

Resource Summary Report

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Unipro UGENE

RRID:SCR_005579

Type: Tool

Proper Citation

Unipro UGENE (RRID:SCR_005579)

Resource Information

URL: <http://ugene.unipro.ru/>

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Description: A multiplatform open-source software to assist molecular biologists without much expertise in bioinformatics to manage, analyze and visualize their data. UGENE integrates widely used bioinformatics tools within a common user interface. The toolkit supports multiple biological data formats and allows the retrieval of data from remote data sources. It provides visualization modules for biological objects such as annotated genome sequences, Next Generation Sequencing (NGS) assembly data, multiple sequence alignments, phylogenetic trees and 3D structures. Most of the integrated algorithms are tuned for maximum performance by the usage of multithreading and special processor instructions. UGENE includes a visual environment for creating reusable workflows that can be launched on local resources or in a High Performance Computing (HPC) environment. UGENE is written in C++ using the Qt framework. The built-in plugin system and structured UGENE API make it possible to extend the toolkit with new functionality.

Abbreviations: UGENE

Resource Type: software resource, software toolkit

Defining Citation: [PMID:22368248](#), [DOI:10.1093/bioinformatics/bts091](#)

Keywords: c++, windows, mac os, linux, bio.tools

Availability: GNU General Public License, v2, Acknowledgement requested

Resource Name: Unipro UGENE

Resource ID: SCR_005579

Alternate IDs: OMICS_01022, biotools:ugene

Alternate URLs: <https://bio.tools/ugene>, <https://sources.debian.org/src/ugene/>

Record Creation Time: 20220129T080231+0000

Record Last Update: 20260905T133235+0000

Ratings and Alerts

No rating or validation information has been found for Unipro UGENE.

No alerts have been found for Unipro UGENE.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 183 mentions in open access literature.

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

Zhilina D, et al. (2026) Dynamic expression of lamin B1 during adult neurogenesis in the vertebrate brain. *Developmental dynamics : an official publication of the American Association of Anatomists*, 255(2), 187.

Mohtasebi S, et al. (2026) Enhanced detection of equine strongyles: Insights from morphological and nemabiome metabarcoding approaches in northern Iran. *Equine veterinary journal*, 58(2), 508.

Pinheiro LCL, et al. (2026) Interplay between CDH1 polymorphisms, haplotypes, and genomic repetitive elements in urothelial bladder cancer prognosis. *Molecular biology reports*, 53(1).

Mbaya-Tshibangu F, et al. (2026) Low-Abundance and Fragmentary *Helicobacter pylori* DNA Detected in Phenotypically Negative Gastric Biopsies Using Targeted Sequencing. *Biomolecules*, 16(6).

Donner J, et al. (2026) Association of the Disheveled 2 (DVL2) Gene c.2044delC Variant with Increased Risk of Canine Cleft Palate. *Animal genetics*, 57(3), e70101.

Bessa Souza MC, et al. (2026) Biosurfactant-Producing Bacteria Isolated from a Microbial Consortium Previously Subjected to Adaptive Laboratory Evolution in Oily Sludge. *Microorganisms*, 14(2).

Ozawa M, et al. (2026) Evidence for Genotype-Associated Differences in Disease Severity and Limitations of Serotype-Based Classification in *Glaesserella parasuis* Revealed by Whole-Genome Sequencing in Japan. *Pathogens (Basel, Switzerland)*, 15(6).

Ghazi-Soltani G, et al. (2026) Functional insights into nucleoside diphosphate kinases encoded by two ndk paralogs in *Waddlia chondrophila*. *Current research in microbial sciences*, 11, 100635.

Janowska MK, et al. (2026) Small heat shock protein HSPB5 uses disorder to bind zinc with high affinity. *The Journal of biological chemistry*, 302(1), 111030.

Yu D, et al. (2026) Susceptibility of naturally human papillomavirus type 16 major capsid protein L1 variants to vaccines and predictions of future evolutionary trends. *Tumour virus research*, 21, 200341.

Anoyatbekova A, et al. (2025) Molecular Detection of Porcine Parvovirus 5 in Domestic Pigs in Russia and Propagation of Field Isolates in Primary Porcine Testicular Cells. *Veterinary sciences*, 12(6).

Jordan S, et al. (2025) Design of genus-specific semi-nested primers for simple and accurate identification of *Enterobacter* strains. *BMC microbiology*, 25(1), 456.

Bykov R, et al. (2025) Molecular Characterization and Epidemiology of Human Noroviruses in the Sverdlovsk Region, Russian Federation. *Viruses*, 17(9).

Chaumeau V, et al. (2025) Identification of Southeast Asian *Anopheles* mosquito species with matrix-assisted laser desorption/ionization time-of-flight mass spectrometry using a cross-correlation approach. *Parasites & vectors*, 18(1), 8.

Salvà-Serra F, et al. (2025) Description of *Pseudomonas imrae* sp. nov., carrying a novel class C β -lactamase gene variant, isolated from gut samples of Atlantic mackerel (*Scomber scombrus*). *Frontiers in microbiology*, 16, 1530878.

Puttonen M, et al. (2025) Fibroblast growth factor receptor expression in hemangioblastomas: A novel therapeutic target. *PloS one*, 20(5), e0323979.

Sami H, et al. (2025) HBV genotype distribution and S gene mutations in HIV-HBV co-infected patients: insights from North India. *Frontiers in cellular and infection microbiology*, 15, 1731472.

D'Amato ME, et al. (2025) Persistence of Ancestral KhoeSan Mitochondrial Patterns in Contemporary South African Populations. *Annals of human genetics*, 89(4), 195.

Zhang S, et al. (2025) Comparative genomics uncovers organellar genome structural divergence in Caryophyllales and reveals widespread non-coding transcription in *Bougainvillea glabra* organellar. *BMC genomics*, 26(1), 722.

Azanbekova M, et al. (2025) Phylogenetic analysis of a 2024 Sheeppox virus isolate from the Almaty region of Kazakhstan and investigation of its pathogenicity in merino sheep. *Frontiers in veterinary science*, 12, 1623187.