

# 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	Proteomic Analysis of Non-human Primate Peripheral Blood Mononuclear Cells During Burkholderia mallei Infection Reveals a Role of Ezrin in Glanders Pathogenesis. <i>Frontiers in Microbiology</i> , 2021, 12, 625211.	3.5	1
2	Targeting p130Cas- and microtubule-dependent MYC regulation sensitizes pancreatic cancer to ERK MAPK inhibition. <i>Cell Reports</i> , 2021, 35, 109291.	6.4	15
3	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
4	Metascape provides a biologist-oriented resource for the analysis of systems-level datasets. <i>Nature Communications</i> , 2019, 10, 1523.	12.8	7,886
5	Identification of a Xist silencing domain by Tiling CRISPR. <i>Scientific Reports</i> , 2019, 9, 2408.	3.3	17
6	Mapping the malaria parasite druggable genome by using in vitro evolution and chemogenomics. <i>Science</i> , 2018, 359, 191-199.	12.6	194
7	Open-source discovery of chemical leads for next-generation chemoprotective antimalarials. <i>Science</i> , 2018, 362, .	12.6	99
8	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
9	A broad analysis of resistance development in the malaria parasite. <i>Nature Communications</i> , 2016, 7, 11901.	12.8	94
10	An Automatic Quality Control Pipeline for High-Throughput Screening Hit Identification. <i>Journal of Biomolecular Screening</i> , 2016, 21, 832-841.	2.6	4
11	High-Throughput Assay and Discovery of Small Molecules that Interrupt Malaria Transmission. <i>Cell Host and Microbe</i> , 2016, 19, 114-126.	11.0	140
12	Meta- and Orthogonal Integration of Influenza Omics Data Defines a Role for UBR4 in Virus Budding. <i>Cell Host and Microbe</i> , 2015, 18, 723-735.	11.0	868
13	Chemical and Biological Properties of Frequent Screening Hits. <i>Journal of Chemical Information and Modeling</i> , 2012, 52, 913-926.	5.4	20
14	Cofactors Required for TLR7- and TLR9-Dependent Innate Immune Responses. <i>Cell Host and Microbe</i> , 2012, 11, 306-318.	11.0	40
15	Imaging of <i>Plasmodium</i> Liver Stages to Drive Next-Generation Antimalarial Drug Discovery. <i>Science</i> , 2011, 334, 1372-1377.	12.6	308
16	In Silico Gene Prioritization by Integrating Multiple Data Sources. <i>PLoS ONE</i> , 2011, 6, e21137.	2.5	57
17	Human host factors required for influenza virus replication. <i>Nature</i> , 2010, 463, 813-817.	27.8	755
18	A Systems-Based Analysis of <i>Plasmodium vivax</i> Lifecycle Transcription from Human to Mosquito. <i>PLoS Neglected Tropical Diseases</i> , 2010, 4, e653.	3.0	96

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19	Chemical-Text Hybrid Search Engines. <i>Journal of Chemical Information and Modeling</i> , 2010, 50, 47-54.	5.4	5
20	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
21	Use of high-density tiling microarrays to identify mutations globally and elucidate mechanisms of drug resistance in <i>Plasmodium falciparum</i> . <i>Genome Biology</i> , 2009, 10, R21.	9.6	120
22	Gene expression signatures and small-molecule compounds link a protein kinase to <i>Plasmodium falciparum</i> motility. <i>Nature Chemical Biology</i> , 2008, 4, 347-356.	8.0	203
23	In silico discovery of transcription regulatory elements in <i>Plasmodium falciparum</i> . <i>BMC Genomics</i> , 2008, 9, 70.	2.8	104
24	Whole genome functional analysis identifies novel components required for mitotic spindle integrity in human cells. <i>Genome Biology</i> , 2008, 9, R44.	9.6	54
25	Global Analysis of Host-Pathogen Interactions that Regulate Early-Stage HIV-1 Replication. <i>Cell</i> , 2008, 135, 49-60.	28.9	881
26	A systematic approach to understand the mechanism of action of the bisthiazolium compound T4 on the human malaria parasite, <i>Plasmodium falciparum</i> . <i>BMC Genomics</i> , 2008, 9, 513.	2.8	58
27	In silico activity profiling reveals the mechanism of action of antimalarials discovered in a high-throughput screen. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 9059-9064.	7.1	400
28	Evidence-Based Annotation of the Malaria Parasite's Genome Using Comparative Expression Profiling. <i>PLoS ONE</i> , 2008, 3, e1570.	2.5	78
29	AUTOMATED MICROSCOPY SCREEN TO IDENTIFY COMPONENTS REQUIRED FOR MITOTIC CELL CYCLE PROGRESSION IN HUMAN CELLS. , 2007, , .		0
30	A role for $\beta$ kinase 2 in bipolar spindle assembly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 16940-16945.	7.1	68
31	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
32	A probability-based approach for the analysis of large-scale RNAi screens. <i>Nature Methods</i> , 2007, 4, 847-849.	19.0	325
33	Exposure of <i>Plasmodium</i> sporozoites to the intracellular concentration of potassium enhances infectivity and reduces cell passage activity. <i>Molecular and Biochemical Parasitology</i> , 2007, 156, 32-40.	1.1	52
34	Profiling the kinome for drug discovery. <i>Drug Discovery Today: Technologies</i> , 2006, 3, 269-276.	4.0	4
35	Learning from the Data: Mining of Large High-Throughput Screening Databases. <i>Journal of Chemical Information and Modeling</i> , 2006, 46, 2381-2395.	5.4	43
36	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

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37	A Systematic Map of Genetic Variation in <i>Plasmodium falciparum</i> . <i>PLoS Pathogens</i> , 2006, 2, e57.	4.7	176
38	An efficient rapid system for profiling the cellular activities of molecular libraries. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 3153-3158.	7.1	173
39	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
40	The <i>Plasmodium falciparum</i> sexual development transcriptome: A microarray analysis using ontology-based pattern identification. <i>Molecular and Biochemical Parasitology</i> , 2005, 143, 67-79.	1.1	295
41	In Vivo Transcriptome of <i>Plasmodium falciparum</i> Reveals Overexpression of Transcripts That Encode Surface Proteins. <i>Journal of Infectious Diseases</i> , 2005, 191, 1196-1203.	4.0	92
42	In silico gene function prediction using ontology-based pattern identification. <i>Bioinformatics</i> , 2005, 21, 1237-1245.	4.1	74
43	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
44	A <i>Plasmodium</i> Gene Family Encoding Maurer's Cleft Membrane Proteins: Structural Properties and Expression Profiling. <i>Genome Research</i> , 2004, 14, 1052-1059.	5.5	133
45	Global analysis of transcript and protein levels across the <i>Plasmodium falciparum</i> life cycle. <i>Genome Research</i> , 2004, 14, 2308-2318.	5.5	394
46	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
47	In vivo transcriptional profiling of <i>Plasmodium falciparum</i> . <i>Malaria Journal</i> , 2004, 3, 30.	2.3	52
48	Discovery of Gene Function by Expression Profiling of the Malaria Parasite Life Cycle. <i>Science</i> , 2003, 301, 1503-1508.	12.6	1,122
49	Algorithms for high-density oligonucleotide array. <i>Current Opinion in Drug Discovery &amp; Development</i> , 2003, 6, 339-45.	1.9	7
50	Excess Polymorphisms in Genes for Membrane Proteins in <i>Plasmodium falciparum</i> . <i>Science</i> , 2002, 298, 216-218.	12.6	80
51	Match-only integral distribution (MOID) algorithm for high-density oligonucleotide array analysis. <i>BMC Bioinformatics</i> , 2002, 3, 3.	2.6	64
52	Monitoring the chromosome 2 intraerythrocytic transcriptome of <i>Plasmodium falciparum</i> using oligonucleotide arrays. <i>American Journal of Tropical Medicine and Hygiene</i> , 2002, 67, 233-243.	1.4	46
53	A Comparison of the Celera and Ensembl Predicted Gene Sets Reveals Little Overlap in Novel Genes. <i>Cell</i> , 2001, 106, 413-415.	28.9	185
54	Mining High-Throughput Screening Data by Novel Knowledge-Based Optimization Analysis. , 0, , 205-233.		1