

J Michael Cherry

List of Publications by Year in descending order

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126
papers

70,582
citations

28736

57
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19470

122
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137
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137
docs citations

137
times ranked

99247
citing authors

#	ARTICLE	IF	CITATIONS
1	ClinGen Variant Curation Interface: a variant classification platform for the application of evidence criteria from ACMG/AMP guidelines. <i>Genome Medicine</i> , 2022, 14, 6.	3.6	34
2	Harmonizing model organism data in the Alliance of Genome Resources. <i>Genetics</i> , 2022, 220, .	1.2	52
3	New data and collaborations at the <i>Saccharomyces</i> Genome Database: updated reference genome, alleles, and the Alliance of Genome Resources. <i>Genetics</i> , 2022, 220, .	1.2	34
4	The Gene Ontology resource: enriching a GOLD mine. <i>Nucleic Acids Research</i> , 2021, 49, D325-D334.	6.5	2,416
5	GA4GH: International policies and standards for data sharing across genomic research and healthcare. <i>Cell Genomics</i> , 2021, 1, 100029.	3.0	94
6	Alliance of Genome Resources Portal: unified model organism research platform. <i>Nucleic Acids Research</i> , 2020, 48, D650-D658.	6.5	145
7	Transcriptome visualization and data availability at the <i>Saccharomyces</i> Genome Database. <i>Nucleic Acids Research</i> , 2020, 48, D743-D748.	6.5	15
8	New developments on the Encyclopedia of DNA Elements (ENCODE) data portal. <i>Nucleic Acids Research</i> , 2020, 48, D882-D889.	6.5	381
9	An atlas of dynamic chromatin landscapes in mouse fetal development. <i>Nature</i> , 2020, 583, 744-751.	13.7	257
10	Perspectives on ENCODE. <i>Nature</i> , 2020, 583, 693-698.	13.7	123
11	Expanded encyclopaedias of DNA elements in the human and mouse genomes. <i>Nature</i> , 2020, 583, 699-710.	13.7	1,252
12	Data Sanitization to Reduce Private Information Leakage from Functional Genomics. <i>Cell</i> , 2020, 183, 905-917.e16.	13.5	28
13	CNN-Peaks: ChIP-Seq peak detection pipeline using convolutional neural networks that imitate human visual inspection. <i>Scientific Reports</i> , 2020, 10, 7933.	1.6	14
14	Incorporation of a unified protein abundance dataset into the <i>Saccharomyces</i> genome database. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	1.4	2
15	Integrative Meta-Assembly Pipeline (IMAP): Chromosome-level genome assembler combining multiple de novo assemblies. <i>PLoS ONE</i> , 2019, 14, e0221858.	1.1	3
16	Integration of macromolecular complex data into the <i>Saccharomyces</i> Genome Database. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	1.4	7
17	The ENCODE Portal as an Epigenomics Resource. <i>Current Protocols in Bioinformatics</i> , 2019, 68, e89.	25.8	23
18	RNAcentral: a hub of information for non-coding RNA sequences. <i>Nucleic Acids Research</i> , 2019, 47, D221-D229.	6.5	153

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19	The Gene Ontology Resource: 20 years and still GOing strong. <i>Nucleic Acids Research</i> , 2019, 47, D330-D338.	6.5	3,474
20	The Encyclopedia of DNA elements (ENCODE): data portal update. <i>Nucleic Acids Research</i> , 2018, 46, D794-D801.	6.5	1,559
21	Saccharomyces genome database informs human biology. <i>Nucleic Acids Research</i> , 2018, 46, D736-D742.	6.5	27
22	Updated regulation curation model at the Saccharomyces Genome Database. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, .	1.4	2
23	Prevention of data duplication for high throughput sequencing repositories. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, .	1.4	9
24	XenMine: A genomic interaction tool for the Xenopus community. <i>Developmental Biology</i> , 2017, 426, 155-164.	0.9	6
25	Active Interaction Mapping Reveals the Hierarchical Organization of Autophagy. <i>Molecular Cell</i> , 2017, 65, 761-774.e5.	4.5	31
26	Expansion of the Gene Ontology knowledgebase and resources. <i>Nucleic Acids Research</i> , 2017, 45, D331-D338.	6.5	1,838
27	Evaluating the Clinical Validity of Gene-Disease Associations: An Evidence-Based Framework Developed by the Clinical Genome Resource. <i>American Journal of Human Genetics</i> , 2017, 100, 895-906.	2.6	403
28	Outreach and online training services at the Saccharomyces Genome Database. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	1.4	6
29	Curated protein information in the Saccharomyces genome database. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	1.4	17
30	RNAcentral: a comprehensive database of non-coding RNA sequences. <i>Nucleic Acids Research</i> , 2017, 45, D128-D134.	6.5	174
31	SnoVault and encodedD: A novel object-based storage system and applications to ENCODE metadata. <i>PLoS ONE</i> , 2017, 12, e0175310.	1.1	14
32	Principles of metadata organization at the ENCODE data coordination center. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw001.	1.4	40
33	Integration of new alternative reference strain genome sequences into the Saccharomyces genome database. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw074.	1.4	15
34	From one to many: expanding the <i>Saccharomyces cerevisiae</i> reference genome panel. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw020.	1.4	9
35	Providing Access to Genomic Variant Knowledge in a Healthcare Setting: A Vision for the ClinGen Electronic Health Records Workgroup. <i>Clinical Pharmacology and Therapeutics</i> , 2016, 99, 157-160.	2.3	15
36	ENCODE data at the ENCODE portal. <i>Nucleic Acids Research</i> , 2016, 44, D726-D732.	6.5	500

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37	TheSaccharomycesGenome Database Variant Viewer. Nucleic Acids Research, 2016, 44, D698-D702.	6.5	23
38	Ontology application and use at the ENCODE DCC. Database: the Journal of Biological Databases and Curation, 2015, 2015, .	1.4	42
39	AGAPE (Automated Genome Analysis PipelinE) for Pan-Genome Analysis of Saccharomyces cerevisiae. PLoS ONE, 2015, 10, e0120671.	1.1	73
40	The <i>Saccharomyces</i> Genome Database: A Tool for Discovery. Cold Spring Harbor Protocols, 2015, 2015, pdb.top083840.	0.2	24
41	RNAcentral: an international database of ncRNA sequences. Nucleic Acids Research, 2015, 43, D123-D129.	6.5	103
42	TheSaccharomycesGenome Database: Exploring Biochemical Pathways and Mutant Phenotypes. Cold Spring Harbor Protocols, 2015, 2015, pdb.prot088898.	0.2	5
43	The <i>Saccharomyces</i> Genome Database: Advanced Searching Methods and Data Mining. Cold Spring Harbor Protocols, 2015, 2015, pdb.prot088906.	0.2	10
44	TheSaccharomycesGenome Database: Gene Product Annotation of Function, Process, and Component. Cold Spring Harbor Protocols, 2015, 2015, pdb.prot088914.	0.2	6
45	The <i>Saccharomyces</i> Genome Database: Exploring Genome Features and Their Annotations. Cold Spring Harbor Protocols, 2015, 2015, pdb.prot088922.	0.2	2
46	<i>Saccharomyces</i> genome database provides new regulation data. Nucleic Acids Research, 2014, 42, D717-D725.	6.5	59
47	The Reference Genome Sequence of<i>Saccharomyces cerevisiae</i>: Then and Now. G3: Genes, Genomes, Genetics, 2014, 4, 389-398.	0.8	369
48	H3K4me3 Breadth Is Linked to Cell Identity and Transcriptional Consistency. Cell, 2014, 158, 673-688.	13.5	404
49	A gene ontology inferred from molecular networks. Nature Biotechnology, 2013, 31, 38-45.	9.4	184
50	The YeastGenome app: the Saccharomyces Genome Database at your fingertips. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat004.	1.4	11
51	The new modern era of yeast genomics: community sequencing and the resulting annotation of multiple Saccharomyces cerevisiae strains at the Saccharomyces Genome Database. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat012.	1.4	40
52	A guide to best practices for Gene Ontology (GO) manual annotation. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat054-bat054.	1.4	135
53	DATABASE, The Journal of Biological Databases and Curation, is now the official journal of the International Society for Biocuration. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat077-bat077.	1.4	1
54	InterMOD: integrated data and tools for the unification of model organism research. Scientific Reports, 2013, 3, 1802.	1.6	25

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55	CvManGO, a method for leveraging computational predictions to improve literature-based Gene Ontology annotations. Database: the Journal of Biological Databases and Curation, 2012, 2012, bas001.	1.4	9
56	Annotation of functional variation in personal genomes using RegulomeDB. Genome Research, 2012, 22, 1790-1797.	2.4	2,335
57	In the beginning there was babble. Autophagy, 2012, 8, 1165-1167.	4.3	14
58	YeastMine—an integrated data warehouse for Saccharomyces cerevisiae data as a multipurpose tool-kit. Database: the Journal of Biological Databases and Curation, 2012, 2012, bar062.	1.4	282
59	Considerations for creating and annotating the budding yeast Genome Map at SGD: a progress report. Database: the Journal of Biological Databases and Curation, 2012, 2012, bar057-bar057.	1.4	10
60	Saccharomyces Genome Database: the genomics resource of budding yeast. Nucleic Acids Research, 2012, 40, D700-D705.	6.5	1,649
61	Toward an interactive article: integrating journals and biological databases. BMC Bioinformatics, 2011, 12, 175.	1.2	12
62	Using computational predictions to improve literature-based Gene Ontology annotations: a feasibility study. Database: the Journal of Biological Databases and Curation, 2011, 2011, bar004-bar004.	1.4	16
63	Towards BioDBcore: a community-defined information specification for biological databases. Database: the Journal of Biological Databases and Curation, 2011, 2011, baq027-baq027.	1.4	30
64	Towards BioDBcore: a community-defined information specification for biological databases. Nucleic Acids Research, 2011, 39, D7-D10.	6.5	32
65	Saccharomyces Genome Database provides mutant phenotype data. Nucleic Acids Research, 2010, 38, D433-D436.	6.5	108
66	New mutant phenotype data curation system in the Saccharomyces Genome Database. Database: the Journal of Biological Databases and Curation, 2009, 2009, bap001-bap001.	1.4	23
67	The Gene Ontology's Reference Genome Project: A Unified Framework for Functional Annotation across Species. PLoS Computational Biology, 2009, 5, e1000431.	1.5	148
68	Functional annotations for the Saccharomyces cerevisiae genome: the knowns and the known unknowns. Trends in Microbiology, 2009, 17, 286-294.	3.5	49
69	Combining guilt-by-association and guilt-by-profiling to predict Saccharomyces cerevisiae gene function. Genome Biology, 2008, 9, S7.	13.9	78
70	Expanded protein information at SGD: new pages and proteome browser. Nucleic Acids Research, 2007, 35, D468-D471.	6.5	69
71	Gene Ontology annotations at SGD: new data sources and annotation methods. Nucleic Acids Research, 2007, 36, D577-D581.	6.5	218
72	Mining experimental evidence of molecular function claims from the literature. Bioinformatics, 2007, 23, 3232-3240.	1.8	11

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73	Saccharomyces cerevisiae S288C genome annotation: a working hypothesis. <i>Yeast</i> , 2006, 23, 857-865.	0.8	99
74	Tetrahymena Genome Database (TGD): a new genomic resource for Tetrahymena thermophila research. <i>Nucleic Acids Research</i> , 2006, 34, D500-D503.	6.5	107
75	The Gene Ontology (GO) project in 2006. <i>Nucleic Acids Research</i> , 2006, 34, D322-D326.	6.5	923
76	Macronuclear Genome Sequence of the Ciliate Tetrahymena thermophila, a Model Eukaryote. <i>PLoS Biology</i> , 2006, 4, e286.	2.6	657
77	Genome Snapshot: a new resource at the Saccharomyces Genome Database (SGD) presenting an overview of the Saccharomyces cerevisiae genome. <i>Nucleic Acids Research</i> , 2006, 34, D442-D445.	6.5	91
78	PatMatch: a program for finding patterns in peptide and nucleotide sequences. <i>Nucleic Acids Research</i> , 2005, 33, W262-W266.	6.5	162
79	Inference of combinatorial regulation in yeast transcriptional networks: A case study of sporulation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 1998-2003.	3.3	95
80	GO::TermFinder--open source software for accessing Gene Ontology information and finding significantly enriched Gene Ontology terms associated with a list of genes. <i>Bioinformatics</i> , 2004, 20, 3710-3715.	1.8	1,782
81	Saccharomyces genome database: Underlying principles and organisation. <i>Briefings in Bioinformatics</i> , 2004, 5, 9-22.	3.2	83
82	Fungal BLAST and Model Organism BLASTP Best Hits: new comparison resources at the Saccharomyces Genome Database (SGD). <i>Nucleic Acids Research</i> , 2004, 33, D374-D377.	6.5	46
83	Saccharomyces Genome Database (SGD) provides tools to identify and analyze sequences from Saccharomyces cerevisiae and related sequences from other organisms. <i>Nucleic Acids Research</i> , 2004, 32, 311D-314.	6.5	258
84	A short study on the success of the Gene Ontology. <i>Web Semantics</i> , 2004, 1, 235-240.	2.2	61
85	SOURCE: a unified genomic resource of functional annotations, ontologies, and gene expression data. <i>Nucleic Acids Research</i> , 2003, 31, 219-223.	6.5	376
86	Saccharomyces Genome Database (SGD) provides biochemical and structural information for budding yeast proteins. <i>Nucleic Acids Research</i> , 2003, 31, 216-218.	6.5	57
87	Saccharomyces Genome Database (SGD) provides secondary gene annotation using the Gene Ontology (GO). <i>Nucleic Acids Research</i> , 2002, 30, 69-72.	6.5	322
88	Saccharomyces genome database. <i>Methods in Enzymology</i> , 2002, 350, 329-346.	0.4	188
89	A systematic approach to reconstructing transcription networks in Saccharomyces cerevisiae. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 16893-16898.	3.3	84
90	Identification of unstable transcripts in Arabidopsis by cDNA microarray analysis: Rapid decay is associated with a group of touch- and specific clock-controlled genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 11513-11518.	3.3	200

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91	Microarray data quality analysis: lessons from the AFGC project. Arabidopsis Functional Genomics Consortium. <i>Plant Molecular Biology</i> , 2002, 48, 119-132.	2.0	76
92	Microarray data quality analysis: lessons from the AFGC project. , 2002, , 119-131.		2
93	Genome comparisons highlight similarity and diversity within the eukaryotic kingdoms. <i>Current Opinion in Chemical Biology</i> , 2001, 5, 86-89.	2.8	19
94	Saccharomyces Genome Database provides tools to survey gene expression and functional analysis data. <i>Nucleic Acids Research</i> , 2001, 29, 80-81.	6.5	61
95	The Stanford Microarray Database. <i>Nucleic Acids Research</i> , 2001, 29, 152-155.	6.5	415
96	Gene Ontology: tool for the unification of biology. <i>Nature Genetics</i> , 2000, 25, 25-29.	9.4	34,499
97	The Genome Sequence of <i>Drosophila melanogaster</i> . <i>Science</i> , 2000, 287, 2185-2195.	6.0	5,566
98	Comparative Genomics of the Eukaryotes. <i>Science</i> , 2000, 287, 2204-2215.	6.0	1,573
99	Integrating functional genomic information into the Saccharomyces Genome Database. <i>Nucleic Acids Research</i> , 2000, 28, 77-80.	6.5	93
100	Using the Saccharomyces Genome Database (SGD) for analysis of protein similarities and structure. <i>Nucleic Acids Research</i> , 1999, 27, 74-78.	6.5	66
101	Unified display of <i>Arabidopsis thaliana</i> physical maps from AtDB, the A.thaliana database. <i>Nucleic Acids Research</i> , 1999, 27, 79-84.	6.5	15
102	Expanding yeast knowledge online. , 1998, 14, 1453-1469.		11
103	<i>Arabidopsis thaliana</i> : A Model Plant for Genome Analysis. , 1998, 282, 662-682.		397
104	Comparison of the Complete Protein Sets of Worm and Yeast: Orthology and Divergence. , 1998, 282, 2022-2028.		404
105	SGD: Saccharomyces Genome Database. <i>Nucleic Acids Research</i> , 1998, 26, 73-79.	6.5	912
106	AtDB, the <i>Arabidopsis thaliana</i> database, and graphical-web-display of progress by the Arabidopsis Genome Initiative. <i>Nucleic Acids Research</i> , 1998, 26, 80-84.	6.5	29
107	Objective: The Complete Sequence of a Plant Genome. <i>Plant Cell</i> , 1997, 9, 476.	3.1	6
108	GENETICS: Yeast as a Model Organism. <i>Science</i> , 1997, 277, 1259-1260.	6.0	362

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109	Genetic and physical maps of <i>Saccharomyces cerevisiae</i> . <i>Nature</i> , 1997, 387, 67-73.	13.7	145
110	Molecular linguistics: Extracting information from gene and protein sequences. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1997, 94, 5506-5507.	3.3	31
111	Characteristics of Amino Acids. <i>Current Protocols in Molecular Biology</i> , 1996, 33, Appendix 1C.	2.9	7
112	The arabidopsis database moves to Stanford. <i>Plant Molecular Biology Reporter</i> , 1996, 14, 6-8.	1.0	2
113	Computer Manipulation of DNA and Protein Sequences. <i>Current Protocols in Molecular Biology</i> , 1995, 30, Unit7.7.	2.9	2
114	ACEDB: A Tool for Biological Information. , 1994, , 347-356.		4
115	An integrated RFLP map of <i>Arabidopsis thaliana</i> . <i>Advances in Cellular and Molecular Biology of Plants</i> , 1994, , 159-162.	0.2	1
116	An integrated genetic/RFLP map of the <i>Arabidopsis thaliana</i> genome. <i>Plant Journal</i> , 1993, 3, 745-754.	2.8	123
117	An integrated genetic/RFLP map of the <i>Arabidopsis thaliana</i> genome. , 1993, 3, 745.		2
118	AAtDB, an <i>Arabidopsis thaliana</i> database. <i>Plant Molecular Biology Reporter</i> , 1992, 10, 308-309.	1.0	20
119	Appendix D: Codon Usage Table for <i>Xenopus laevis</i> . <i>Methods in Cell Biology</i> , 1991, 36, 675-677.	0.5	46
120	<i>Saccharomyces cerevisiae</i> homoserine kinase is homologous to prokaryotic homoserine kinases. <i>Gene</i> , 1990, 96, 177-180.	1.0	10
121	Mutational analysis of conserved nucleotides in a self-splicing group I intron. <i>Journal of Molecular Biology</i> , 1990, 215, 345-358.	2.0	73
122	Genetic Dissection of an RNA Enzyme. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 1987, 52, 173-180.	2.0	18
123	The internally located telomeric sequences in the germ-line chromosomes of tetrahymena are at the ends of transposon-like elements. <i>Cell</i> , 1985, 43, 747-758.	13.5	110
124	Computational Methods and Bioinformatic Tools. , 0, , 769-904.		0
125	Gene function, metabolic pathways and comparative genomics in yeast. , 0, , .		1
126	A Short Study on the Success of the Gene Ontology. <i>SSRN Electronic Journal</i> , 0, , .	0.4	3