

# Katherine Wolstencroft

## List of Publications by Year in descending order

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Version: 2024-02-01

54  
papers

11,657  
citations

377584

21  
h-index

388640

36  
g-index

59  
all docs

59  
docs citations

59  
times ranked

25531  
citing authors

#	ARTICLE	IF	CITATIONS
1	Establishing a consensus for the hallmarks of cancer based on gene ontology and pathway annotations. BMC Bioinformatics, 2021, 22, 178.	1.2	15
2	Large-scale zero-shot learning in the wild: Classifying zoological illustrations. Ecological Informatics, 2021, 62, 101222.	2.3	5
3	Design of a FAIR digital data health infrastructure in Africa for COVID-19 reporting and research. Genetics & Genomics Next, 2021, 2, e10050.	0.8	27
4	Perspectives on automated composition of workflows in the life sciences. F1000Research, 2021, 10, 897.	0.8	7
5	Semantic annotation of natural history collections. Web Semantics, 2019, 59, 100462.	2.2	13
6	Automated Semantic Annotation of Species Names in Handwritten Texts. Lecture Notes in Computer Science, 2019, , 667-680.	1.0	1
7	Linking natural history collections. , 2018, , .		0
8	From Handwritten Manuscripts to Linked Data. Lecture Notes in Computer Science, 2018, , 330-334.	1.0	2
9	Towards a Digital Infrastructure for Illustrated Handwritten Archives. Lecture Notes in Computer Science, 2018, , 155-166.	1.0	11
10	FAIRDOMHub: a repository and collaboration environment for sharing systems biology research. Nucleic Acids Research, 2017, 45, D404-D407.	6.5	98
11	Identifiers for the 21st century: How to design, provision, and reuse persistent identifiers to maximize utility and impact of life science data. PLoS Biology, 2017, 15, e2001414.	2.6	97
12	The FAIR Guiding Principles for scientific data management and stewardship. Scientific Data, 2016, 3, 160018.	2.4	8,670
13	A comprehensive gene expression analysis at sequential stages of in vitro cardiac differentiation from isolated MESP1-expressing-mesoderm progenitors. Scientific Reports, 2016, 6, 19386.	1.6	53
14	A physiome interoperability roadmap for personalized drug development. Interface Focus, 2016, 6, 20150094.	1.5	8
15	The evolution of standards and data management practices in systems biology. Molecular Systems Biology, 2015, 11, 851.	3.2	35
16	Multidisciplinary Collaboration to Facilitate Hypotheses Generation in Huntington's Disease. , 2015, , .		3
17	SEEK: a systems biology data and model management platform. BMC Systems Biology, 2015, 9, 33.	3.0	75
18	Structuring research methods and data with the research object model: genomics workflows as a case study. Journal of Biomedical Semantics, 2014, 5, 41.	0.9	26

#	ARTICLE	IF	CITATIONS
19	Track Introduction: Scientific Workflows. Lecture Notes in Computer Science, 2014, , 404-406.	1.0	0
20	The Taverna workflow suite: designing and executing workflows of Web Services on the desktop, web or in the cloud. Nucleic Acids Research, 2013, 41, W557-W561.	6.5	567
21	Stealthy annotation of experimental biology by spreadsheets. Concurrency Computation Practice and Experience, 2013, 25, 467-480.	1.4	3
22	Semantic Data and Models Sharing in Systems Biology: The Just Enough Results Model and the SEEK Platform. Lecture Notes in Computer Science, 2013, , 212-227.	1.0	6
23	Semantic Web, Interoperability. , 2013, , 1921-1925.		2
24	Toward interoperable bioscience data. Nature Genetics, 2012, 44, 121-126.	9.4	362
25	RightField: Semantic enrichment of Systems Biology data using spreadsheets. , 2012, , .		1
26	Populous: a tool for building OWL ontologies from templates. BMC Bioinformatics, 2012, 13, S5.	1.2	25
27	RightField: Scientific Knowledge Acquisition by Stealth through Ontology-Enabled Spreadsheets. Lecture Notes in Computer Science, 2012, , 438-441.	1.0	1
28	The Taverna Workbench: Integrating and analysing biological and clinical data with computerised workflows. EMBnet Journal, 2012, 18, 18.	0.2	0
29	Opening new gateways to workflows for life scientists. Studies in Health Technology and Informatics, 2012, 175, 131-41.	0.2	5
30	The SEEK. Methods in Enzymology, 2011, 500, 629-655.	0.4	44
31	OneStop:JWS Online's access point to SBML,SBGN and MIRIAM compliant annotation. Nature Precedings, 2011, , .	0.1	0
32	An experimental workflow development platform for historical document digitisation and analysis. , 2011, , .		7
33	RightField: embedding ontology annotation in spreadsheets. Bioinformatics, 2011, 27, 2021-2022.	1.8	69
34	Community-driven computational biology with Debian Linux. BMC Bioinformatics, 2010, 11, S5.	1.2	42
35	BioCatalogue: a universal catalogue of web services for the life sciences. Nucleic Acids Research, 2010, 38, W689-W694.	6.5	185
36	Functional Units: Abstractions for Web Service Annotations. , 2010, , .		5

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37	The Evolution of myExperiment. , 2010, , .		11
38	BioCatalogue: A Curated Web Service Registry For The Life Science Community. Nature Precedings, 2009, , .	0.1	13
39	Benchmarking workflow discovery: a case study from bioinformatics. Concurrency Computation Practice and Experience, 2009, 21, 2052-2069.	1.4	8
40	The data playground: An intuitive workflow specification environment. Future Generation Computer Systems, 2009, 25, 453-459.	4.9	8
41	Analysing Scientific Workflows: Why Workflows Not Only Connect Web Services. , 2009, , .		27
42	Metadata Management in the Taverna Workflow System. , 2008, , .		30
43	Solutions for data integration in functional genomics: a critical assessment and case study. Briefings in Bioinformatics, 2008, 9, 532-544.	3.2	23
44	Data curation + process curation=data integration + science. Briefings in Bioinformatics, 2008, 9, 506-517.	3.2	53
45	Towards dynamic database infrastructures for mouse genetics. , 2008, , .		1
46	The Data Playground: An Intuitive Workflow Specification Environment. , 2007, , .		13
47	A systematic strategy for large-scale analysis of genotypeâ€“phenotype correlations: identification of candidate genes involved in African trypanosomiasis. Nucleic Acids Research, 2007, 35, 5625-5633.	6.5	51
48	The <SUP align=right>my</SUP>Grid ontology: bioinformatics service discovery. International Journal of Bioinformatics Research and Applications, 2007, 3, 303.	0.1	72
49	Applying OWL Reasoning to Genomic Data. , 2007, , 225-248.		14
50	Knowledge Discovery for Biology with Taverna. , 2007, , 355-395.		12
51	Taverna: a tool for building and running workflows of services. Nucleic Acids Research, 2006, 34, W729-W732.	6.5	758
52	Semantic Annotation of Natural History Collections. SSRN Electronic Journal, 0, , .	0.4	1
53	A Workflow for the Semantic Annotation of Field Books and Specimen Labels. Biodiversity Information Science and Standards, 0, 2, e25839.	0.0	0
54	The Semantic Field Book Annotator. Biodiversity Information Science and Standards, 0, 3, .	0.0	0