

Yingyao Zhou

List of Publications by Year in descending order

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54
papers

16,071
citations

94433

37
h-index

175258

52
g-index

57
all docs

57
docs citations

57
times ranked

22913
citing authors

#	ARTICLE	IF	CITATIONS
1	Metascape provides a biologist-oriented resource for the analysis of systems-level datasets. Nature Communications, 2019, 10, 1523.	12.8	7,886
2	Discovery of Gene Function by Expression Profiling of the Malaria Parasite Life Cycle. Science, 2003, 301, 1503-1508.	12.6	1,122
3	Global Analysis of Host-Pathogen Interactions that Regulate Early-Stage HIV-1 Replication. Cell, 2008, 135, 49-60.	28.9	881
4	Meta- and Orthogonal Integration of Influenza Omics Data Defines a Role for UBR4 in Virus Budding. Cell Host and Microbe, 2015, 18, 723-735.	11.0	868
5	Human host factors required for influenza virus replication. Nature, 2010, 463, 813-817.	27.8	755
6	<i>In silico</i> activity profiling reveals the mechanism of action of antimalarials discovered in a high-throughput screen. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 9059-9064.	7.1	400
7	Global analysis of transcript and protein levels across the Plasmodium falciparum life cycle. Genome Research, 2004, 14, 2308-2318.	5.5	394
8	A probability-based approach for the analysis of large-scale RNAi screens. Nature Methods, 2007, 4, 847-849.	19.0	325
9	Imaging of Plasmodium Liver Stages to Drive Next-Generation Antimalarial Drug Discovery. Science, 2011, 334, 1372-1377.	12.6	308
10	The Plasmodium falciparum sexual development transcriptome: A microarray analysis using ontology-based pattern identification. Molecular and Biochemical Parasitology, 2005, 143, 67-79.	1.1	295
11	Gene expression signatures and small-molecule compounds link a protein kinase to Plasmodium falciparum motility. Nature Chemical Biology, 2008, 4, 347-356.	8.0	203
12	Mapping the malaria parasite druggable genome by using in vitro evolution and chemogenomics. Science, 2018, 359, 191-199.	12.6	194
13	A Comparison of the Celera and Ensembl Predicted Gene Sets Reveals Little Overlap in Novel Genes. Cell, 2001, 106, 413-415.	28.9	185
14	A Systematic Map of Genetic Variation in Plasmodium falciparum. PLoS Pathogens, 2006, 2, e57.	4.7	176
15	An efficient rapid system for profiling the cellular activities of molecular libraries. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 3153-3158.	7.1	173
16	High-Throughput Assay and Discovery of Small Molecules that Interrupt Malaria Transmission. Cell Host and Microbe, 2016, 19, 114-126.	11.0	140
17	A Plasmodium Gene Family Encoding Maurer's Cleft Membrane Proteins: Structural Properties and Expression Profiling. Genome Research, 2004, 14, 1052-1059.	5.5	133
18	Use of high-density tiling microarrays to identify mutations globally and elucidate mechanisms of drug resistance in Plasmodium falciparum. Genome Biology, 2009, 10, R21.	9.6	120

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19	In silico discovery of transcription regulatory elements in Plasmodium falciparum. BMC Genomics, 2008, 9, 70.	2.8	104
20	Open-source discovery of chemical leads for next-generation chemoprotective antimalarials. Science, 2018, 362, .	12.6	99
21	A Systems-Based Analysis of Plasmodium vivax Lifecycle Transcription from Human to Mosquito. PLoS Neglected Tropical Diseases, 2010, 4, e653.	3.0	96
22	A broad analysis of resistance development in the malaria parasite. Nature Communications, 2016, 7, 11901.	12.8	94
23	In Vivo Transcriptome of Plasmodium falciparum Reveals Overexpression of Transcripts That Encode Surface Proteins. Journal of Infectious Diseases, 2005, 191, 1196-1203.	4.0	92
24	Excess Polymorphisms in Genes for Membrane Proteins in Plasmodium falciparum. Science, 2002, 298, 216-218.	12.6	80
25	Evidence-Based Annotation of the Malaria Parasite's Genome Using Comparative Expression Profiling. PLoS ONE, 2008, 3, e1570.	2.5	78
26	In silico gene function prediction using ontology-based pattern identification. Bioinformatics, 2005, 21, 1237-1245.	4.1	74
27	A role for Î²B kinase 2 in bipolar spindle assembly. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 16940-16945.	7.1	68
28	Match-only integral distribution (MOID) algorithm for high-density oligonucleotide array analysis. BMC Bioinformatics, 2002, 3, 3.	2.6	64
29	A systematic approach to understand the mechanism of action of the bisthiazolium compound T4 on the human malaria parasite, Plasmodium falciparum. BMC Genomics, 2008, 9, 513.	2.8	58
30	In Silico Gene Prioritization by Integrating Multiple Data Sources. PLoS ONE, 2011, 6, e21137.	2.5	57
31	Whole genome functional analysis identifies novel components required for mitotic spindle integrity in human cells. Genome Biology, 2008, 9, R44.	9.6	54
32	In vivo transcriptional profiling of Plasmodium falciparum. Malaria Journal, 2004, 3, 30.	2.3	52
33	Exposure of Plasmodium sporozoites to the intracellular concentration of potassium enhances infectivity and reduces cell passage activity. Molecular and Biochemical Parasitology, 2007, 156, 32-40.	1.1	52
34	Monitoring the chromosome 2 intraerythrocytic transcriptome of Plasmodium falciparum using oligonucleotide arrays.. American Journal of Tropical Medicine and Hygiene, 2002, 67, 233-243.	1.4	46
35	Learning from the Data: Mining of Large High-Throughput Screening Databases. Journal of Chemical Information and Modeling, 2006, 46, 2381-2395.	5.4	43
36	Cofactors Required for TLR7- and TLR9-Dependent Innate Immune Responses. Cell Host and Microbe, 2012, 11, 306-318.	11.0	40

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37	Novel Statistical Approach for Primary High-Throughput Screening Hit Selection. <i>Journal of Chemical Information and Modeling</i> , 2005, 45, 1784-1790.	5.4	39
38	Large-Scale Annotation of Small-Molecule Libraries Using Public Databases. <i>Journal of Chemical Information and Modeling</i> , 2007, 47, 1386-1394.	5.4	37
39	Identification of Small Molecule and Genetic Modulators of AON-Induced Dystrophin Exon Skipping by High-Throughput Screening. <i>PLoS ONE</i> , 2009, 4, e8348.	2.5	27
40	Leveraging two-way probe-level block design for identifying differential gene expression with high-density oligonucleotide arrays. <i>BMC Bioinformatics</i> , 2004, 5, 42.	2.6	25
41	Systems-based analysis of RIG-I-dependent signalling identifies KHSRP as an inhibitor of RIG-I receptor activation. <i>Nature Microbiology</i> , 2017, 2, 17022.	13.3	25
42	Chemical and Biological Properties of Frequent Screening Hits. <i>Journal of Chemical Information and Modeling</i> , 2012, 52, 913-926.	5.4	20
43	Purifying the Masses: Integrating Prepurification Quality Control, High-Throughput LC/MS Purification, and Compound Plating To Feed High-Throughput Screening. <i>ACS Combinatorial Science</i> , 2005, 7, 210-217.	3.3	18
44	Identification of a Xist silencing domain by Tiling CRISPR. <i>Scientific Reports</i> , 2019, 9, 2408.	3.3	17
45	Targeting p130Cas- and microtubule-dependent MYC regulation sensitizes pancreatic cancer to ERK MAPK inhibition. <i>Cell Reports</i> , 2021, 35, 109291.	6.4	15
46	Dexamethasone inhibits respiratory syncytial virus-driven mucus production while increasing viral replication without altering antiviral interferon signaling. <i>Virology</i> , 2020, 540, 195-206.	2.4	11
47	Algorithms for high-density oligonucleotide array. <i>Current Opinion in Drug Discovery & Development</i> , 2003, 6, 339-45.	1.9	7
48	Just-in-Time Purification: An Effective Solution for Cherry-Picking and Purifying Active Compounds from Large Legacy Libraries. <i>Journal of Biomolecular Screening</i> , 2006, 11, 933-939.	2.6	6
49	Chemical-Text Hybrid Search Engines. <i>Journal of Chemical Information and Modeling</i> , 2010, 50, 47-54.	5.4	5
50	Profiling the kinome for drug discovery. <i>Drug Discovery Today: Technologies</i> , 2006, 3, 269-276.	4.0	4
51	An Automatic Quality Control Pipeline for High-Throughput Screening Hit Identification. <i>Journal of Biomolecular Screening</i> , 2016, 21, 832-841.	2.6	4
52	Proteomic Analysis of Non-human Primate Peripheral Blood Mononuclear Cells During <i>Burkholderia mallei</i> Infection Reveals a Role of Ezrin in Glanders Pathogenesis. <i>Frontiers in Microbiology</i> , 2021, 12, 625211.	3.5	1
53	Mining High-Throughput Screening Data by Novel Knowledge-Based Optimization Analysis. , 0, , 205-233.		1
54	AUTOMATED MICROSCOPY SCREEN TO IDENTIFY COMPONENTS REQUIRED FOR MITOTIC CELL CYCLE PROGRESSION IN HUMAN CELLS. , 2007, , .		0