

Elizabeth Ann Winzeler

List of Publications by Citations

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220
papers

24,774
citations

63
h-index

156
g-index

238
ext. papers

28,065
ext. citations

13.1
avg, IF

6.29
L-index

#	Paper	IF	Citations
220	Functional profiling of the <i>Saccharomyces cerevisiae</i> genome. <i>Nature</i> , 2002 , 418, 387-91	50.4	3278
219	Functional characterization of the <i>S. cerevisiae</i> genome by gene deletion and parallel analysis. <i>Science</i> , 1999 , 285, 901-6	33.3	3254
218	Genomics, gene expression and DNA arrays. <i>Nature</i> , 2000 , 405, 827-36	50.4	1695
217	A genome-wide transcriptional analysis of the mitotic cell cycle. <i>Molecular Cell</i> , 1998 , 2, 65-73	17.6	1659
216	Discovery of gene function by expression profiling of the malaria parasite life cycle. <i>Science</i> , 2003 , 301, 1503-8	33.3	1010
215	Spiroindolones, a potent compound class for the treatment of malaria. <i>Science</i> , 2010 , 329, 1175-80	33.3	883
214	Replication dynamics of the yeast genome. <i>Science</i> , 2001 , 294, 115-21	33.3	622
213	Genomic profiling of drug sensitivities via induced haploinsufficiency. <i>Nature Genetics</i> , 1999 , 21, 278-83	36.3	472
212	The core meiotic transcriptome in budding yeasts. <i>Nature Genetics</i> , 2000 , 26, 415-23	36.3	378
211	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, 9059-64	11.5	361
210	Global analysis of transcript and protein levels across the <i>Plasmodium falciparum</i> life cycle. <i>Genome Research</i> , 2004 , 14, 2308-18	9.7	354
209	Spirotetrahydro beta-carbolines (spiroindolones): a new class of potent and orally efficacious compounds for the treatment of malaria. <i>Journal of Medicinal Chemistry</i> , 2010 , 53, 5155-64	8.3	332
208	Protein pathway and complex clustering of correlated mRNA and protein expression analyses in <i>Saccharomyces cerevisiae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 3107-12	11.5	307
207	Large-scale identification of single-feature polymorphisms in complex genomes. <i>Genome Research</i> , 2003 , 13, 513-23	9.7	307
206	Direct allelic variation scanning of the yeast genome. <i>Science</i> , 1998 , 281, 1194-7	33.3	306
205	Targeting <i>Plasmodium</i> PI(4)K to eliminate malaria. <i>Nature</i> , 2013 , 504, 248-253	50.4	291
204	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	1.9	258

203	A novel multiple-stage antimalarial agent that inhibits protein synthesis. <i>Nature</i> , 2015 , 522, 315-20	50.4	250
202	The activities of current antimalarial drugs on the life cycle stages of Plasmodium: a comparative study with human and rodent parasites. <i>PLoS Medicine</i> , 2012 , 9, e1001169	11.6	249
201	Imaging of Plasmodium liver stages to drive next-generation antimalarial drug discovery. <i>Science</i> , 2011 , 334, 1372-7	33.3	243
200	Molecular mechanism for switching of P. falciparum invasion pathways into human erythrocytes. <i>Science</i> , 2005 , 309, 1384-7	33.3	224
199	A plant-like kinase in Plasmodium falciparum regulates parasite egress from erythrocytes. <i>Science</i> , 2010 , 328, 910-2	33.3	221
198	Antimalarial drug discovery - approaches and progress towards new medicines. <i>Nature Reviews Microbiology</i> , 2013 , 11, 849-62	22.2	202
197	Distinct physiological states of Plasmodium falciparum in malaria-infected patients. <i>Nature</i> , 2007 , 450, 1091-5	50.4	186
196	Gene expression signatures and small-molecule compounds link a protein kinase to Plasmodium falciparum motility. <i>Nature Chemical Biology</i> , 2008 , 4, 347-56	11.7	178
195	Diversity-oriented synthesis yields novel multistage antimalarial inhibitors. <i>Nature</i> , 2016 , 538, 344-349	50.4	172
194	Open Source Drug Discovery with the Malaria Box Compound Collection for Neglected Diseases and Beyond. <i>PLoS Pathogens</i> , 2016 , 12, e1005763	7.6	167
193	Selective and specific inhibition of the plasmodium falciparum lysyl-tRNA synthetase by the fungal secondary metabolite cladosporin. <i>Cell Host and Microbe</i> , 2012 , 11, 654-63	23.4	165
192	Plasmodium circumsporozoite protein promotes the development of the liver stages of the parasite. <i>Cell</i> , 2007 , 131, 492-504	56.2	164
191	A systematic map of genetic variation in Plasmodium falciparum. <i>PLoS Pathogens</i> , 2006 , 2, e57	7.6	159
190	Na(+) regulation in the malaria parasite Plasmodium falciparum involves the cation ATPase PfATP4 and is a target of the spiroindolone antimalarials. <i>Cell Host and Microbe</i> , 2013 , 13, 227-37	23.4	153
189	Mitotic evolution of Plasmodium falciparum shows a stable core genome but recombination in antigen families. <i>PLoS Genetics</i> , 2013 , 9, e1003293	6	149
188	malERA: An updated research agenda for malaria elimination and eradication. <i>PLoS Medicine</i> , 2017 , 14, e1002456	11.6	148
187	Genetic diversity in yeast assessed with whole-genome oligonucleotide arrays. <i>Genetics</i> , 2003 , 163, 79-89		148
186	Mapping the malaria parasite druggable genome by using in vitro evolution and chemogenomics. <i>Science</i> , 2018 , 359, 191-199	33.3	124

185	A Plasmodium gene family encoding Maurer's cleft membrane proteins: structural properties and expression profiling. <i>Genome Research</i> , 2004 , 14, 1052-9	9.7	122
184	Use of high-density tiling microarrays to identify mutations globally and elucidate mechanisms of drug resistance in Plasmodium falciparum. <i>Genome Biology</i> , 2009 , 10, R21	18.3	114
183	Malaria research in the post-genomic era. <i>Nature</i> , 2008 , 455, 751-6	50.4	110
182	Common PIEZO1 Allele in African Populations Causes RBC Dehydration and Attenuates Plasmodium Infection. <i>Cell</i> , 2018 , 173, 443-455.e12	56.2	104
181	KAF156 is an antimalarial clinical candidate with potential for use in prophylaxis, treatment, and prevention of disease transmission. <i>Antimicrobial Agents and Chemotherapy</i> , 2014 , 58, 5060-7	5.9	101
180	Synthesis and biological evaluation of epidithio-, epitetrahydro-, and bis-(methylthio)diketopiperazines: synthetic methodology, enantioselective total synthesis of epicoccin G, 8,8-Tepi-ent-rostratin B, gliotoxin, gliotoxin G, emethallicin E, and haematocin and discovery of novel thioether-containing dihydroquinolizidine alkaloids. <i>Journal of the American Chemical Society</i> , 2012 , 134, 1211-1221	16.4	101
179	The Plasmodium eukaryotic initiation factor-2alpha kinase IK2 controls the latency of sporozoites in the mosquito salivary glands. <i>Journal of Experimental Medicine</i> , 2010 , 207, 1465-74	16.6	99
178	Validation of isoleucine utilization targets in Plasmodium falciparum. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 1627-32	11.5	99
177	High-Throughput Assay and Discovery of Small Molecules that Interrupt Malaria Transmission. <i>Cell Host and Microbe</i> , 2016 , 19, 114-26	23.4	94
176	Piperaquine resistance is associated with a copy number variation on chromosome 5 in drug-pressured Plasmodium falciparum parasites. <i>Antimicrobial Agents and Chemotherapy</i> , 2011 , 55, 3908-16	5.9	93
175	Imidazolopiperazines: hit to lead optimization of new antimalarial agents. <i>Journal of Medicinal Chemistry</i> , 2011 , 54, 5116-30	8.3	88
174	In silico discovery of transcription regulatory elements in Plasmodium falciparum. <i>BMC Genomics</i> , 2008 , 9, 70	4.5	88
173	The Ume6 regulon coordinates metabolic and meiotic gene expression in yeast. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 13431-6	11.5	88
172	Previously uncharacterized genes in the UV- and MMS-induced DNA damage response in yeast. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 10605-10	11.5	87
171	Whole-genome sequencing and microarray analysis of ex vivo Plasmodium vivax reveal selective pressure on putative drug resistance genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 20045-50	11.5	84
170	A systems-based analysis of Plasmodium vivax lifecycle transcription from human to mosquito. <i>PLoS Neglected Tropical Diseases</i> , 2010 , 4, e653	4.8	84
169	In vivo transcriptome of Plasmodium falciparum reveals overexpression of transcripts that encode surface proteins. <i>Journal of Infectious Diseases</i> , 2005 , 191, 1196-203	7	83
168	Application of high-density array-based signature-tagged mutagenesis to discover novel Yersinia virulence-associated genes. <i>Infection and Immunity</i> , 2001 , 69, 7810-9	3.7	80

167	Imidazolopiperazines: lead optimization of the second-generation antimalarial agents. <i>Journal of Medicinal Chemistry</i> , 2012 , 55, 4244-73	8.3	75
166	Excess polymorphisms in genes for membrane proteins in <i>Plasmodium falciparum</i> . <i>Science</i> , 2002 , 298, 216-8	33.3	73
165	A chemical genomic analysis of decoquinate, a <i>Plasmodium falciparum</i> cytochrome b inhibitor. <i>ACS Chemical Biology</i> , 2011 , 6, 1214-22	4.9	72
164	Experimentally induced blood-stage <i>Plasmodium vivax</i> infection in healthy volunteers. <i>Journal of Infectious Diseases</i> , 2013 , 208, 1688-94	7	71
163	Targeting the ERAD pathway via inhibition of signal peptide peptidase for antiparasitic therapeutic design. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 21486-91	11.5	71
162	A broad analysis of resistance development in the malaria parasite. <i>Nature Communications</i> , 2016 , 7, 11901	17.4	70
161	Evidence-based annotation of the malaria parasite genome using comparative expression profiling. <i>PLoS ONE</i> , 2008 , 3, e1570	3.7	70
160	UDP-galactose and acetyl-CoA transporters as <i>Plasmodium</i> multidrug resistance genes. <i>Nature Microbiology</i> , 2016 , 1, 16166	26.6	67
159	In silico gene function prediction using ontology-based pattern identification. <i>Bioinformatics</i> , 2005 , 21, 1237-45	7.2	65
158	Treasures and traps in genome-wide data sets: case examples from yeast. <i>Nature Reviews Genetics</i> , 2002 , 3, 653-61	30.1	63
157	Antimalarial activity of single-dose DSM265, a novel plasmodium dihydroorotate dehydrogenase inhibitor, in patients with uncomplicated <i>Plasmodium falciparum</i> or <i>Plasmodium vivax</i> malaria infection: a proof-of-concept, open-label, phase 2a study. <i>Lancet Infectious Diseases</i> , 2018 , 18, 874-883	25.5	62
156	High-Throughput Luciferase-Based Assay for the Discovery of Therapeutics That Prevent Malaria. <i>ACS Infectious Diseases</i> , 2016 , 2, 281-293	5.5	61
155	Discovery of HDAC inhibitors with potent activity against multiple malaria parasite life cycle stages. <i>European Journal of Medicinal Chemistry</i> , 2014 , 82, 204-13	6.8	61
154	A high throughput screen for next-generation leads targeting malaria parasite transmission. <i>Nature Communications</i> , 2018 , 9, 3805	17.4	61
153	Open-source discovery of chemical leads for next-generation chemoprotective antimalarials. <i>Science</i> , 2018 , 362,	33.3	60
152	A Variant PfCRT Isoform Can Contribute to Resistance to the First-Line Partner Drug Piperaquine. <i>MBio</i> , 2017 , 8,	7.8	58
151	Genome-wide nucleosome mapping of <i>Plasmodium falciparum</i> reveals histone-rich coding and histone-poor intergenic regions and chromatin remodeling of core and subtelomeric genes. <i>BMC Genomics</i> , 2009 , 10, 610	4.5	58
150	Mutations in the P-type cation-transporter ATPase 4, PfATP4, mediate resistance to both aminopyrazole and spiroindolone antimalarials. <i>ACS Chemical Biology</i> , 2015 , 10, 413-20	4.9	57

149	KAI407, a potent non-8-aminoquinoline compound that kills <i>Plasmodium cynomolgi</i> early dormant liver stage parasites in vitro. <i>Antimicrobial Agents and Chemotherapy</i> , 2014 , 58, 1586-95	5.9	56
148	Using genetic methods to define the targets of compounds with antimalarial activity. <i>Journal of Medicinal Chemistry</i> , 2013 , 56, 7761-71	8.3	53
147	Drug resistance genomics of the antimalarial drug artemisinin. <i>Genome Biology</i> , 2014 , 15, 544	18.3	53
146	Parallel identification of new genes in <i>Saccharomyces cerevisiae</i> . <i>Genome Research</i> , 2002 , 12, 1210-20	9.7	53
145	A high resolution case study of a patient with recurrent <i>Plasmodium vivax</i> infections shows that relapses were caused by meiotic siblings. <i>PLoS Neglected Tropical Diseases</i> , 2014 , 8, e2882	4.8	52
144	Functional analysis of the yeast genome. <i>Current Opinion in Genetics and Development</i> , 1997 , 7, 771-6	4.9	52
143	A systematic approach to understand the mechanism of action of the bithiazolium compound T4 on the human malaria parasite, <i>Plasmodium falciparum</i> . <i>BMC Genomics</i> , 2008 , 9, 513	4.5	51
142	Lysyl-tRNA synthetase as a drug target in malaria and cryptosporidiosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 7015-7020	11.5	50
141	Synthesis of (+)-7,20-Diisocyanoadociane and Liver-Stage Antiplasmodial Activity of the Isocyanoterpene Class. <i>Journal of the American Chemical Society</i> , 2016 , 138, 7268-71	16.4	50
140	Genome scanning of Amazonian <i>Plasmodium falciparum</i> shows subtelomeric instability and clindamycin-resistant parasites. <i>Genome Research</i> , 2010 , 20, 1534-44	9.7	48
139	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	1.9	47
138	Development of a Potent Inhibitor of the <i>Plasmodium</i> Proteasome with Reduced Mammalian Toxicity. <i>Journal of Medicinal Chemistry</i> , 2017 , 60, 6721-6732	8.3	46
137	<i>Plasmodium falciparum</i> : genome wide perturbations in transcript profiles among mixed stage cultures after chloroquine treatment. <i>Experimental Parasitology</i> , 2007 , 117, 87-92	2.1	46
136	In vivo transcriptional profiling of <i>Plasmodium falciparum</i> . <i>Malaria Journal</i> , 2004 , 3, 30	3.6	46
135	Direct transfer of whole genomes from bacteria to yeast. <i>Nature Methods</i> , 2013 , 10, 410-2	21.6	45
134	Microarray-based comparative genomic analyses of the human malaria parasite <i>Plasmodium falciparum</i> using Affymetrix arrays. <i>Molecular and Biochemical Parasitology</i> , 2005 , 144, 177-86	1.9	45
133	CRISPR-Cas9-modified <i>pfmdr1</i> protects <i>Plasmodium falciparum</i> asexual blood stages and gametocytes against a class of piperazine-containing compounds but potentiates artemisinin-based combination therapy partner drugs. <i>Molecular Microbiology</i> , 2016 , 101, 381-93	4.1	45
132	Discovery of a Quinoline-4-carboxamide Derivative with a Novel Mechanism of Action, Multistage Antimalarial Activity, and Potent in Vivo Efficacy. <i>Journal of Medicinal Chemistry</i> , 2016 , 59, 9672-9685	8.3	45

131	Open Source Drug Discovery: Highly Potent Antimalarial Compounds Derived from the Tres Cantos Arylpyrroles. <i>ACS Central Science</i> , 2016 , 2, 687-701	16.8	44
130	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. <i>Journal of Medicinal Chemistry</i> , 2016 , 59, 9890-9905	8.3	43
129	Fluorescence-based expression monitoring using microarrays. <i>Methods in Enzymology</i> , 1999 , 306, 3-18	1.7	41
128	Monitoring the chromosome 2 intraerythrocytic transcriptome of Plasmodium falciparum using oligonucleotide arrays. <i>American Journal of Tropical Medicine and Hygiene</i> , 2002 , 67, 233-43	3.2	41
127	The paradoxical population genetics of Plasmodium falciparum. <i>Trends in Parasitology</i> , 2002 , 18, 266-72	6.4	40
126	Infection of laboratory-colonized Anopheles darlingi mosquitoes by Plasmodium vivax. <i>American Journal of Tropical Medicine and Hygiene</i> , 2014 , 90, 612-616	3.2	39
125	Use of flow cytometry to identify a Caulobacter 4.5 S RNA temperature-sensitive mutant defective in the cell cycle. <i>Journal of Molecular Biology</i> , 1995 , 251, 346-65	6.5	39
124	Identification of pathogen genomic variants through an integrated pipeline. <i>BMC Bioinformatics</i> , 2014 , 15, 63	3.6	37
123	Target Validation and Identification of Novel Boronate Inhibitors of the Plasmodium falciparum Proteasome. <i>Journal of Medicinal Chemistry</i> , 2018 , 61, 10053-10066	8.3	37
122	Selective Whole-Genome Amplification Is a Robust Method That Enables Scalable Whole-Genome Sequencing of Plasmodium vivax From Unprocessed Clinical Samples. <i>MBio</i> , 2017 , 8,	7.8	36
121	Using in Vitro Evolution and Whole Genome Analysis To Discover Next Generation Targets for Antimalarial Drug Discovery. <i>ACS Infectious Diseases</i> , 2018 , 4, 301-314	5.5	35
120	Whole genome sequencing analysis of Plasmodium vivax using whole genome capture. <i>BMC Genomics</i> , 2012 , 13, 262	4.5	34
119	Large-scale annotation of small-molecule libraries using public databases. <i>Journal of Chemical Information and Modeling</i> , 2007 , 47, 1386-94	6.1	33
118	Advances in omics-based methods to identify novel targets for malaria and other parasitic protozoan infections. <i>Genome Medicine</i> , 2019 , 11, 63	14.4	32
117	Mutations in the Plasmodium falciparum Cyclic Amine Resistance Locus (PFCARL) Confer Multidrug Resistance. <i>MBio</i> , 2016 , 7,	7.8	32
116	Comparative chemical genomics reveal that the spiroindolone antimalarial KAE609 (Cipargamin) is a P-type ATPase inhibitor. <i>Scientific Reports</i> , 2016 , 6, 27806	4.9	31
115	Phenotypic Screens in Antimalarial Drug Discovery. <i>Trends in Parasitology</i> , 2016 , 32, 697-707	6.4	31
114	Applied systems biology and malaria. <i>Nature Reviews Microbiology</i> , 2006 , 4, 145-51	22.2	31

113	Niemann-Pick type C1-related protein is a druggable target required for parasite membrane homeostasis. <i>ELife</i> , 2019 , 8,	8.9	31
112	Covalent Plasmodium falciparum-selective proteasome inhibitors exhibit a low propensity for generating resistance in vitro and synergize with multiple antimalarial agents. <i>PLoS Pathogens</i> , 2019 , 15, e1007722	7.6	30
111	Target identification and validation of novel antimalarials. <i>Future Microbiology</i> , 2011 , 6, 693-704	2.9	30
110	Validation of the protein kinase CLK3 as a multistage cross-species malarial drug target. <i>Science</i> , 2019 , 365,	33.3	29
109	Regulatory motifs uncovered among gene expression clusters in Plasmodium falciparum. <i>Molecular and Biochemical Parasitology</i> , 2007 , 153, 19-30	1.9	29
108	Combining Stage Specificity and Metabolomic Profiling to Advance Antimalarial Drug Discovery. <i>Cell Chemical Biology</i> , 2020 , 27, 158-171.e3	8.2	29
107	Dual RNA-seq identifies human mucosal immunity protein Mucin-13 as a hallmark of Plasmodium exoerythrocytic infection. <i>Nature Communications</i> , 2019 , 10, 488	17.4	27
106	Inhibition of Resistance-Refractory P. falciparum Kinase PKG Delivers Prophylactic, Blood Stage, and Transmission-Blocking Antiplasmodial Activity. <i>Cell Chemical Biology</i> , 2020 , 27, 806-816.e8	8.2	26
105	Coordinated functions of WSS1, PSY2 and TOF1 in the DNA damage response. <i>Nucleic Acids Research</i> , 2004 , 32, 6519-30	20.1	26
104	Plasmodium falciparum Cyclic Amine Resistance Locus (PFCARL), a Resistance Mechanism for Two Distinct Compound Classes. <i>ACS Infectious Diseases</i> , 2016 , 2, 816-826	5.5	26
103	Hexahydroquinolines are antimalarial candidates with potent blood-stage and transmission-blocking activity. <i>Nature Microbiology</i> , 2017 , 2, 1403-1414	26.6	25
102	The genomic architecture of antimalarial drug resistance. <i>Briefings in Functional Genomics</i> , 2019 , 18, 314-338	17.9	25
101	Lead optimization of imidazopyrazines: a new class of antimalarial with activity on Plasmodium liver stages. <i>ACS Medicinal Chemistry Letters</i> , 2014 , 5, 947-50	4.3	24
100	A Novel Pyrazolopyridine with in Vivo Activity in Plasmodium berghei- and Plasmodium falciparum-Infected Mouse Models from Structure-Activity Relationship Studies around the Core of Recently Identified Antimalarial Imidazopyridazines. <i>Journal of Medicinal Chemistry</i> , 2015 , 58, 8713-22	8.3	23
99	Next-Generation Sequencing of Plasmodium vivax Patient Samples Shows Evidence of Direct Evolution in Drug-Resistance Genes. <i>ACS Infectious Diseases</i> , 2015 , 1, 367-79	5.5	22
98	A key role for lipoic acid synthesis during Plasmodium liver stage development. <i>Cellular Microbiology</i> , 2013 , 15, 1585-604	3.9	22
97	Discovery of novel 1H-imidazol-2-yl-pyrimidine-4,6-diamines as potential antimalarials. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2010 , 20, 4027-31	2.9	22
96	Nuclear repositioning precedes promoter accessibility and is linked to the switching frequency of a Plasmodium falciparum invasion gene. <i>Cell Host and Microbe</i> , 2012 , 12, 739-50	23.4	20

95	Bacterial genome reduction using the progressive clustering of deletions via yeast sexual cycling. <i>Genome Research</i> , 2015 , 25, 435-44	9.7	19
94	Leveraging two-way probe-level block design for identifying differential gene expression with high-density oligonucleotide arrays. <i>BMC Bioinformatics</i> , 2004 , 5, 42	3.6	19
93	One-pot, multi-component synthesis and structure-activity relationships of peptoid-based histone deacetylase (HDAC) inhibitors targeting malaria parasites. <i>European Journal of Medicinal Chemistry</i> , 2018 , 158, 801-813	6.8	19
92	Esterase mutation is a mechanism of resistance to antimalarial compounds. <i>Nature Communications</i> , 2017 , 8, 14240	17.4	18
91	Genomics, systems biology and drug development for infectious diseases. <i>Molecular BioSystems</i> , 2007 , 3, 841-8		18
90	Using expression information to discover new drug and vaccine targets in the malaria parasite <i>Plasmodium falciparum</i> . <i>Pharmacogenomics</i> , 2005 , 6, 17-26	2.6	18
89	MalDA, Accelerating Malaria Drug Discovery. <i>Trends in Parasitology</i> , 2021 , 37, 493-507	6.4	18
88	Multistage and transmission-blocking targeted antimalarials discovered from the open-source MMV Pandemic Response Box. <i>Nature Communications</i> , 2021 , 12, 269	17.4	18
87	Genetic analysis of primaquine tolerance in a patient with relapsing vivax malaria. <i>Emerging Infectious Diseases</i> , 2013 , 19, 802-5	10.2	17
86	Identification of non-CSP antigens bearing CD8 epitopes in mice immunized with irradiated sporozoites. <i>Vaccine</i> , 2011 , 29, 7335-42	4.1	17
85	A novel promoter motif for <i>Caulobacter</i> cell cycle-controlled DNA replication genes. <i>Journal of Molecular Biology</i> , 1996 , 264, 412-25	6.5	17
84	Translation of the leaderless <i>Caulobacter</i> dnaX mRNA. <i>Journal of Bacteriology</i> , 1997 , 179, 3981-8	3.5	16
83	Genome wide analysis of inbred mouse lines identifies a locus containing Ppar-gamma as contributing to enhanced malaria survival. <i>PLoS ONE</i> , 2010 , 5, e10903	3.7	16
82	The antimalarial resistome - finding new drug targets and their modes of action. <i>Current Opinion in Microbiology</i> , 2020 , 57, 49-55	7.9	16
81	Evolution of resistance in vitro reveals mechanisms of artemisinin activity in. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 ,	11.5	16
80	Rapid Chagas Disease Drug Target Discovery Using Directed Evolution in Drug-Sensitive Yeast. <i>ACS Chemical Biology</i> , 2017 , 12, 422-434	4.9	15
79	Kalkipyronone B, a marine cyanobacterial β pyrone possessing cytotoxic and anti-fungal activities. <i>Phytochemistry</i> , 2016 , 122, 113-118	4	15
78	Systems analysis of host-parasite interactions. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2015 , 7, 381-400	6.6	15

77	Cell-based optimization of novel benzamides as potential antimalarial leads. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2009 , 19, 6970-4	2.9	15
76	Functional analysis of the yeast genome by precise deletion and parallel phenotypic characterization. <i>Novartis Foundation Symposium</i> , 2000 , 229, 105-9; discussion 109-11		15
75	Large-scale mutagenesis and functional genomics in yeast. <i>Functional and Integrative Genomics</i> , 2002 , 2, 193-8	3.8	15
74	In vitro selection predicts malaria parasite resistance to dihydroorotate dehydrogenase inhibitors in a mouse infection model. <i>Science Translational Medicine</i> , 2019 , 11,	17.5	15
73	Structure-Activity and Structure-Toxicity Relationships of Peptoid-Based Histone Deacetylase Inhibitors with Dual-Stage Antiplasmodial Activity. <i>ChemMedChem</i> , 2019 , 14, 912-926	3.7	14
72	Probing the Open Global Health Chemical Diversity Library for Multistage-Active Starting Points for Next-Generation Antimalarials. <i>ACS Infectious Diseases</i> , 2020 , 6, 613-628	5.5	14
71	Accessible and distinct decoquinate derivatives active against Mycobacterium tuberculosis and apicomplexan parasites. <i>Communications Chemistry</i> , 2018 , 1,	6.3	14
70	Elucidating genetic diversity with oligonucleotide arrays. <i>Chromosome Research</i> , 2005 , 13, 225-35	4.4	13
69	Exploration of the Resistome and Druggable Genome Reveals New Mechanisms of Drug Resistance and Antimalarial Targets. <i>Microbiology Insights</i> , 2018 , 11, 1178636118808529	2.5	13
68	Targeted disruption of a ring-infected erythrocyte surface antigen (RESA)-like export protein gene in <i>Plasmodium falciparum</i> confers stable chondroitin 4-sulfate cytoadherence capacity. <i>Journal of Biological Chemistry</i> , 2014 , 289, 34408-21	5.4	12
67	Exploration of <i>Plasmodium vivax</i> transmission dynamics and recurrent infections in the Peruvian Amazon using whole genome sequencing. <i>Genome Medicine</i> , 2018 , 10, 52	14.4	11
66	Chemogenomics identifies acetyl-coenzyme A synthetase as a target for malaria treatment and prevention. <i>Cell Chemical Biology</i> , 2021 ,	8.2	11
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