

Lynn M Schriml

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.

72
papers

16,577
citations

31
h-index

81
g-index

81
ext. papers

20,818
ext. citations

17
avg, IF

7.8
L-index

#	Paper	IF	Citations
72	Darwinian genomics and diversity in the tree of life.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022 , 119,	11.5	2
71	MixS-SA: a MixS extension defining the minimum information standard for sequence data from symbiont-associated micro-organisms. <i>ISME Communications</i> , 2022 , 2,		1
70	A community approach to the cancer-variant-interpretation bottleneck. <i>Nature Cancer</i> , 2022 , 3, 522-525	15.4	0
69	Reporting guidelines for human microbiome research: the STORMS checklist. <i>Nature Medicine</i> , 2021 , 27, 1885-1892	50.5	19
68	The Human Disease Ontology 2022 update. <i>Nucleic Acids Research</i> , 2021 ,	20.1	11
67	Annotating unknown species of urban microorganisms on a global scale unveils novel functional diversity and local environment association. <i>Environmental Research</i> , 2021 , 207, 112183	7.9	0
66	OBO Foundry in 2021: operationalizing open data principles to evaluate ontologies. <i>Database: the Journal of Biological Databases and Curation</i> , 2021 , 2021,	5	7
65	COVID-19 biomarkers and their overlap with comorbidities in a disease biomarker data model. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	2
64	A global metagenomic map of urban microbiomes and antimicrobial resistance. <i>Cell</i> , 2021 , 184, 3376-3393	36.17	42
63	Microbiome Metadata Standards: Report of the National Microbiome Data Collaborative Workshop and Follow-On Activities. <i>MSystems</i> , 2021 , 6,	7.6	7
62	Response to Biesecker et al. <i>American Journal of Human Genetics</i> , 2021 , 108, 1807-1808	11	0
61	COVID-19 pandemic reveals the peril of ignoring metadata standards. <i>Scientific Data</i> , 2020 , 7, 188	8.2	30
60	A harmonized meta-knowledgebase of clinical interpretations of somatic genomic variants in cancer. <i>Nature Genetics</i> , 2020 , 52, 448-457	36.3	58
59	Wikidata as a knowledge graph for the life sciences. <i>ELife</i> , 2020 , 9,	8.9	24
58	Toward unrestricted use of public genomic data. <i>Science</i> , 2019 , 363, 350-352	33.3	25
57	Consent insufficient for data release-Response. <i>Science</i> , 2019 , 364, 446	33.3	4
56	Parasite microbiome project: Grand challenges. <i>PLoS Pathogens</i> , 2019 , 15, e1008028	7.6	22

55	Minimum Information about an Uncultivated Virus Genome (MIUViG). <i>Nature Biotechnology</i> , 2019 , 37, 29-37	44.5	180
54	Human Disease Ontology 2018 update: classification, content and workflow expansion. <i>Nucleic Acids Research</i> , 2019 , 47, D955-D962	20.1	177
53	ECO, the Evidence & Conclusion Ontology: community standard for evidence information. <i>Nucleic Acids Research</i> , 2019 , 47, D1186-D1194	20.1	42
52	FoodOn: a harmonized food ontology to increase global food traceability, quality control and data integration. <i>Npj Science of Food</i> , 2018 , 2, 23	6.3	83
51	Disease Ontology: improving and unifying disease annotations across species. <i>DMM Disease Models and Mechanisms</i> , 2018 , 11,	4.1	42
50	Molecular, phenotypic, and sample-associated data to describe pluripotent stem cell lines and derivatives. <i>Scientific Data</i> , 2017 , 4, 170030	8.2	31
49	Genomic Methods and Microbiological Technologies for Profiling Novel and Extreme Environments for the Extreme Microbiome Project (XMP). <i>Journal of Biomolecular Techniques</i> , 2017 , 28, 31-39	1.1	31
48	Minimum information about a single amplified genome (MISAG) and a metagenome-assembled genome (MIMAG) of bacteria and archaea. <i>Nature Biotechnology</i> , 2017 , 35, 725-731	44.5	648
47	Wikidata as a semantic framework for the Gene Wiki initiative. <i>Database: the Journal of Biological Databases and Curation</i> , 2016 , 2016,	5	37
46	Integrated Genomic Analysis of Diverse Induced Pluripotent Stem Cells from the Progenitor Cell Biology Consortium. <i>Stem Cell Reports</i> , 2016 , 7, 110-25	8	72
45	The Human Phenotype Ontology: Semantic Unification of Common and Rare Disease. <i>American Journal of Human Genetics</i> , 2015 , 97, 111-24	11	147
44	Disease Ontology 2015 update: an expanded and updated database of human diseases for linking biomedical knowledge through disease data. <i>Nucleic Acids Research</i> , 2015 , 43, D1071-8	20.1	403
43	The Disease Ontology: fostering interoperability between biological and clinical human disease-related data. <i>Mammalian Genome</i> , 2015 , 26, 584-9	3.2	50
42	Generating a focused view of disease ontology cancer terms for pan-cancer data integration and analysis. <i>Database: the Journal of Biological Databases and Curation</i> , 2015 , 2015, bav032	5	32
41	Genomic standards consortium projects. <i>Standards in Genomic Sciences</i> , 2014 , 9, 599-601		21
40	Report of the 14th Genomic Standards Consortium Meeting, Oxford, UK, September 17-21, 2012.. <i>Standards in Genomic Sciences</i> , 2014 , 9, 1236-1250		1
39	Standardized metadata for human pathogen/vector genomic sequences. <i>PLoS ONE</i> , 2014 , 9, e99979	3.7	25
38	MixS-BE: a MixS extension defining a minimum information standard for sequence data from the built environment. <i>ISME Journal</i> , 2014 , 8, 1-3	11.9	109

37	Genomic Standards Consortium Projects. <i>Standards in Genomic Sciences</i> , 2014 , 9, 599-601		23
36	Structure, function and diversity of the healthy human microbiome. <i>Nature</i> , 2012 , 486, 207-14	50.4	6938
35	Disease Ontology: a backbone for disease semantic integration. <i>Nucleic Acids Research</i> , 2012 , 40, D940-620.1		562
34	A framework for human microbiome research. <i>Nature</i> , 2012 , 486, 215-21	50.4	1722
33	The Metadata Coverage Index (MCI): A standardized metric for quantifying database metadata richness. <i>Standards in Genomic Sciences</i> , 2012 , 6, 438-47		6
32	Report of the 13(th) Genomic Standards Consortium Meeting, Shenzhen, China, March 4-7, 2012. <i>Standards in Genomic Sciences</i> , 2012 , 6, 276-86		1
31	RCN4GSC Workshop Report: Managing Data at the Interface of Biodiversity and (Meta)Genomics, March 2011. <i>Standards in Genomic Sciences</i> , 2012 , 7, 159-65		5
30	Minimum information about a marker gene sequence (MIMARKS) and minimum information about any (x) sequence (MIxS) specifications. <i>Nature Biotechnology</i> , 2011 , 29, 415-20	44.5	445
29	The Translational Medicine Ontology and Knowledge Base: driving personalized medicine by bridging the gap between bench and bedside. <i>Journal of Biomedical Semantics</i> , 2011 , 2 Suppl 2, S1	2.2	55
28	The Genomic Standards Consortium. <i>PLoS Biology</i> , 2011 , 9, e1001088	9.7	143
27	GeMInA, Genomic Metadata for Infectious Agents, a geospatial surveillance pathogen database. <i>Nucleic Acids Research</i> , 2010 , 38, D754-64	20.1	20
26	Metagenomes and metatranscriptomes from the L4 long-term coastal monitoring station in the Western English Channel. <i>Standards in Genomic Sciences</i> , 2010 , 3, 183-93		22
25	Metagenomics: A founding finds its feet. <i>Standards in Genomic Sciences</i> , 2010 , 3, 212-3		
24	Meeting Report from the Genomic Standards Consortium (GSC) Workshop 9. <i>Standards in Genomic Sciences</i> , 2010 , 3, 216-24		2
23	Meeting Report from the Genomic Standards Consortium (GSC) Workshop 10. <i>Standards in Genomic Sciences</i> , 2010 , 3, 225-31		7
22	Meeting Report: "Metagenomics, Metadata and Meta-analysis" (M3) Workshop at the Pacific Symposium on Biocomputing 2010. <i>Standards in Genomic Sciences</i> , 2010 , 2, 357-60		2
21	Habitat-Lite: a GSC case study based on free text terms for environmental metadata. <i>OMICS A Journal of Integrative Biology</i> , 2008 , 12, 129-36	3.8	34
20	Laying the foundation for a Genomic Rosetta Stone: creating information hubs through the use of consensus identifiers. <i>OMICS A Journal of Integrative Biology</i> , 2008 , 12, 123-7	3.8	11

19	Database resources of the National Center for Biotechnology Information. <i>Nucleic Acids Research</i> , 2005 , 33, D39-45	20.1	343
18	Development and evaluation of an automated annotation pipeline and cDNA annotation system. <i>Genome Research</i> , 2003 , 13, 1542-51	9.7	24
17	Human disease genes and their cloned mouse orthologs: exploration of the FANTOM2 cDNA sequence data set. <i>Genome Research</i> , 2003 , 13, 1496-500	9.7	6
16	Connecting sequence and biology in the laboratory mouse. <i>Genome Research</i> , 2003 , 13, 1505-19	9.7	14
15	Database resources of the National Center for Biotechnology. <i>Nucleic Acids Research</i> , 2003 , 31, 28-33	20.1	682
14	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs. <i>Nature</i> , 2002 , 420, 563-73	50.4	1350
13	Database resources of the National Center for Biotechnology Information: 2002 update. <i>Nucleic Acids Research</i> , 2002 , 30, 13-6	20.1	167
12	An ATP-binding cassette gene (ABCG3) closely related to the multidrug transporter ABCG2 (MXR/ABCP) has an unusual ATP-binding domain. <i>Mammalian Genome</i> , 2001 , 12, 86-8	3.2	27
11	A radiation hybrid map of mouse genes. <i>Nature Genetics</i> , 2001 , 29, 201-5	36.3	61
10	Identifying and characterizing a five-gene cluster of ATP-binding cassette transporters mapping to human chromosome 17q24: a new subgroup within the ABCA subfamily. <i>GeneScreen</i> , 2001 , 1, 157-164		15
9	Functional annotation of a full-length mouse cDNA collection. <i>Nature</i> , 2001 , 409, 685-90	50.4	560
8	Use of denaturing HPLC to map human and murine genes and to validate single-nucleotide polymorphisms. <i>BioTechniques</i> , 2000 , 28, 740-5	2.5	18
7	Identification of 18 mouse ABC genes and characterization of the ABC superfamily in <i>Mus musculus</i> . <i>Genomics</i> , 2000 , 64, 24-31	4.3	25
6	Mutational spectra of PTEN/MMAC1 gene: a tumor suppressor with lipid phosphatase activity. <i>Journal of the National Cancer Institute</i> , 1999 , 91, 1922-32	9.7	433
5	Dating the origin of the CCR5-Delta32 AIDS-resistance allele by the coalescence of haplotypes. <i>American Journal of Human Genetics</i> , 1998 , 62, 1507-15	11	428
4	Wikidata as a linked-data hub for Biodiversity data. <i>Biodiversity Information Science and Standards</i> , 2013 , 3, 1-15		4
3	Annotating public fungal ITS sequences from the built environment according to the MixS-Built Environment standard. Report from a May 23-24, 2016 workshop (Gothenburg, Sweden). <i>MycoKeys</i> , 2016 , 16, 1-15	2.4	13
2	A harmonized meta-knowledgebase of clinical interpretations of cancer genomic variants		5

1 Wikidata as a FAIR knowledge graph for the life sciences

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