Elizabeth Ann Winzeler

List of Publications by Year
in descending order

218	30,095	13068	5227
papers	citations	68 h-index	165 g-index

238	238	238	24641
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Functional profiling of the Saccharomyces cerevisiae genome. Nature, 2002, 418, 387-391.	13.7	3,938
2	Functional Characterization of the S. cerevisiae Genome by Gene Deletion and Parallel Analysis. Science, 1999, 285, 901-906.	6.0	3,761
3	A Genome-Wide Transcriptional Analysis of the Mitotic Cell Cycle. Molecular Cell, 1998, 2, 65-73.	4.5	1,927
4	Genomics, gene expression and DNA arrays. Nature, 2000, 405, 827-836.	13.7	1,893
5	Discovery of Gene Function by Expression Profiling of the Malaria Parasite Life Cycle. Science, 2003, 301, 1503-1508.	6.0	1,122
6	Spiroindolones, a Potent Compound Class for the Treatment of Malaria. Science, 2010, 329, 1175-1180.	6.0	1,031
7	Replication Dynamics of the Yeast Genome. Science, 2001, 294, 115-121.	6.0	736
8	Genomic profiling of drug sensitivities via induced haploinsufficiency. Nature Genetics, 1999, 21, 278-283.	9.4	533
9	The core meiotic transcriptome in budding yeasts. Nature Genetics, 2000, 26, 415-423.	9.4	430
10	In silico 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.	3.3	400
11	Global analysis of transcript and protein levels across the Plasmodium falciparum life cycle. Genome Research, 2004, 14, 2308-2318.	2.4	394
12	Spirotetrahydro Î²-Carbolines (Spiroindolones): A New Class of Potent and Orally Efficacious Compounds for the Treatment of Malaria. Journal of Medicinal Chemistry, 2010, 53, 5155-5164.	2.9	381
13	Targeting Plasmodium PI(4)K to eliminate malaria. Nature, 2013, 504, 248-253.	13.7	377
14	Direct Allelic Variation Scanning of the Yeast Genome. , 1998, 281, 1194-1197.		368
15	A novel multiple-stage antimalarial agent that inhibits protein synthesis. Nature, 2015, 522, 315-320.	13.7	353
16	Protein pathway and complex clustering of correlated mRNA and protein expression analyses in Saccharomyces cerevisiae. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 3107-3112.	3.3	346
17	Large-Scale Identification of Single-Feature Polymorphisms in Complex Genomes. Genome Research, 2003, 13, 513-523.	2.4	345
18	Imaging of Plasmodium Liver Stages to Drive Next-Generation Antimalarial Drug Discovery. Science, 2011, 334, 1372-1377.	6.0	308

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19	The Activities of Current Antimalarial Drugs on the Life Cycle Stages of Plasmodium: A Comparative Study with Human and Rodent Parasites. PLoS Medicine, 2012, 9, e1001169.	3.9	301
20	The Plasmodium falciparum sexual development transcriptome: A microarray analysis using ontology-based pattern identification. Molecular and Biochemical Parasitology, 2005, 143, 67-79.	0.5	295
21	A Plant-Like Kinase in Plasmodium falciparum Regulates Parasite Egress from Erythrocytes. Science, 2010, 328, 910-912.	6.0	263
22	Molecular Mechanism for Switching of P. falciparum Invasion Pathways into Human Erythrocytes. Science, 2005, 309, 1384-1387.	6.0	247
23	Antimalarial drug discovery â€" approaches and progress towards new medicines. Nature Reviews Microbiology, 2013, 11, 849-862.	13.6	244
24	Open Source Drug Discovery with the Malaria Box Compound Collection for Neglected Diseases and Beyond. PLoS Pathogens, 2016, 12, e1005763.	2.1	244
25	malERA: An updated research agenda for malaria elimination and eradication. PLoS Medicine, 2017, 14, e1002456.	3.9	221
26	Distinct physiological states of Plasmodium falciparum in malaria-infected patients. Nature, 2007, 450, 1091-1095.	13.7	220
27	Diversity-oriented synthesis yields novel multistage antimalarial inhibitors. Nature, 2016, 538, 344-349.	13.7	214
28	Gene expression signatures and small-molecule compounds link a protein kinase to Plasmodium falciparum motility. Nature Chemical Biology, 2008, 4, 347-356.	3.9	203
29	Selective and Specific Inhibition of the Plasmodium falciparum Lysyl-tRNA Synthetase by the Fungal Secondary Metabolite Cladosporin. Cell Host and Microbe, 2012, 11, 654-663.	5.1	202
30	Mapping the malaria parasite druggable genome by using in vitro evolution and chemogenomics. Science, 2018, 359, 191-199.	6.0	194
31	Mitotic Evolution of Plasmodium falciparum Shows a Stable Core Genome but Recombination in Antigen Families. PLoS Genetics, 2013, 9, e1003293.	1.5	192
32	Plasmodium Circumsporozoite Protein Promotes the Development of the Liver Stages of the Parasite. Cell, 2007, 131, 492-504.	13.5	187
33	Na+ Regulation in the Malaria Parasite Plasmodium falciparum Involves the Cation ATPase PfATP4 and Is a Target of the Spiroindolone Antimalarials. Cell Host and Microbe, 2013, 13, 227-237.	5.1	185
34	A Systematic Map of Genetic Variation in Plasmodium falciparum. PLoS Pathogens, 2006, 2, e57.	2.1	176
35	Common PIEZO1 Allele in African Populations Causes RBC Dehydration and Attenuates Plasmodium Infection. Cell, 2018, 173, 443-455.e12.	13.5	176
36	Genetic Diversity in Yeast Assessed With Whole-Genome Oligonucleotide Arrays. Genetics, 2003, 163, 79-89.	1.2	171

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37	High-Throughput Assay and Discovery of Small Molecules that Interrupt Malaria Transmission. Cell Host and Microbe, 2016, 19, 114-126.	5.1	140
38	A Plasmodium Gene Family Encoding Maurer's Cleft Membrane Proteins: Structural Properties and Expression Profiling. Genome Research, 2004, 14, 1052-1059.	2.4	133
39	Malaria research in the post-genomic era. Nature, 2008, 455, 751-756.	13.7	133
40	Validation of isoleucine utilization targets in Plasmodium falciparum. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 1627-1632.	3.3	123
41	KAF156 Is an Antimalarial Clinical Candidate with Potential for Use in Prophylaxis, Treatment, and Prevention of Disease Transmission. Antimicrobial Agents and Chemotherapy, 2014, 58, 5060-5067.	1.4	122
42	The Plasmodium eukaryotic initiation factor-2Î± kinase IK2 controls the latency of sporozoites in the mosquito salivary glands. Journal of Experimental Medicine, 2010, 207, 1465-1474.	4.2	121
43	Use of high-density tiling microarrays to identify mutations globally and elucidate mechanisms of drug resistance in Plasmodium falciparum. Genome Biology, 2009, 10, R21.	13.9	120
44	Synthesis and Biological Evaluation of Epidithio-, Epitetrathio-, and bis-(Methylthio)diketopiperazines: Synthetic Methodology, Enantioselective Total Synthesis of Epicoccin G, 8,8â€²-epi-ent-Rostratin B, Gliotoxin, Gliotoxin G, Emethallicin E, and Haematocin and Discovery of New Antiviral and Antimalarial Agents. Journal of the American Chemical Society, 2012, 134, 17320-17332.	6.6	113
45	The Ume6 regulon coordinates metabolic and meiotic gene expression in yeast. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 13431-13436.	3.3	107
46	Antimalarial activity of single-dose DSM265, a novel plasmodium dihydroorotate dehydrogenase inhibitor, in patients with uncomplicated Plasmodium falciparum or Plasmodium vivax malaria infection: a proof-of-concept, open-label, phase 2a study. Lancet Infectious Diseases, The, 2018, 18, 874-883.	4.6	106
47	In silico discovery of transcription regulatory elements in Plasmodium falciparum. BMC Genomics, 2008, 9, 70.	1.2	104
48	Piperaquine Resistance Is Associated with a Copy Number Variation on Chromosome 5 in Drug-Pressured Plasmodium falciparum Parasites. Antimicrobial Agents and Chemotherapy, 2011, 55, 3908-3916.	1.4	102
49	UDP-galactose and acetyl-CoA transporters as Plasmodium multidrug resistance genes. Nature Microbiology, 2016, 1, 16166.	5.9	102
50	Whole-genome sequencing and microarray analysis of ex vivo Plasmodium vivax reveal selective pressure on putative drug resistance genes. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 20045-20050.	3.3	99
51	Open-source discovery of chemical leads for next-generation chemoprotective antimalarials. Science, 2018, 362, .	6.0	99
52	Previously uncharacterized genes in the UV- and MMS-induced DNA damage response in yeast. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 10605-10610.	3.3	98
53	A Systems-Based Analysis of Plasmodium vivax Lifecycle Transcription from Human to Mosquito. PLoS Neglected Tropical Diseases, 2010, 4, e653.	1.3	96
54	A broad analysis of resistance development in the malaria parasite. Nature Communications, 2016, 7, 11901.	5.8	94

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55	Lysyl-tRNA synthetase as a drug target in malaria and cryptosporidiosis. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 7015-7020.	3.3	94
56	In Vivo Transcriptome ofPlasmodium falciparumReveals Overexpression of Transcripts That Encode Surface Proteins. Journal of Infectious Diseases, 2005, 191, 1196-1203.	1.9	92
57	A high throughput screen for next-generation leads targeting malaria parasite transmission. Nature Communications, 2018, 9, 3805.	5.8	92
58	Application of High-Density Array-Based Signature-Tagged Mutagenesis To Discover Novel Yersinia Virulence-Associated Genes. Infection and Immunity, 2001, 69, 7810-7819.	1.0	91
59	Imidazolopiperazines: Hit to Lead Optimization of New Antimalarial Agents. Journal of Medicinal Chemistry, 2011, 54, 5116-5130.	2.9	91
60	Targeting the ERAD pathway via inhibition of signal peptide peptidase for antiparasitic therapeutic design. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 21486-21491.	3.3	89
61	Experimentally Induced Blood-Stage Plasmodium vivax Infection in Healthy Volunteers. Journal of Infectious Diseases, 2013, 208, 1688-1694.	1.9	87
62	A Chemical Genomic Analysis of Decoquinate, a Plasmodium falciparum Cytochrome b Inhibitor. ACS Chemical Biology, 2011, 6, 1214-1222.	1.6	84
63	High-Throughput Luciferase-Based Assay for the Discovery of Therapeutics That Prevent Malaria. ACS Infectious Diseases, 2016, 2, 281-293.	1.8	84
64	Imidazolopiperazines: Lead Optimization of the Second-Generation Antimalarial Agents. Journal of Medicinal Chemistry, 2012, 55, 4244-4273.	2.9	83
65	A Variant PfCRT Isoform Can Contribute to Plasmodium falciparum Resistance to the First-Line Partner Drug Piperaquine. MBio, 2017, 8, .	1.8	82
66	Excess Polymorphisms in Genes for Membrane Proteins inPlasmodium falciparum. Science, 2002, 298, 216-218.	6.0	80
67	Evidence-Based Annotation of the Malaria Parasite's Genome Using Comparative Expression Profiling. PLoS ONE, 2008, 3, e1570.	1.1	78
68	Mutations in the P-Type Cation-Transporter ATPase 4, PfATP4, Mediate Resistance to Both Aminopyrazole and Spiroindolone Antimalarials. ACS Chemical Biology, 2015, 10, 413-420.	1.6	75
69	In silico gene function prediction using ontology-based pattern identification. Bioinformatics, 2005, 21, 1237-1245.	1.8	74
70	Treasures and traps in genome-wide data sets: case examples from yeast. Nature Reviews Genetics, 2002, 3, 653-661.	7.7	72
71	A High Resolution Case Study of a Patient with Recurrent Plasmodium vivax Infections Shows That Relapses Were Caused by Meiotic Siblings. PLoS Neglected Tropical Diseases, 2014, 8, e2882.	1.3	70
72	Development of a Potent Inhibitor of the Plasmodium Proteasome with Reduced Mammalian Toxicity. Journal of Medicinal Chemistry, 2017, 60, 6721-6732.	2.9	70

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73	Discovery of HDAC inhibitors with potent activity against multiple malaria parasite life cycle stages. European Journal of Medicinal Chemistry, 2014, 82, 204-213.	2.6	68
74	Open Source Drug Discovery: Highly Potent Antimalarial Compounds Derived from the Tres Cantos Arylpyrroles. ACS Central Science, 2016, 2, 687-701.	5.3	68
75	Genome-wide nucleosome mapping of Plasmodium falciparum reveals histone-rich coding and histone-poor intergenic regions and chromatin remodeling of core and subtelomeric genes. BMC Genomics, 2009, 10, 610.	1.2	67
76	Drug resistance genomics of the antimalarial drug artemisinin. Genome Biology, 2014, 15, 544.	3.8	66
77	Discovery of a Quinoline-4-carboxamide Derivative with a Novel Mechanism of Action, Multistage Antimalarial Activity, and Potent in Vivo Efficacy. Journal of Medicinal Chemistry, 2016, 59, 9672-9685.	2.9	66
78	The genomic architecture of antimalarial drug resistance. Briefings in Functional Genomics, 2019, 18, 314-328.	1.3	66
79	Direct transfer of whole genomes from bacteria to yeast. Nature Methods, 2013, 10, 410-412.	9.0	64
80	Synthesis of (+)-7,20-Diisocyanoadociane and Liver-Stage Antiplasmodial Activity of the Isocyanoterpene Class. Journal of the American Chemical Society, 2016, 138, 7268-7271.	6.6	64
81	Parallel Identification of New Genes in Saccharomyces cerevisiae. Genome Research, 2002, 12, 1210-1220.	2.4	61
82	KAI407, a Potent Non-8-Aminoquinoline Compound That Kills Plasmodium cynomolgi Early Dormant Liver Stage ParasitesIn Vitro. Antimicrobial Agents and Chemotherapy, 2014, 58, 1586-1595.	1.4	61
83	Multistage and transmission-blocking targeted antimalarials discovered from the open-source MMV Pandemic Response Box. Nature Communications, 2021, 12, 269.	5.8	61
84	Using in Vitro Evolution and Whole Genome Analysis To Discover Next Generation Targets for Antimalarial Drug Discovery. ACS Infectious Diseases, 2018, 4, 301-314.	1.8	60
85	Functional analysis of the yeast genome. Current Opinion in Genetics and Development, 1997, 7, 771-776.	1.5	59
86	Genome scanning of Amazonian Plasmodium falciparum shows subtelomeric instability and clindamycin-resistant parasites. Genome Research, 2010, 20, 1534-1544.	2.4	59
87	Using Genetic Methods To Define the Targets of Compounds with Antimalarial Activity. Journal of Medicinal Chemistry, 2013, 56, 7761-7771.	2.9	59
88	Selective Whole-Genome Amplification Is a Robust Method That Enables Scalable Whole-Genome Sequencing of Plasmodium vivax from Unprocessed Clinical Samples. MBio, 2017, 8, .	1.8	59
89	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.	1.2	58
90	Covalent Plasmodium falciparum-selective proteasome inhibitors exhibit a low propensity for generating resistance in vitro and synergize with multiple antimalarial agents. PLoS Pathogens, 2019, 15, e1007722.	2.1	58

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91	CRISPRâ€Cas9â€modified pfmdr1 protects Plasmodium falciparum asexual blood stages and gametocytes against a class of piperazineâ€containing compounds but potentiates artemisininâ€based combination therapy partner drugs. Molecular Microbiology, 2016, 101, 381-393.	1.2	56
92	Inhibition of Resistance-Refractory P. falciparum Kinase PKG Delivers Prophylactic, Blood Stage, and Transmission-Blocking Antiplasmodial Activity. Cell Chemical Biology, 2020, 27, 806-816.e8.	2.5	56
93	Systems analysis of hostâ€“parasite interactions. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2015, 7, 381-400.	6.6	55
94	Target Validation and Identification of Novel Boronate Inhibitors of the Plasmodium falciparum Proteasome. Journal of Medicinal Chemistry, 2018, 61, 10053-10066.	2.9	54
95	Advances in omics-based methods to identify novel targets for malaria and other parasitic protozoan infections. Genome Medicine, 2019, 11, 63.	3.6	54
96	Combining Stage Specificity and Metabolomic Profiling to Advance Antimalarial Drug Discovery. Cell Chemical Biology, 2020, 27, 158-171.e3.	2.5	54
97	In vivo transcriptional profiling of Plasmodium falciparum. Malaria Journal, 2004, 3, 30.	0.8	52
98	Microarray-based comparative genomic analyses of the human malaria parasite Plasmodium falciparum using Affymetrix arrays. Molecular and Biochemical Parasitology, 2005, 144, 177-186.	0.5	52
99	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.	0.5	52
100	Identification of a Potential Antimalarial Drug Candidate from a Series of 2-Aminopyrazines by Optimization of Aqueous Solubility and Potency across the Parasite Life Cycle. Journal of Medicinal Chemistry, 2016, 59, 9890-9905.	2.9	51
101	Validation of the protein kinase Pf CLK3 as a multistage cross-species malarial drug target. Science, 2019, 365, .	6.0	51
102	MalDA, Accelerating Malaria Drug Discovery. Trends in Parasitology, 2021, 37, 493-507.	1.5	51
103	Plasmodium Niemann-Pick type C1-related protein is a druggable target required for parasite membrane homeostasis. ELife, 2019, 8, .	2.8	51
104	Infection of Laboratory-Colonized Anopheles darlingi Mosquitoes by Plasmodium vivax. American Journal of Tropical Medicine and Hygiene, 2014, 90, 612-616.	0.6	50
105	Plasmodium falciparum: Genome wide perturbations in transcript profiles among mixed stage cultures after chloroquine treatment. Experimental Parasitology, 2007, 117, 87-92.	0.5	49
106	Mutations in the Plasmodium falciparum Cyclic Amine Resistance Locus (PfCARL) Confer Multidrug Resistance. MBio, 2016, 7, .	1.8	49
107	Phenotypic Screens in Antimalarial Drug Discovery. Trends in Parasitology, 2016, 32, 697-707.	1.5	48
108	Esterase mutation is a mechanism of resistance to antimalarial compounds. Nature Communications, 2017, 8, 14240.	5.8	47

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109	Hexahydroquinolines are antimalarial candidates with potent blood-stage and transmission-blocking activity. Nature Microbiology, 2017, 2, 1403-1414.	5.9	47
110	Whole genome sequencing analysis of Plasmodium vivax using whole genome capture. BMC Genomics, 2012, 13, 262.	1.2	46
111	Identification of pathogen genomic variants through an integrated pipeline. BMC Bioinformatics, 2014, 15, 63.	1.2	46
112	Monitoring the chromosome 2 intraerythrocytic transcriptome of Plasmodium falciparum using oligonucleotide arrays.. American Journal of Tropical Medicine and Hygiene, 2002, 67, 233-243.	0.6	46
113	[1] Fluorescence-based expression monitoring using microarrays. Methods in Enzymology, 1999, 306, 3-18.	0.4	45
114	The paradoxical population genetics of Plasmodium falciparum. Trends in Parasitology, 2002, 18, 266-272.	1.5	45
115	Dual RNA-seq identifies human mucosal immunity protein Mucin-13 as a hallmark of Plasmodium exoerythrocytic infection. Nature Communications, 2019, 10, 488.	5.8	45
116	Use of Flow cytometry to identify aCaulobacter4.5 S RNA Temperature-sensitive Mutant Defective in the Cell Cycle. Journal of Molecular Biology, 1995, 251, 346-365.	2.0	41
117	Chemogenomics identifies acetyl-coenzyme A synthetase as a target for malaria treatment and prevention. Cell Chemical Biology, 2022, 29, 191-201.e8.	2.5	39
118	Comparative chemical genomics reveal that the spiroindolone antimalarial KAE609 (Cipargamin) is a P-type ATPase inhibitor. Scientific Reports, 2016, 6, 27806.	1.6	38
119	Applied systems biology and malaria. Nature Reviews Microbiology, 2006, 4, 145-151.	13.6	37
120	Large-Scale Annotation of Small-Molecule Libraries Using Public Databases. Journal of Chemical Information and Modeling, 2007, 47, 1386-1394.	2.5	37
121	A key role for lipoic acid synthesis duringPlasmodiumliver stage development. Cellular Microbiology, 2013, 15, 1585-1604.	1.1	36
122	Prioritization of Molecular Targets for Antimalarial Drug Discovery. ACS Infectious Diseases, 2021, 7, 2764-2776.	1.8	35
123	Plasmodium falciparum Cyclic Amine Resistance Locus (PfCARL), a Resistance Mechanism for Two Distinct Compound Classes. ACS Infectious Diseases, 2016, 2, 816-826.	1.8	34
124	The antimalarial resistome â€“ finding new drug targets and their modes of action. Current Opinion in Microbiology, 2020, 57, 49-55.	2.3	34
125	Coordinated functions of WSS1, PSY2 and TOF1 in the DNA damage response. Nucleic Acids Research, 2004, 32, 6519-6530.	6.5	33
126	A Novel Pyrazolopyridine with in Vivo Activity in Plasmodium berghei- and Plasmodium falciparum-Infected Mouse Models from Structureâ€“Activity Relationship Studies around the Core of Recently Identified Antimalarial Imidazopyridazines. Journal of Medicinal Chemistry, 2015, 58, 8713-8722.	2.9	32

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127	Regulatory motifs uncovered among gene expression clusters in Plasmodium falciparum. Molecular and Biochemical Parasitology, 2007, 153, 19-30.	0.5	31
128	Target identification and validation of novel antimalarials. Future Microbiology, 2011, 6, 693-704.	1.0	30
129	Lead Optimization of Imidazopyrazines: A New Class of Antimalarial with Activity on Plasmodium Liver Stages. ACS Medicinal Chemistry Letters, 2014, 5, 947-950.	1.3	30
130	Next-Generation Sequencing of Plasmodium vivax Patient Samples Shows Evidence of Direct Evolution in Drug-Resistance Genes. ACS Infectious Diseases, 2015, 1, 367-379.	1.8	30
131	Accessible and distinct decoquinate derivatives active against Mycobacterium tuberculosis and apicomplexan parasites. Communications Chemistry, 2018, 1, .	2.0	30
132	In vitro selection predicts malaria parasite resistance to dihydroorotate dehydrogenase inhibitors in a mouse infection model. Science Translational Medicine, 2019, 11, .	5.8	30
133	Evolution of resistance in vitro reveals mechanisms of artemisinin activity in Toxoplasma gondii. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 26881-26891.	3.3	30
134	One-pot, multi-component synthesis and structure-activity relationships of peptoid-based histone deacetylase (HDAC) inhibitors targeting malaria parasites. European Journal of Medicinal Chemistry, 2018, 158, 801-813.	2.6	29
135	Bacterial genome reduction using the progressive clustering of deletions via yeast sexual cycling. Genome Research, 2015, 25, 435-444.	2.4	27
136	Exploration of Plasmodium vivax transmission dynamics and recurrent infections in the Peruvian Amazon using whole genome sequencing. Genome Medicine, 2018, 10, 52.	3.6	27
137	Pan-active imidazolopiperazine antimalarials target the Plasmodium falciparum intracellular secretory pathway. Nature Communications, 2020, 11, 1780.	5.8	27
138	Rapid Chagas Disease Drug Target Discovery Using Directed Evolution in Drug-Sensitive Yeast. ACS Chemical Biology, 2017, 12, 422-434.	1.6	26
139	Probing the Open Global Health Chemical Diversity Library for Multistage-Active Starting Points for Next-Generation Antimalarials. ACS Infectious Diseases, 2020, 6, 613-628.	1.8	26
140	Leveraging two-way probe-level block design for identifying differential gene expression with high-density oligonucleotide arrays. BMC Bioinformatics, 2004, 5, 42.	1.2	25
141	Discovery of novel 1H-imidazol-2-yl-pyrimidine-4,6-diamines as potential antimalarials. Bioorganic and Medicinal Chemistry Letters, 2010, 20, 4027-4031.	1.0	25
142	Reaction hijacking of tyrosine tRNA synthetase as a new whole-of-life-cycle antimalarial strategy. Science, 2022, 376, 1074-1079.	6.0	25
143	Nuclear Repositioning Precedes Promoter Accessibility and Is Linked to the Switching Frequency of a Plasmodium falciparum Invasion Gene. Cell Host and Microbe, 2012, 12, 739-750.	5.1	24
144	Structureâ€“Activity and Structureâ€“Toxicity Relationships of Peptoidâ€Based Histone Deacetylase Inhibitors with Dualâ€Stage Antiplasmodial Activity. ChemMedChem, 2019, 14, 912-926.	1.6	24

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145	Potent Antimalarials with Development Potential Identified by Structure-Guided Computational Optimization of a Pyrrole-Based Dihydroorotate Dehydrogenase Inhibitor Series. Journal of Medicinal Chemistry, 2021, 64, 6085-6136.	2.9	24
146	Genomics, systems biology and drug development for infectious diseases. Molecular BioSystems, 2007, 3, 841.	2.9	22
147	Genome Wide Analysis of Inbred Mouse Lines Identifies a Locus Containing Ppar-Î³ as Contributing to Enhanced Malaria Survival. PLoS ONE, 2010, 5, e10903.	1.1	22
148	Genetic Analysis of Primaquine Tolerance in a Patient with Relapsing Vivax Malaria. Emerging Infectious Diseases, 2013, 19, 802-805.	2.0	21
149	Cyclization-blocked proguanil as a strategy to improve the antimalarial activity of atovaquone. Communications Biology, 2019, 2, 166.	2.0	20
150	Synthesis and Structureâ€“Activity Relationship of Dual-Stage Antimalarial Pyrazolo[3,4-b]pyridines. Journal of Medicinal Chemistry, 2020, 63, 11902-11919.	2.9	20
151	A Novel Promoter Motif forCaulobacterCell Cycle-controlled DNA Replication Genes. Journal of Molecular Biology, 1996, 264, 412-425.	2.0	19
152	Using expression information to discover new drug and vaccine targets in the malaria parasitePlasmodium falciparum. Pharmacogenomics, 2005, 6, 17-26.	0.6	19
153	Identification of non-CSP antigens bearing CD8 epitopes in mice immunized with irradiated sporozoites. Vaccine, 2011, 29, 7335-7342.	1.7	19
154	Kalkipyrone B, a marine cyanobacterial Î³-pyrone possessing cytotoxic and anti-fungal activities. Phytochemistry, 2016, 122, 113-118.	1.4	19
155	Design of proteasome inhibitors with oral efficacy in vivo against Plasmodium falciparum and selectivity over the human proteasome. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	19
156	Human Aurora kinase inhibitor Hesperadin reveals epistatic interaction between Plasmodium falciparum PfArk1 and PfNek1 kinases. Communications Biology, 2020, 3, 701.	2.0	18
157	Large-scale mutagenesis and functional genomics in yeast. Functional and Integrative Genomics, 2002, 2, 193-198.	1.4	17
158	Targeted Disruption of a Ring-infected Erythrocyte Surface Antigen (RESA)-like Export Protein Gene in Plasmodium falciparum Confers Stable Chondroitin 4-Sulfate Cytoadherence Capacity. Journal of Biological Chemistry, 2014, 289, 34408-34421.	1.6	16
159	Optimal 10-Aminoartemisinins With Potent Transmission-Blocking Capabilities for New Artemisinin Combination Therapiesâ€“Activities Against Blood Stage P. falciparum Including PfKI3 C580Y Mutants and Liver Stage P. berghei Parasites. Frontiers in Chemistry, 2019, 7, 901.	1.8	16
160	PfMFR3: A Multidrug-Resistant Modulator in Plasmodium falciparum. ACS Infectious Diseases, 2021, 7, 811-825.	1.8	16
161	Translation of the leaderless Caulobacter dnaX mRNA. Journal of Bacteriology, 1997, 179, 3981-3988.	1.0	16
162	Elucidating genetic diversity with oligonucleotide arrays. Chromosome Research, 2005, 13, 225-235.	1.0	15

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163	Functional Analysis of the Yeast Genome by Precise Deletion and Parallel Phenotypic Characterization. Novartis Foundation Symposium, 2008, 229, 105-111.	1.2	15
164	Cell-based optimization of novel benzamides as potential antimalarial leads. Bioorganic and Medicinal Chemistry Letters, 2009, 19, 6970-6974.	1.0	15
165	Exploration of the Plasmodium falciparum Resistome and Druggable Genome Reveals New Mechanisms of Drug Resistance and Antimalarial Targets. Microbiology Insights, 2018, 11, 117863611880852.	0.9	15
166	Fluorescence anisotropy decay of ethidium bound to nucleosome core particles. 2. The Torsional Motion of the DNA is highly constrained and sensitive to pH. Biochemistry, 1991, 30, 5304-5313.	1.2	14
167	Design and Synthesis of Terephthalic Acidâ€Based Histone Deacetylase Inhibitors with Dualâ€Stage Antiâ€• Plasmodium Activity. ChemMedChem, 2017, 12, 1627-1636.	1.6	14
168	A consensus-based and readable extension of Linear Code for Reaction Rules (LiCoRR). Beilstein Journal of Organic Chemistry, 2020, 16, 2645-2662.	1.3	14
169	The Plasmodium falciparum ABC transporter ABCI3 confers parasite strain-dependent pleiotropic antimalarial drug resistance. Cell Chemical Biology, 2022, 29, 824-839.e6.	2.5	14
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