

Catherine A Ball

List of Publications by Year in descending order

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Version: 2024-02-01

44
papers

43,827
citations

236612

25
h-index

329751

37
g-index

45
all docs

45
docs citations

45
times ranked

65478
citing authors

#	ARTICLE	IF	CITATIONS
1	Gene Ontology: tool for the unification of biology. <i>Nature Genetics</i> , 2000, 25, 25-29.	9.4	34,499
2	Minimum information about a microarray experiment (MIAME)â€”toward standards for microarray data. <i>Nature Genetics</i> , 2001, 29, 365-371.	9.4	3,750
3	Identification of Genes Periodically Expressed in the Human Cell Cycle and Their Expression in Tumors. <i>Molecular Biology of the Cell</i> , 2002, 13, 1977-2000.	0.9	1,352
4	Promoting coherent minimum reporting guidelines for biological and biomedical investigations: the MIBBI project. <i>Nature Biotechnology</i> , 2008, 26, 889-896.	9.4	506
5	Repeatability of published microarray gene expression analyses. <i>Nature Genetics</i> , 2009, 41, 149-155.	9.4	477
6	Comparison of the Complete Protein Sets of Worm and Yeast: Orthology and Divergence. , 1998, 282, 2022-2028.		404
7	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
8	The Stanford Microarray Database: data access and quality assessment tools. <i>Nucleic Acids Research</i> , 2003, 31, 94-96.	6.5	297
9	TB database: an integrated platform for tuberculosis research. <i>Nucleic Acids Research</i> , 2009, 37, D499-D508.	6.5	201
10	Saccharomyces genome database. <i>Methods in Enzymology</i> , 2002, 350, 329-346.	0.4	188
11	A simple spreadsheet-based, MIAME-supportive format for microarray data: MAGE-TAB. <i>BMC Bioinformatics</i> , 2006, 7, 489.	1.2	185
12	The Stanford Microarray Database accommodates additional microarray platforms and data formats. <i>Nucleic Acids Research</i> , 2004, 33, D580-D582.	6.5	175
13	Standards for Microarray Data. <i>Science</i> , 2002, 298, 539b-539.	6.0	147
14	The Stanford Microarray Database: implementation of new analysis tools and open source release of software. <i>Nucleic Acids Research</i> , 2007, 35, D766-D770.	6.5	146
15	Microarray databases: standards and ontologies. <i>Nature Genetics</i> , 2002, 32, 469-473.	9.4	133
16	Minimum information specification for in situ hybridization and immunohistochemistry experiments (MISFISHIE). <i>Nature Biotechnology</i> , 2008, 26, 305-312.	9.4	111
17	TB database 2010: Overview and update. <i>Tuberculosis</i> , 2010, 90, 225-235.	0.8	106
18	Submission of Microarray Data to Public Repositories. <i>PLoS Biology</i> , 2004, 2, e317.	2.6	102

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19	Clustering of 770,000 genomes reveals post-colonial population structure of North America. <i>Nature Communications</i> , 2017, 8, 14238.	5.8	99
20	The Functional Genomics Experiment model (FuGE): an extensible framework for standards in functional genomics. <i>Nature Biotechnology</i> , 2007, 25, 1127-1133.	9.4	96
21	Implementation of GenePattern within the Stanford Microarray Database. <i>Nucleic Acids Research</i> , 2009, 37, D898-D901.	6.5	96
22	Data Standards for Omics Data: The Basis of Data Sharing and Reuse. <i>Methods in Molecular Biology</i> , 2011, 719, 31-69.	0.4	73
23	MGED Standards: Work in Progress. <i>OMICS A Journal of Integrative Biology</i> , 2006, 10, 138-144.	1.0	54
24	Funding high-throughput data sharing. <i>Nature Biotechnology</i> , 2004, 22, 1179-1183.	9.4	49
25	An open letter to the scientific journals. <i>Bioinformatics</i> , 2002, 18, 1409-1409.	1.8	40
26	A Prospective Analysis of Genetic Variants Associated with Human Lifespan. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2863-2878.	0.8	40
27	PortEco: a resource for exploring bacterial biology through high-throughput data and analysis tools. <i>Nucleic Acids Research</i> , 2014, 42, D677-D684.	6.5	25
28	Domain-Specific Data Sharing in Neuroscience: What Do We Have to Learn from Each Other?. <i>Neuroinformatics</i> , 2008, 6, 117-121.	1.5	24
29	Genome comparisons highlight similarity and diversity within the eukaryotic kingdoms. <i>Current Opinion in Chemical Biology</i> , 2001, 5, 86-89.	2.8	19
30	Development of the Minimum Information Specification for In Situ Hybridization and Immunohistochemistry Experiments (MISFISHIE). <i>OMICS A Journal of Integrative Biology</i> , 2006, 10, 205-208.	1.0	19
31	The Stanford Microarray Database: A User's Guide. , 2006, 338, 191-208.		16
32	Annotare—a tool for annotating high-throughput biomedical investigations and resulting data. <i>Bioinformatics</i> , 2010, 26, 2470-2471.	1.8	14
33	Expanding yeast knowledge online. , 1998, 14, 1453-1469.		11
34	A guide to microarray experiments—an open letter to the scientific journals. <i>Lancet, The</i> , 2002, 360, 1019.	6.3	11
35	Storage and Retrieval of Microarray Data and Open Source Microarray Database Software. <i>Molecular Biotechnology</i> , 2005, 30, 239-252.	1.3	11
36	Are we stuck in the standards?. <i>Nature Biotechnology</i> , 2006, 24, 1374-1376.	9.4	9

#	ARTICLE	IF	CITATIONS
37	The history and geographic distribution of a KCNQ1 atrial fibrillation risk allele. Nature Communications, 2021, 12, 6442.	5.8	7
38	Minimum information about a functional genomics experiment: the state of microarray standards and their extension to other technologies. Drug Discovery Today: TARGETS, 2004, 3, 159-164.	0.5	5
39	The XBabelPhish MAGE-ML and XML Translator. BMC Bioinformatics, 2008, 9, 28.	1.2	3
40	OntologyWidget – a reusable, embeddable widget for easily locating ontology terms. BMC Bioinformatics, 2007, 8, 338.	1.2	2
41	Microarray Databases: Storage and Retrieval of Microarray Data. , 2003, 224, 235-248.		1
42	Computational Methods and Bioinformatic Tools. , 0, , 769-904.		0
43	MAGE-OM: An object model for the communication of microarray data. , 2006, , .		0
44	What are Microarrays?. , 0, , 369-387.		0