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

Funding:

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

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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 147 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>dkNET</u>.

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.

Dossmann L, et al. (2024) Specific DNMT3C flanking sequence preferences facilitate methylation of young murine retrotransposons. Communications biology, 7(1), 582.

Hidvégi N, et al. (2024) Expression responses of XTH genes in tomato and potato to environmental mechanical forces: focus on behavior in response to rainfall, wind and touch. Plant signaling & behavior, 19(1), 2360296.

Sun Y, et al. (2024) Demographic and zoological drivers of infectome diversity in companion cats with ascites. mSystems, 9(9), e0063624.

Cafardi JM, et al. (2024) Vertical Transmission of Hepatitis C Virus Among Women With a History of Injection Opioid Use. Clinical infectious diseases : an official publication of the Infectious Diseases Society of America, 79(3), 701.

Umotoy JC, et al. (2024) Inhibition of HIV-1 replication by nanobodies targeting tetraspanin CD9. iScience, 27(10), 110958.

Baji? V, et al. (2024) mtDNA "nomenclutter" and its consequences on the interpretation of genetic data. BMC ecology and evolution, 24(1), 110.

Quinones-Olvera N, et al. (2024) Diverse and abundant phages exploit conjugative plasmids. Nature communications, 15(1), 3197.

Pontes A, et al. (2024) Tracking alternative versions of the galactose gene network in the genus Saccharomyces and their expansion after domestication. iScience, 27(2), 108987.

Chaumeau V, et al. (2024) Identification of Southeast Asian Anopheles mosquito species using MALDI-TOF mass spectrometry. PloS one, 19(7), e0305167.

Wang G, et al. (2024) Identification of endothelial and mesenchymal FOXF1 enhancers involved in alveolar capillary dysplasia. Nature communications, 15(1), 5233.

Nazarova A, et al. (2024) Leeches Baicalobdella torquata feed on hemolymph but have a low effect on the cellular immune response of amphipod Eulimnogammarus verrucosus from Lake Baikal. PeerJ, 12, e17348.

Ferreira RC, et al. (2024) Reconstructing Prehistoric Viral Genomes from Neanderthal Sequencing Data. Viruses, 16(6).

Litov AG, et al. (2024) Extensive Diversity of Viruses in Millipedes Collected in the Dong Nai Biosphere Reserve (Vietnam). Viruses, 16(9).

Andriyanov P, et al. (2024) Large-scale genomic analysis of Elizabethkingia anophelis. BMC genomics, 25(1), 1015.

Du R, et al. (2024) A de novo homozygous missense mutation of the GUSB gene leads to mucopolysaccharidosis type VII identification in a family with twice adverse pregnancy outcomes due to non-immune hydrops fetalis. Molecular genetics and metabolism reports, 38, 101033.

Tsishevskaya AA, et al. (2024) Untranslated Regions of a Segmented Kindia Tick Virus Genome Are Highly Conserved and Contain Multiple Regulatory Elements for Viral Replication. Microorganisms, 12(2).

Gholampour Z, et al. (2024) Application of High-Throughput Sequencing for Comprehensive Virome Profiling in Grapevines Shows Yellows in Iran. Viruses, 16(2).

Wang T, et al. (2024) Digenic CHD7 and SMCHD1 inheritance Unveils phenotypic variability in a family mainly presenting with hypogonadotropic hypogonadism. Heliyon, 10(1), e23272.

Luna N, et al. (2024) Microbial community dynamics in blood, faeces and oral secretions of neotropical bats in Casanare, Colombia. Scientific reports, 14(1), 25808.