Lynn M Schriml

List of Publications by Year
in descending order

74 papers	23,377 citations	94433 37 h-index	85541 71 g-index
81 all docs	81 docs citations	81 times ranked	33531 citing authors

#	Article	IF	Citations
1	The Human Disease Ontology 2022 update. Nucleic Acids Research, 2022, 50, D1255-D1261.	14.5	92
2	Annotating unknown species of urban microorganisms on a global scale unveils novel functional diversity and local environment association. Environmental Research, 2022, 207, 112183.	7.5	7
3	Darwinian genomics and diversity in the tree of life. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	19
4	MIxS-SA: a MIxS extension defining the minimum information standard for sequence data from symbiont-associated micro-organisms. ISME Communications, 2022, 2, .	4.2	3
5	eP063: Genetic variants associated with childhood cancers: Curation initiatives of the ClinGen Somatic Cancer Pediatric Taskforce. Genetics in Medicine, 2022, 24, S41-S42.	2.4	0
6	A decade of <i>GigaScience</i>: 10 years of the evolving genomic and biomedical standards landscape. GigaScience, 2022, 11, .	6.4	3
7	A community approach to the cancer-variant-interpretation bottleneck. Nature Cancer, 2022, 3, 522-525.	13.2	3
8	Microbiome Metadata Standards: Report of the National Microbiome Data Collaborative's Workshop and Follow-On Activities. MSystems, 2021, 6, .	3.8	28
9	COVID-19 biomarkers and their overlap with comorbidities in a disease biomarker data model. Briefings in Bioinformatics, 2021, 22, .	6.5	11
10	A global metagenomic map of urban microbiomes and antimicrobial resistance. Cell, 2021, 184, 3376-3393.e17.	28.9	164
11	Abstract 210: Advancing knowledgebase representation of pediatric cancer variants through ClinGen/CIViC collaboration. , 2021, , .		0
12	Response to Biesecker etÂal.. American Journal of Human Genetics, 2021, 108, 1807-1808.	6.2	3
13	OBO Foundry in 2021: operationalizing open data principles to evaluate ontologies. Database: the Journal of Biological Databases and Curation, 2021, 2021, .	3.0	77
14	Reporting guidelines for human microbiome research: the STORMS checklist. Nature Medicine, 2021, 27, 1885-1892.	30.7	170
15	Etiology context of rare diseases in the Human Disease Ontology. , 2021, , .		0
16	COVID-19 pandemic reveals the peril of ignoring metadata standards. Scientific Data, 2020, 7, 188.	5.3	56
17	A harmonized meta-knowledgebase of clinical interpretations of somatic genomic variants in cancer. Nature Genetics, 2020, 52, 448-457.	21.4	104
18	Wikidata as a knowledge graph for the life sciences. ELife, 2020, 9, .	6.0	76

#	Article	IF	Citations
19	Parasite microbiome project: Grand challenges. PLoS Pathogens, 2019, 15, e1008028.	4.7	50
20	Toward unrestricted use of public genomic data. Science, 2019, 363, 350-352.	12.6	45
21	Consent insufficient for data releaseâ€"Response. Science, 2019, 364, 446-446.	12.6	5
22	Minimum Information about an Uncultivated Virus Genome (MIUViG). Nature Biotechnology, 2019, 37, 29-37.	17.5	414
23	Human Disease Ontology 2018 update: classification, content and workflow expansion. Nucleic Acids Research, 2019, 47, D955-D962.	14.5	383
24	ECO, the Evidence & Conclusion Ontology: community standard for evidence information. Nucleic Acids Research, 2019, 47, D1186-D1194.	14.5	67
25	FoodOn: a harmonized food ontology to increase global food traceability, quality control and data integration. Npj Science of Food, 2018, 2, 23.	5.5	164
26	Augmenting the disease ontology improves and unifies disease annotations across species. DMM Disease Models and Mechanisms, 2018, 11, .	2.4	81
27	Molecular, phenotypic, and sample-associated data to describe pluripotent stem cell lines and derivatives. Scientific Data, 2017, 4, 170030.	5.3	48
28	Minimum information about a single amplified genome (MISAG) and a metagenome-assembled genome (MIMAG) of bacteria and archaea. Nature Biotechnology, 2017, 35, 725-731.	17.5	1,512
29	Genomic Methods and Microbiological Technologies for Profiling Novel and Extreme Environments for the Extreme Microbiome Project (XMP). Journal of Biomolecular Techniques, 2017, 28, 31-39.	1.5	53
30	Wikidata as a semantic framework for the Gene Wiki initiative. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw015.	3.0	47
31	Integrated Genomic Analysis of Diverse Induced Pluripotent Stem Cells from the Progenitor Cell Biology Consortium. Stem Cell Reports, 2016, 7, 110-125.	4.8	101
32	Generating a focused view of disease ontology cancer terms for pan-cancer data integration and analysis. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav032-bav032.	3.0	40
33	The Human Phenotype Ontology: Semantic Unification of Common and Rare Disease. American Journal of Human Genetics, 2015, 97, 111-124.	6.2	203
34	Disease Ontology 2015 update: an expanded and updated database of human diseases for linking biomedical knowledge through disease data. Nucleic Acids Research, 2015, 43, D1071-D1078.	14.5	498
35	The Disease Ontology: fostering interoperability between biological and clinical human disease-related data. Mammalian Genome, 2015, 26, 584-589.	2.2	60
36	Standardized Metadata for Human Pathogen/Vector Genomic Sequences. PLoS ONE, 2014, 9, e99979.	2.5	34

#	Article	IF	Citations
37	MIxS-BE: a MIxS extension defining a minimum information standard for sequence data from the built environment. ISME Journal, 2014, 8, 1-3.	9.8	127
38	Genomic Standards Consortium Projects. Standards in Genomic Sciences, 2014, 9, 599-601.	1.5	26
39	Report of the 14th Genomic Standards Consortium Meeting, Oxford, UK, September 17-21, 2012.. Standards in Genomic Sciences, 2014, 9, 1236-1250.	1.5	1
40	Genomic Standards Consortium Projects. Standards in Genomic Sciences, 2014, 9, 599-601.	1.5	29
41	The Metadata Coverage Index (MCI): A standardized metric for quantifying database metadata richness. Standards in Genomic Sciences, 2012, 6, 444-453.	1.5	8
42	Report of the 13th Genomic Standards Consortium Meeting, Shenzhen, China, March 4â€"7, 2012.. Standards in Genomic Sciences, 2012, 6, 276-286.	1.5	3
43	RCN4GSC Workshop Report: Managing Data at the Interface of Biodiversity and (Meta)Genomics, March 2011. Standards in Genomic Sciences, 2012, 7, 159-165.	1.5	5
44	Structure, function and diversity of the healthy human microbiome. Nature, 2012, 486, 207-214.	27.8	9,614
45	Disease Ontology: a backbone for disease semantic integration. Nucleic Acids Research, 2012, 40, D940-D946.	14.5	793
46	A framework for human microbiome research. Nature, 2012, 486, 215-221.	27.8	2,249
47	Minimum information about a marker gene sequence (MIMARKS) and minimum information about any (x) sequence (MIxS) specifications. Nature Biotechnology, 2011, 29, 415-420.	17.5	608
48	The Translational Medicine Ontology and Knowledge Base: driving personalized medicine by bridging the gap between bench and bedside. Journal of Biomedical Semantics, 2011, 2, S1.	1.6	68
49	The Genomic Standards Consortium. PLoS Biology, 2011, 9, e1001088.	5.6	180
50	Metagenomes and metatranscriptomes from the L4 long-term coastal monitoring station in the Western English Channel. Standards in Genomic Sciences, 2010, 3, 183-193.	1.5	28
51	Metagenomics: A foundling finds its feet.. Standards in Genomic Sciences, 2010, 3, 212-213.	1.5	1
52	Meeting Report from the Genomic Standards Consortium (GSC) Workshop 9. Standards in Genomic Sciences, 2010, 3, 216-224.	1.5	3
53	Meeting Report from the Genomic Standards Consortium (GSC) Workshop 10. Standards in Genomic Sciences, 2010, 3, 225-231.	1.5	8
54	Meeting Report: â€œMetagenomics, Metadata and Meta-analysisâ€•(M3) Workshop at the Pacific Symposium on Biocomputing 2010. Standards in Genomic Sciences, 2010, 2, 357-360.	1.5	2

#	Article	IF	Citations
55	GeMInA, Genomic Metadata for Infectious Agents, a geospatial surveillance pathogen database. Nucleic Acids Research, 2010, 38, D754-D764.	14.5	25
56	Habitat-Lite: A GSC Case Study Based on Free Text Terms for Environmental Metadata. OMICS A Journal of Integrative Biology, 2008, 12, 129-136.	2.0	39
57	Laying the Foundation for a Genomic Rosetta Stone: Creating Information Hubs through the Use of Consensus Identifiers. OMICS A Journal of Integrative Biology, 2008, 12, 123-127.	2.0	12
58	Database resources of the National Center for Biotechnology Information. Nucleic Acids Research, 2004, 33, D39-D45.	14.5	369
59	Development and Evaluation of an Automated Annotation Pipeline and cDNA Annotation System. Genome Research, 2003, 13, 1542-1551.	5.5	34
60	Human Disease Genes and Their Cloned Mouse Orthologs: Exploration of the FANTOM2 cDNA Sequence Data Set. Genome Research, 2003, 13, 1496-1500.	5.5	7
61	Connecting Sequence and Biology in the Laboratory Mouse. Genome Research, 2003, 13, 1505-1519.	5.5	18
62	Database resources of the National Center for Biotechnology. Nucleic Acids Research, 2003, 31, 28-33.	14.5	879
63	Database resources of the National Center for Biotechnology Information: 2002 update. Nucleic Acids Research, 2002, 30, 13-16.	14.5	184
64	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs. Nature, 2002, 420, 563-573.	27.8	1,548
65	Functional annotation of a full-length mouse cDNA collection. Nature, 2001, 409, 685-690.	27.8	653
66	An ATP-binding cassette gene (ABCG3) closely related to the multidrug transporter ABCG2 (MXR/ABCP) has an unusual ATP-binding domain. Mammalian Genome, 2001, 12, 86-88.	2.2	32
67	A radiation hybrid map of mouse genes. Nature Genetics, 2001, 29, 201-205.	21.4	93
68	Identifying and characterizing a five-gene cluster of ATP-binding cassette transporters mapping to human chromosome 17q24: a new subgroup within the ABCA subfamily. GeneScreen, 2001, 1, 157-164.	0.6	20
69	Use of Denaturing HPLC to Map Human and Murine Genes and to Validate Single-Nucleotide Polymorphisms. BioTechniques, 2000, 28, 740-745.	1.8	21
70	Identification of 18 Mouse ABC Genes and Characterization of the ABC Superfamily in Mus musculus. Genomics, 2000, 64, 24-31.	2.9	28
71	Mutational Spectra of PTEN/MMAC1 Gene: a Tumor Suppressor With Lipid Phosphatase Activity. Journal of the National Cancer Institute, 1999, 91, 1922-1932.	6.3	473
72	Dating the Origin of the CCR5-Î"32 AIDS-Resistance Allele by the Coalescence of Haplotypes. American Journal of Human Genetics, 1998, 62, 1507-1515.	6.2	507

#	Article	IF	Citations
73	Wikidata as a linked-data hub for Biodiversity dataÂ. Biodiversity Information Science and Standards, 0, 3, .	0.0	8
74	Annotating public fungal ITS sequences from the built environment according to the MIxS-Built Environment standard â€" a report from a May 23-24, 2016 workshop (Gothenburg, Sweden). MycoKeys, 0, 16, 1-15.	1.9	16