

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 toolkit, software resource

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: 20260803T040416+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 170 mentions in open access literature.

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

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.

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.

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

Berdieva M, et al. (2025) Transcriptomic Analysis of Cold-Induced Temporary Cysts in Marine Dinoflagellate *Prorocentrum cordatum*. *International journal of molecular sciences*, 26(12).

Safwat MS, et al. (2025) Ancient and dominant: a novel feline immunodeficiency virus subtype "X-EGY" identified in Egyptian cats associated with high prevalence. *BMC veterinary research*, 21(1), 497.

Liu C, et al. (2025) Characterization of Novel WFS1 Variants in Three Diabetes Pedigrees. *Journal of diabetes*, 17(7), e70114.

Leonildi A, et al. (2025) Phenotypic and Molecular Characterization of Pyomelanin-Producing *Acinetobacter baumannii* ST2Pas;ST1816/ST195Oxf Causing the First European Nosocomial Outbreak. *Microorganisms*, 13(3).

Paião HGO, et al. (2025) Phylogenetic Analysis of Varicella-Zoster Virus in Cerebrospinal Fluid from Individuals with Acute Central Nervous System Infection: An Exploratory Study. *Viruses*, 17(2).

Liao Y, et al. (2025) Cell division protein CdpA organises and anchors the midcell ring in haloarchaea. *Nature communications*, 16(1), 5076.

Brugneti F, et al. (2025) Elucidation of "Twig Canker and Shoot Blight" (TCSB) in Peach Caused by *Diaporthe amygdali* in the North of Italy in Emilia-Romagna. *Physiologia plantarum*, 177(4), e70428.

Bulatov Y, et al. (2025) Camelpox Virus in Western Kazakhstan: Isolation and Phylogenetic Analysis of a New Strain. *Viruses*, 17(9).

Di Sora N, et al. (2025) "The Last of Them": Entomopathogenic Effect of *Akanthomyces muscarius* on the Scale Insect Pest *Toumeyella parvicornis* Under Laboratory Conditions, a Potential Biological Control Candidate. *Physiologia plantarum*, 177(5), e70533.

Martínez C, et al. (2025) New Coronavirus in Colombian Caribbean Bats: In Silico Analysis Reveals Possible Risk of Interspecific Jumping. *Viruses*, 17(10).

Omonijo FA, et al. (2025) Small nucleolar RNA dysregulation and potential roles in bovine subclinical mastitis. *Journal of animal science and biotechnology*, 16(1), 124.