

# Mark D Wilkinson

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

85  
papers

7,492  
citations

24  
h-index

86  
g-index

113  
ext. papers

10,240  
ext. citations

4.8  
avg, IF

5.07  
L-index

#	Paper	IF	Citations
85	Semantic modelling of common data elements for rare disease registries, and a prototype workflow for their deployment over registry data.. <i>Journal of Biomedical Semantics</i> , <b>2022</b> , 13, 9	2.2	0
84	Endogenous indole-3-acetamide levels contribute to the crosstalk between auxin and abscisic acid, and trigger plant stress responses in Arabidopsis. <i>Journal of Experimental Botany</i> , <b>2021</b> , 72, 459-475	7	10
83	FAIR Principles: Interpretations and Implementation Considerations. <i>Data Intelligence</i> , <b>2020</b> , 2, 10-29	3	66
82	BioHackathon 2015: Semantics of data for life sciences and reproducible research. <i>F1000Research</i> , <b>2020</b> , 9, 136	3.6	2
81	Evaluating FAIR maturity through a scalable, automated, community-governed framework. <i>Scientific Data</i> , <b>2019</b> , 6, 174	8.2	41
80	Robust and automatic definition of microbiome states. <i>PeerJ</i> , <b>2019</b> , 7, e6657	3.1	4
79	Virulence- and signaling-associated genes display a preference for long 3'UTRs during rice infection and metabolic stress in the rice blast fungus. <i>New Phytologist</i> , <b>2019</b> , 221, 399-414	9.8	3
78	Genome-wide analysis of the H3K27me3 epigenome and transcriptome in Brassica rapa. <i>GigaScience</i> , <b>2019</b> , 8,	7.6	10
77	MECP2 variation in Rett syndrome-An overview of current coverage of genetic and phenotype data within existing databases. <i>Human Mutation</i> , <b>2018</b> , 39, 914-924	4.7	12
76	Extracting Diagnostic Knowledge from MedLine Plus: A Comparison between MetaMap and cTAKES Approaches. <i>Current Bioinformatics</i> , <b>2018</b> , 13, 573-582	4.7	3
75	Genome-wide polyadenylation site mapping datasets in the rice blast fungus Magnaporthe oryzae. <i>Scientific Data</i> , <b>2018</b> , 5, 180271	8.2	2
74	MDPbiome: microbiome engineering through prescriptive perturbations. <i>Bioinformatics</i> , <b>2018</b> , 34, i838-i847	8.4	9
73	A design framework and exemplar metrics for FAIRness. <i>Scientific Data</i> , <b>2018</b> , 5, 180118	8.2	90
72	Preparing Data at the Source to Foster Interoperability across Rare Disease Resources. <i>Advances in Experimental Medicine and Biology</i> , <b>2017</b> , 1031, 165-179	3.6	8
71	Molecular characterization of a novel ssRNA ourmia-like virus from the rice blast fungus Magnaporthe oryzae. <i>Archives of Virology</i> , <b>2017</b> , 162, 891-895	2.6	19
70	Cloudy, increasingly FAIR; revisiting the FAIR Data guiding principles for the European Open Science Cloud. <i>Information Services and Use</i> , <b>2017</b> , 37, 49-56	0.5	138
69	Publishing FAIR Data: An Exemplar Methodology Utilizing PHI-Base. <i>Frontiers in Plant Science</i> , <b>2016</b> , 7, 641	6.2	15

68	The FAIR Guiding Principles for scientific data management and stewardship. <i>Scientific Data</i> , <b>2016</b> , 3, 160018	8.2	4154
67	Diagnostic Knowledge Extraction from MedlinePlus: An Application for Infectious Diseases. <i>Advances in Intelligent Systems and Computing</i> , <b>2015</b> , 79-87	0.4	7
66	Enhanced reproducibility of SADI web service workflows with Galaxy and Docker. <i>GigaScience</i> , <b>2015</b> , 4, 59	7.6	11
65	VPS13D Gene Variant Is Associated with Altered IL-6 Production and Mortality in Septic Shock. <i>Journal of Innate Immunity</i> , <b>2015</b> , 7, 545-53	6.9	7
64	Quantitative evaluation of bias in PCR amplification and next-generation sequencing derived from metabarcoding samples. <i>Analytical and Bioanalytical Chemistry</i> , <b>2015</b> , 407, 1841-8	4.4	77
63	Automatic detection and resolution of measurement-unit conflicts in aggregated data. <i>BMC Medical Genomics</i> , <b>2014</b> , 7 Suppl 1, S12	3.7	3
62	Leveraging Applications of Formal Methods, Verification and Validation. Specialized Techniques and Applications. <i>Lecture Notes in Computer Science</i> , <b>2014</b> ,	0.9	2
61	The relationship between host lifespan and pathogen reservoir potential: an analysis in the system <i>Arabidopsis thaliana</i> --cucumber mosaic virus. <i>PLoS Pathogens</i> , <b>2014</b> , 10, e1004492	7.6	40
60	Nanopublishing Clinical Diagnoses: Tracking Diagnostic Knowledge Base Content and Utilization <b>2014</b> ,		1
59	The SemanticScience Integrated Ontology (SIO) for biomedical research and knowledge discovery. <i>Journal of Biomedical Semantics</i> , <b>2014</b> , 5, 14	2.2	101
58	Bioinformatics Tools for Next-Generation RNA Sequencing Analysis <b>2014</b> , 371-391		1
57	Executing SADI services in Galaxy. <i>Journal of Biomedical Semantics</i> , <b>2014</b> , 5, 42	2.2	6
56	Automatically exposing OpenLifeData via SADI semantic Web Services. <i>Journal of Biomedical Semantics</i> , <b>2014</b> , 5, 46	2.2	10
55	BioHackathon series in 2011 and 2012: penetration of ontology and linked data in life science domains. <i>Journal of Biomedical Semantics</i> , <b>2014</b> , 5, 5	2.2	42
54	Automatic Annotation of Bioinformatics Workflows with Biomedical Ontologies. <i>Lecture Notes in Computer Science</i> , <b>2014</b> , 464-478	0.9	2
53	The 3rd DBCLS BioHackathon: improving life science data integration with Semantic Web technologies. <i>Journal of Biomedical Semantics</i> , <b>2013</b> , 4, 6	2.2	22
52	OPPL-Galaxy, a Galaxy tool for enhancing ontology exploitation as part of bioinformatics workflows. <i>Journal of Biomedical Semantics</i> , <b>2013</b> , 4, 2	2.2	2
51	Health Web Science. <i>Foundations and Trends in Web Science</i> , <b>2013</b> , 4, 269-419	0	3

50	The emergent discipline of health web science. <i>Journal of Medical Internet Research</i> , <b>2013</b> , 15, e166	7.6	19
49	The SADI Personal Health Lens: A Web Browser-Based System for Identifying Personally Relevant Drug Interactions. <i>JMIR Research Protocols</i> , <b>2013</b> , 2, e14	2	7
48	Genomics data resources: frameworks and standards. <i>Methods in Molecular Biology</i> , <b>2012</b> , 856, 489-511	1.4	2
47	Extending and encoding existing biological terminologies and datasets for use in the reasoned semantic web. <i>Journal of Biomedical Semantics</i> , <b>2012</b> , 3, 6	2.2	4
46	SPARQL assist language-neutral query composer. <i>BMC Bioinformatics</i> , <b>2012</b> , 13 Suppl 1, S2	3.6	7
45	Analysis of a multilevel diagnosis decision support system and its implications: a case study. <i>Computational and Mathematical Methods in Medicine</i> , <b>2012</b> , 2012, 367345	2.8	13
44	OWL-DL Domain-Models as Abstract Workflows. <i>Lecture Notes in Computer Science</i> , <b>2012</b> , 56-66	0.9	6
43	Bioscientific Data Processing and Modeling. <i>Lecture Notes in Computer Science</i> , <b>2012</b> , 7-11	0.9	
42	The Semantic Automated Discovery and Integration (SADI) Web service Design-Pattern, API and Reference Implementation. <i>Nature Precedings</i> , <b>2011</b> ,		2
41	The 2nd DBCLS BioHackathon: interoperable bioinformatics Web services for integrated applications. <i>Journal of Biomedical Semantics</i> , <b>2011</b> , 2, 4	2.2	15
40	The Semantic Automated Discovery and Integration (SADI) Web service Design-Pattern, API and Reference Implementation. <i>Journal of Biomedical Semantics</i> , <b>2011</b> , 2, 8	2.2	77
39	OWL2Perl: creating Perl modules from OWL class definitions. <i>Bioinformatics</i> , <b>2010</b> , 26, 2357-8	7.2	2
38	SADI, SHARE, and the in silico scientific method. <i>BMC Bioinformatics</i> , <b>2010</b> , 11 Suppl 12, S7	3.6	25
37	The DBCLS BioHackathon: standardization and interoperability for bioinformatics web services and workflows. The DBCLS BioHackathon Consortium*. <i>Journal of Biomedical Semantics</i> , <b>2010</b> , 1, 8	2.2	24
36	Semantically-Guided Workflow Construction in Taverna: The SADI and BioMoby Plug-Ins. <i>Lecture Notes in Computer Science</i> , <b>2010</b> , 301-312	0.9	14
35	Tools in Scientific Workflow Composition. <i>Lecture Notes in Computer Science</i> , <b>2010</b> , 258-260	0.9	2
34	Moby and Moby 2: creatures of the deep (web). <i>Briefings in Bioinformatics</i> , <b>2009</b> , 10, 114-28	13.4	18
33	Social tagging in the life sciences: characterizing a new metadata resource for bioinformatics. <i>BMC Bioinformatics</i> , <b>2009</b> , 10, 313	3.6	12

32	Optimization of Distributed SPARQL Queries Using EdmondsRAlgorithm and PrimR Algorithm <b>2009</b>		9
31	SADI Semantic Web Services - Cause you canR always GET what you want! <b>2009</b> ,		13
30	SHARE: A Semantic Web Query Engine for Bioinformatics. <i>Lecture Notes in Computer Science</i> , <b>2009</b> , 367-369		21
29	Semi-automatic web service composition for the life sciences using the BioMoby semantic web framework. <i>Journal of Biomedical Informatics</i> , <b>2008</b> , 41, 837-47	10.2	39
28	Interoperability with Moby 1.0--itR better than sharing your toothbrush!. <i>Briefings in Bioinformatics</i> , <b>2008</b> , 9, 220-31	13.4	73
27	Interoperability With Moby 1.0 - ItR Better Than Sharing Your Toothbrush!. <i>Nature Precedings</i> , <b>2008</b> ,		1
26	The generation challenge programme platform: semantic standards and workbench for crop science. <i>International Journal of Plant Genomics</i> , <b>2008</b> , 2008, 369601		3
25	Using a Novel Data Transformation Technique to Provide the EMBOSS Software Suite as Semantic Web Services <b>2007</b> ,		3
24	Tag clouds for summarizing web search results <b>2007</b> ,		97
23	DataBiNS: a BioMoby-based data-mining workflow for biological pathways and non-synonymous SNPs. <i>Bioinformatics</i> , <b>2007</b> , 23, 780-2	7.2	6
22	Vcsa1 gene peptides for the treatment of inflammatory and allergic reactions. <i>Recent Patents on Inflammation and Allergy Drug Discovery</i> , <b>2007</b> , 1, 124-32	5.4	8
21	BioMoby extensions to the Taverna workflow management and enactment software. <i>BMC Bioinformatics</i> , <b>2006</b> , 7, 523	3.6	41
20	iHOPerator: user-scripting a personalized bioinformatics Web, starting with the iHOP website. <i>BMC Bioinformatics</i> , <b>2006</b> , 7, 534	3.6	14
19	The Life Sciences Semantic Web is full of creeps!. <i>Briefings in Bioinformatics</i> , <b>2006</b> , 7, 275-86	13.4	65
18	Gbrowse Moby: a Web-based browser for BioMoby Services. <i>Source Code for Biology and Medicine</i> , <b>2006</b> , 1, 4	1.9	16
17	FAST, CHEAP AND OUT OF CONTROL: A ZERO CURATION MODEL FOR ONTOLOGY DEVELOPMENT <b>2005</b> ,		6
16	BioMOBY successfully integrates distributed heterogeneous bioinformatics Web Services. The PlaNet exemplar case. <i>Plant Physiology</i> , <b>2005</b> , 138, 5-17	6.6	71
15	Comparison of ESTs from juvenile and adult phases of the giant unicellular green alga <i>Acetabularia acetabulum</i> . <i>BMC Plant Biology</i> , <b>2004</b> , 4, 3	5.3	18

14	Applying Semantic Web Services to Bioinformatics: Experiences Gained, Lessons Learnt. <i>Lecture Notes in Computer Science</i> , <b>2004</b> , 350-364	0.9	34
13	Genquire: genome annotation browser/editor. <i>Bioinformatics</i> , <b>2002</b> , 18, 1398-9	7.2	8
12	BioMOBY: an open source biological web services proposal. <i>Briefings in Bioinformatics</i> , <b>2002</b> , 3, 331-41	13.4	252
11	The Bioperl toolkit: Perl modules for the life sciences. <i>Genome Research</i> , <b>2002</b> , 12, 1611-8	9.7	1234
10	Different Roles of Flowering-Time Genes in the Activation of Floral Initiation Genes in Arabidopsis. <i>Plant Cell</i> , <b>1997</b> , 9, 1921	11.6	9
9	Unusual Floral Organs Controls Meristem Identity and Organ Primordia Fate in Arabidopsis. <i>Plant Cell</i> , <b>1995</b> , 7, 1485	11.6	31
8	Parallels between UNUSUAL FLORAL ORGANS and FIMBRIATA, genes controlling flower development in Arabidopsis and Antirrhinum. <i>Plant Cell</i> , <b>1995</b> , 7, 1501-10	11.6	163
7	Interoperability and FAIRness through a novel combination of Web technologies		3
6	Interoperability and FAIRness through a novel combination of Web technologies. <i>PeerJ Computer Science</i> , <b>3</b> , e110	2.7	38
5	BioHackathon series in 2013 and 2014: improvements of semantic interoperability in life science data and services. <i>F1000Research</i> , <b>8</b> , 1677	3.6	
4	A design framework and exemplar metrics for FAIRness		2
3	Evaluating FAIR-Compliance Through an Objective, Automated, Community-Governed Framework		5
2	Evaluating FAIR Maturity Through a Scalable, Automated, Community-Governed Framework		3
1	Semantic modelling of Common Data Elements for Rare Disease registries, and a prototype workflow for their deployment over registry data		1