

Lynn M Schriml

List of Publications by Year in descending order

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Version: 2024-02-01

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	Structure, function and diversity of the healthy human microbiome. <i>Nature</i> , 2012, 486, 207-214.	27.8	9,614
2	A framework for human microbiome research. <i>Nature</i> , 2012, 486, 215-221.	27.8	2,249
3	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs. <i>Nature</i> , 2002, 420, 563-573.	27.8	1,548
4	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.	17.5	1,512
5	Database resources of the National Center for Biotechnology. <i>Nucleic Acids Research</i> , 2003, 31, 28-33.	14.5	879
6	Disease Ontology: a backbone for disease semantic integration. <i>Nucleic Acids Research</i> , 2012, 40, D940-D946.	14.5	793
7	Functional annotation of a full-length mouse cDNA collection. <i>Nature</i> , 2001, 409, 685-690.	27.8	653
8	Minimum information about a marker gene sequence (MIMARKS) and minimum information about any (x) sequence (MIxS) specifications. <i>Nature Biotechnology</i> , 2011, 29, 415-420.	17.5	608
9	Dating the Origin of the CCR5- Δ 32 AIDS-Resistance Allele by the Coalescence of Haplotypes. <i>American Journal of Human Genetics</i> , 1998, 62, 1507-1515.	6.2	507
10	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-D1078.	14.5	498
11	Mutational Spectra of PTEN/MMAC1 Gene: a Tumor Suppressor With Lipid Phosphatase Activity. <i>Journal of the National Cancer Institute</i> , 1999, 91, 1922-1932.	6.3	473
12	Minimum Information about an Uncultivated Virus Genome (MIUViG). <i>Nature Biotechnology</i> , 2019, 37, 29-37.	17.5	414
13	Human Disease Ontology 2018 update: classification, content and workflow expansion. <i>Nucleic Acids Research</i> , 2019, 47, D955-D962.	14.5	383
14	Database resources of the National Center for Biotechnology Information. <i>Nucleic Acids Research</i> , 2004, 33, D39-D45.	14.5	369
15	The Human Phenotype Ontology: Semantic Unification of Common and Rare Disease. <i>American Journal of Human Genetics</i> , 2015, 97, 111-124.	6.2	203
16	Database resources of the National Center for Biotechnology Information: 2002 update. <i>Nucleic Acids Research</i> , 2002, 30, 13-16.	14.5	184
17	The Genomic Standards Consortium. <i>PLoS Biology</i> , 2011, 9, e1001088.	5.6	180
18	Reporting guidelines for human microbiome research: the STORMS checklist. <i>Nature Medicine</i> , 2021, 27, 1885-1892.	30.7	170

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19	FoodOn: a harmonized food ontology to increase global food traceability, quality control and data integration. <i>Npj Science of Food</i> , 2018, 2, 23.	5.5	164
20	A global metagenomic map of urban microbiomes and antimicrobial resistance. <i>Cell</i> , 2021, 184, 3376-3393.e17.	28.9	164
21	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.	9.8	127
22	A harmonized meta-knowledgebase of clinical interpretations of somatic genomic variants in cancer. <i>Nature Genetics</i> , 2020, 52, 448-457.	21.4	104
23	Integrated Genomic Analysis of Diverse Induced Pluripotent Stem Cells from the Progenitor Cell Biology Consortium. <i>Stem Cell Reports</i> , 2016, 7, 110-125.	4.8	101
24	A radiation hybrid map of mouse genes. <i>Nature Genetics</i> , 2001, 29, 201-205.	21.4	93
25	The Human Disease Ontology 2022 update. <i>Nucleic Acids Research</i> , 2022, 50, D1255-D1261.	14.5	92
26	Augmenting the disease ontology improves and unifies disease annotations across species. <i>DMM Disease Models and Mechanisms</i> , 2018, 11, .	2.4	81
27	OBO Foundry in 2021: operationalizing open data principles to evaluate ontologies. <i>Database: the Journal of Biological Databases and Curation</i> , 2021, 2021, .	3.0	77
28	Wikidata as a knowledge graph for the life sciences. <i>ELife</i> , 2020, 9, .	6.0	76
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, S1.	1.6	68
30	ECO, the Evidence & Conclusion Ontology: community standard for evidence information. <i>Nucleic Acids Research</i> , 2019, 47, D1186-D1194.	14.5	67
31	The Disease Ontology: fostering interoperability between biological and clinical human disease-related data. <i>Mammalian Genome</i> , 2015, 26, 584-589.	2.2	60
32	COVID-19 pandemic reveals the peril of ignoring metadata standards. <i>Scientific Data</i> , 2020, 7, 188.	5.3	56
33	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.	1.5	53
34	Parasite microbiome project: Grand challenges. <i>PLoS Pathogens</i> , 2019, 15, e1008028.	4.7	50
35	Molecular, phenotypic, and sample-associated data to describe pluripotent stem cell lines and derivatives. <i>Scientific Data</i> , 2017, 4, 170030.	5.3	48
36	Wikidata as a semantic framework for the Gene Wiki initiative. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw015.	3.0	47

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37	Toward unrestricted use of public genomic data. <i>Science</i> , 2019, 363, 350-352.	12.6	45
38	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-bav032.	3.0	40
39	Habitat-Lite: A GSC Case Study Based on Free Text Terms for Environmental Metadata. <i>OMICS A Journal of Integrative Biology</i> , 2008, 12, 129-136.	2.0	39
40	Development and Evaluation of an Automated Annotation Pipeline and cDNA Annotation System. <i>Genome Research</i> , 2003, 13, 1542-1551.	5.5	34
41	Standardized Metadata for Human Pathogen/Vector Genomic Sequences. <i>PLoS ONE</i> , 2014, 9, e99979.	2.5	34
42	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, 86-88.	2.2	32
43	Genomic Standards Consortium Projects. <i>Standards in Genomic Sciences</i> , 2014, 9, 599-601.	1.5	29
44	Identification of 18 Mouse ABC Genes and Characterization of the ABC Superfamily in <i>Mus musculus</i> . <i>Genomics</i> , 2000, 64, 24-31.	2.9	28
45	Metagenomes and metatranscriptomes from the L4 long-term coastal monitoring station in the Western English Channel. <i>Standards in Genomic Sciences</i> , 2010, 3, 183-193.	1.5	28
46	Microbiome Metadata Standards: Report of the National Microbiome Data Collaborative's Workshop and Follow-On Activities. <i>MSystems</i> , 2021, 6, .	3.8	28
47	Genomic Standards Consortium Projects. <i>Standards in Genomic Sciences</i> , 2014, 9, 599-601.	1.5	26
48	GeMInA, Genomic Metadata for Infectious Agents, a geospatial surveillance pathogen database. <i>Nucleic Acids Research</i> , 2010, 38, D754-D764.	14.5	25
49	Use of Denaturing HPLC to Map Human and Murine Genes and to Validate Single-Nucleotide Polymorphisms. <i>BioTechniques</i> , 2000, 28, 740-745.	1.8	21
50	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.	0.6	20
51	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, .	7.1	19
52	Connecting Sequence and Biology in the Laboratory Mouse. <i>Genome Research</i> , 2003, 13, 1505-1519.	5.5	18
53	Annotating public fungal ITS sequences from the built environment according to the MlxS-Built Environment standard "a report from a May 23-24, 2016 workshop (Gothenburg, Sweden). <i>MycKeys</i> , 0, 16, 1-15.	1.9	16
54	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, 123-127.	2.0	12

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55	COVID-19 biomarkers and their overlap with comorbidities in a disease biomarker data model. Briefings in Bioinformatics, 2021, 22, .	6.5	11
56	Meeting Report from the Genomic Standards Consortium (GSC) Workshop 10. Standards in Genomic Sciences, 2010, 3, 225-231.	1.5	8
57	The Metadata Coverage Index (MCI): A standardized metric for quantifying database metadata richness. Standards in Genomic Sciences, 2012, 6, 444-453.	1.5	8
58	Wikidata as a linked-data hub for Biodiversity data. Biodiversity Information Science and Standards, 0, 3, .	0.0	8
59	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
60	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
61	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
62	Consent insufficient for data release. Science, 2019, 364, 446-446.	12.6	5
63	Meeting Report from the Genomic Standards Consortium (GSC) Workshop 9. Standards in Genomic Sciences, 2010, 3, 216-224.	1.5	3
64	Report of the 13th Genomic Standards Consortium Meeting, Shenzhen, China, March 4-7, 2012.. Standards in Genomic Sciences, 2012, 6, 276-286.	1.5	3
65	Response to Biesecker et al.. American Journal of Human Genetics, 2021, 108, 1807-1808.	6.2	3
66	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
67	A decade of GigaScience: 10 years of the evolving genomic and biomedical standards landscape. GigaScience, 2022, 11, .	6.4	3
68	A community approach to the cancer-variant-interpretation bottleneck. Nature Cancer, 2022, 3, 522-525.	13.2	3
69	Meeting Report: Metagenomics, Metadata and Meta-analysis (M3) Workshop at the Pacific Symposium on Biocomputing 2010. Standards in Genomic Sciences, 2010, 2, 357-360.	1.5	2
70	Metagenomics: A founding finds its feet.. Standards in Genomic Sciences, 2010, 3, 212-213.	1.5	1
71	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
72	Abstract 210: Advancing knowledgebase representation of pediatric cancer variants through ClinGen/CIViC collaboration. , 2021, , .		0

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73	eP063: Genetic variants associated with childhood cancers: Curation initiatives of the ClinGen Somatic Cancer Pediatric Taskforce. <i>Genetics in Medicine</i> , 2022, 24, S41-S42.	2.4	0
74	Etiology context of rare diseases in the Human Disease Ontology. , 2021, , .		0