Unipro UGENE
RRID:SCR_005579
Type: Tool

Proper Citation

Unipro UGENE (RRID:SCR_005579)

Resource Information

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

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.

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Resource Type: Resource, software resource, software toolkit

Keywords: c++, windows, mac os, linux

Resource ID: SCR_005579

References: PMID: 22368248

Availability: GNU General Public License, v2, Acknowledgement requested
Website Status: Last checked up

Alternate IDs: OMICS_01022

Abbreviations: UGENE

Mentions Count: 50

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 50 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch Infrastructure.


Thiyahuddin NM, et al. (2019) Yeast Species in the Oral Cavities of Older People: A Comparison between People Living in Their Own Homes and Those in Rest Homes. Journal of fungi (Basel, Switzerland), 5(2).


Molina R, et al. (2019) Structure of Csx1-cOAcocomplex reveals the basis of RNA decay
Type III-B CRISPR-Cas. Nature communications, 10(1), 4302.


