2023) Notes to the Taxonomic Affiliation of the *Bulbophyllum* Sect. *Physometra* (Orchidaceae, Epidendroideae) Based on Molecular Phylogenetic Analyses. *International journal of molecular sciences*, 24(11).