Resource Summary Report

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JENA: A Semantic Web Framework for Java

RRID:SCR_001766
Type: Tool

Proper Citation

JENA: A Semantic Web Framework for Java (RRID:SCR_001766)

Resource Information

URL: http://jena.sourceforge.net/

Proper Citation: JENA: A Semantic Web Framework for Java (RRID:SCR_001766)

Description: Java framework for building Semantic Web applications, it provides a collection of tools and Java libraries to help you to develop semantic web and linked-data apps, tools and servers. It provides extensive Java libraries for helping developers develop code that handles RDF, RDFS, RDFa, OWL and SPARQL in line with published W3C recommendations. Jena includes a rule-based inference engine to perform reasoning based on OWL and RDFS ontologies, and a variety of storage strategies to store RDF triples in memory or on disk. The Jena Framework includes: * an API for reading, processing and writing RDF data in XML, N-triples and Turtle formats; * an ontology API for handling OWL and RDFS ontologies; * a rule-based inference engine for reasoning with RDF and OWL data sources; * stores to allow large numbers of RDF triples to be efficiently stored on disk; * a query engine compliant with the latest SPARQL specification * servers to allow RDF data to be published to other applications using a variety of protocols, including SPARQL In April 2012, Jena graduated from the Apache incubator process and was approved as a top-level Apache project.

Abbreviations: Jena

Synonyms: Apache Jena

Resource Type: software toolkit, software resource

Keywords: java, inference engine, semantic, software framework, semantic web, rdf, rdfs, rdfa, owl, sparql

Funding:

Availability: Apache License, v2., The community can contribute to this resource

Resource Name: JENA: A Semantic Web Framework for Java

Resource ID: SCR_001766

Alternate IDs: nif-0000-10271

Record Creation Time: 20220129T080209+0000

Record Last Update: 20250412T054634+0000

Ratings and Alerts

No rating or validation information has been found for JENA: A Semantic Web Framework for Java.

No alerts have been found for JENA: A Semantic Web Framework for Java.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 13 mentions in open access literature.

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

Timón S, et al. (2017) Extending XNAT Platform with an Incremental Semantic Framework. Frontiers in neuroinformatics, 11, 57.

Bonnet E, et al. (2013) BiNoM 2.0, a Cytoscape plugin for accessing and analyzing pathways using standard systems biology formats. BMC systems biology, 7, 18.

Levasseur A, et al. (2012) The chordate proteome history database. Evolutionary bioinformatics online, 8, 437.

Dönitz J, et al. (2012) The ontology-based answers (OBA) service: a connector for embedded usage of ontologies in applications. Frontiers in genetics, 3, 197.

Gosal G, et al. (2011) ProKinO: an ontology for integrative analysis of protein kinases in cancer. PloS one, 6(12), e28782.

Jeong E, et al. (2011) CSO validator: improving manual curation workflow for biological pathways. Bioinformatics (Oxford, England), 27(17), 2471.

Qu XA, et al. (2009) Inferring novel disease indications for known drugs by semantically linking drug action and disease mechanism relationships. BMC bioinformatics, 10 Suppl 5(Suppl 5), S4.

French L, et al. (2009) Application and evaluation of automated semantic annotation of gene expression experiments. Bioinformatics (Oxford, England), 25(12), 1543.

Kanagasabai R, et al. (2009) Mining to find the lipid interaction networks involved in Ovarian Cancers. Summit on translational bioinformatics, 2009, 61.

Lemoine F, et al. (2008) GenoQuery: a new querying module for functional annotation in a genomic warehouse. Bioinformatics (Oxford, England), 24(13), i322.

Bug WJ, et al. (2008) The NIFSTD and BIRNLex vocabularies: building comprehensive ontologies for neuroscience. Neuroinformatics, 6(3), 175.

Baker CJ, et al. (2008) Towards ontology-driven navigation of the lipid bibliosphere. BMC bioinformatics, 9 Suppl 1(Suppl 1), S5.

Robertson N, et al. (2007) DiscoverySpace: an interactive data analysis application. Genome biology, 8(1), R6.