

Resource Summary Report

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Taverna

RRID:SCR_004437

Type: Tool

Proper Citation

Taverna (RRID:SCR_004437)

Resource Information

URL: <http://www.taverna.org.uk/>

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Description: An open source and domain independent Workflow Management System ?????? a suite of tools used to design and execute scientific workflows and aid in silico experimentation. Taverna Workbench now has support for service sets, offline workflow editing, workflow validation, improved workflow run monitoring, and the pausing and canceling of workflow runs. The command line tool allows you to run workflows outside of the workbench and is available as a stand-alone download or bundled with the Taverna Workbench 2.2.0 download. The Taverna suite is written in Java and includes the Taverna Engine (used for enacting workflows) that powers both the Taverna Workbench (the desktop client application) and the Taverna Server (which allows remote execution of workflows). Taverna is also available as a Command Line Tool for a quick execution of workflows from a terminal. Taverna 2.2.0 includes * Copy/paste, shortcuts, undo/redo, drag and drop * Animated workflow diagram * Remembers added/removed services * Secure Web services support * Secure access to resources on the web * Up-to-date R support * Intermediate values during workflow runs * myExperiment integration * Excel and csv spreadsheet support * Command line tool

Abbreviations: Taverna

Resource Type: workflow software, data processing software, software resource, software application

Defining Citation: [PMID:18337261](#), [PMID:23640334](#)

Funding: OMII-UK ;
EPSRC ;
BBSRC ;
Microsoft ;
ESRC ;
JISC

Availability: Open unspecified license

Resource Name: Taverna

Resource ID: SCR_004437

Alternate IDs: nlx_43462, OMICS_01146

Record Creation Time: 20220129T080224+0000

Record Last Update: 20260819T044111+0000

Ratings and Alerts

No rating or validation information has been found for Taverna.

No alerts have been found for Taverna.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 30 mentions in open access literature.

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

Mareya CR, et al. (2020) Adaptive defence-related changes in the metabolome of *Sorghum bicolor* cells in response to lipopolysaccharides of the pathogen *Burkholderia andropogonis*. *Scientific reports*, 10(1), 7626.

Tugizimana F, et al. (2019) Time-resolved decoding of metabolic signatures of in vitro growth of the hemibiotrophic pathogen *Colletotrichum sublineolum*. *Scientific reports*, 9(1), 3290.

van der Spek A, et al. (2019) Metabolomics reveals a link between homocysteine and lipid metabolism and leukocyte telomere length: the ENGAGE consortium. *Scientific reports*, 9(1), 11623.

Tugizimana F, et al. (2018) Metabolomic Analysis of Defense-Related Reprogramming in *Sorghum bicolor* in Response to *Colletotrichum sublineolum* Infection Reveals a Functional Metabolic Web of Phenylpropanoid and Flavonoid Pathways. *Frontiers in plant science*, 9, 1840.

Chojnacki S, et al. (2017) Programmatic access to bioinformatics tools from EMBL-EBI update: 2017. *Nucleic acids research*, 45(W1), W550.

Finnegan T, et al. (2016) The Lipopolysaccharide-Induced Metabolome Signature in *Arabidopsis thaliana* Reveals Dynamic Reprogramming of Phytoalexin and Phytoanticipin

Pathways. PloS one, 11(9), e0163572.

Przyby?a P, et al. (2016) Text mining resources for the life sciences. Database : the journal of biological databases and curation, 2016.

Zehl L, et al. (2016) Handling Metadata in a Neurophysiology Laboratory. Frontiers in neuroinformatics, 10, 26.

de Brevern AG, et al. (2015) Trends in IT Innovation to Build a Next Generation Bioinformatics Solution to Manage and Analyse Biological Big Data Produced by NGS Technologies. BioMed research international, 2015, 904541.

Holl S, et al. (2015) Scientific workflow optimization for improved peptide and protein identification. BMC bioinformatics, 16(1), 284.

Leidenberger S, et al. (2015) Mapping present and future potential distribution patterns for a meso-grazer guild in the Baltic Sea. Journal of biogeography, 42(2), 241.

Pernet C, et al. (2015) Improving functional magnetic resonance imaging reproducibility. GigaScience, 4, 15.

Almiñana C, et al. (2014) The battle of the sexes starts in the oviduct: modulation of oviductal transcriptome by X and Y-bearing spermatozoa. BMC genomics, 15(1), 293.

Barnea ER, et al. (2014) Insight into Preimplantation Factor (PIF*) mechanism for embryo protection and development: target oxidative stress and protein misfolding (PDI and HSP) through essential RIKP [corrected] binding site. PloS one, 9(7), e100263.

Malm EK, et al. (2014) APP: an Automated Proteomics Pipeline for the analysis of mass spectrometry data based on multiple open access tools. BMC bioinformatics, 15(1), 441.

Goossen WT, et al. (2014) Detailed clinical models: representing knowledge, data and semantics in healthcare information technology. Healthcare informatics research, 20(3), 163.

Schera F, et al. (2014) The p-medicine portal-a collaboration platform for research in personalised medicine. Ecancermedalscience, 8, 398.

Tugizimana F, et al. (2014) Multi-platform metabolomic analyses of ergosterol-induced dynamic changes in Nicotiana tabacum cells. PloS one, 9(1), e87846.

Dinov ID, et al. (2014) High-throughput neuroimaging-genetics computational infrastructure. Frontiers in neuroinformatics, 8, 41.

Goodman A, et al. (2014) Ten simple rules for the care and feeding of scientific data. PLoS computational biology, 10(4), e1003542.