

Elizabeth Ann Winzeler

List of Publications by Year in Descending Order

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Version: 2024-04-25

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	Adaptive laboratory evolution in <i>S. cerevisiae</i> highlights role of transcription factors in fungal xenobiotic resistance.. <i>Communications Biology</i> , 2022 , 5, 128	6.7	1
219	A novel CSP C-terminal epitope targeted by an antibody with protective activity against <i>Plasmodium falciparum</i> .. <i>PLoS Pathogens</i> , 2022 , 18, e1010409	7.6	0
218	Reaction hijacking of tyrosine tRNA synthetase as a new whole-of-life-cycle antimalarial strategy. <i>Science</i> , 2022 , 376, 1074-1079	33.3	3
217	PFMR3: A Multidrug-Resistant Modulator in. <i>ACS Infectious Diseases</i> , 2021 , 7, 811-825	5.5	4
216	Potent Antimalarials with Development Potential Identified by Structure-Guided Computational Optimization of a Pyrrole-Based Dihydroorotate Dehydrogenase Inhibitor Series. <i>Journal of Medicinal Chemistry</i> , 2021 , 64, 6085-6136	8.3	3
215	MalDA, Accelerating Malaria Drug Discovery. <i>Trends in Parasitology</i> , 2021 , 37, 493-507	6.4	18
214	The <i>Plasmodium falciparum</i> ABC transporter ABCI3 confers parasite strain-dependent pleiotropic antimalarial drug resistance. <i>Cell Chemical Biology</i> , 2021 ,	8.2	3
213	Investigation of the in vitro and in vivo efficacy of peptoid-based HDAC inhibitors with dual-stage antiplasmodial activity. <i>European Journal of Medicinal Chemistry</i> , 2021 , 211, 113065	6.8	3
212	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
211	Identification and Profiling of a Novel Diazaspiro[3.4]octane Chemical Series Active against Multiple Stages of the Human Malaria Parasite and Optimization Efforts. <i>Journal of Medicinal Chemistry</i> , 2021 , 64, 2291-2309	8.3	5
210	Novel Antimalarial Tetrazoles and Amides Active against the Hemoglobin Degradation Pathway in. <i>Journal of Medicinal Chemistry</i> , 2021 , 64, 2739-2761	8.3	2
209	The Novel bis-1,2,4-Triazine MIPS-0004373 Demonstrates Rapid and Potent Activity against All Blood Stages of the Malaria Parasite. <i>Antimicrobial Agents and Chemotherapy</i> , 2021 , 65, e0031121	5.9	3
208	Chemogenomics identifies acetyl-coenzyme A synthetase as a target for malaria treatment and prevention. <i>Cell Chemical Biology</i> , 2021 ,	8.2	11
207	Prioritization of Molecular Targets for Antimalarial Drug Discovery. <i>ACS Infectious Diseases</i> , 2021 , 7, 2764-2776	5.3	3
206	Design of proteasome inhibitors with oral efficacy in vivo against and selectivity over the human proteasome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	1
205	Chemoprotective antimalarials identified through quantitative high-throughput screening of <i>Plasmodium</i> blood and liver stage parasites. <i>Scientific Reports</i> , 2021 , 11, 2121	4.9	7
204	The Key Glycolytic Enzyme Phosphofructokinase Is Involved in Resistance to Antiplasmodial Glycosides. <i>MBio</i> , 2020 , 11,	7.8	2

203	Inhibition of Resistance-Refractory <i>P. falciparum</i> Kinase PKG Delivers Prophylactic, Blood Stage, and Transmission-Blocking Antiplasmodial Activity. <i>Cell Chemical Biology</i> , 2020 , 27, 806-816.e8	8.2	26
202	Synthesis and Bioactivity of Phthalimide Analogs as Potential Drugs to Treat Schistosomiasis, a Neglected Disease of Poverty. <i>Pharmaceuticals</i> , 2020 , 13,	5.2	4
201	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
200	Combining Stage Specificity and Metabolomic Profiling to Advance Antimalarial Drug Discovery. <i>Cell Chemical Biology</i> , 2020 , 27, 158-171.e3	8.2	29
199	SnapShot: Antimalarial Drugs. <i>Cell</i> , 2020 , 183, 554-554.e1	56.2	1
198	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
197	Human Aurora kinase inhibitor Hesperadin reveals epistatic interaction between <i>Plasmodium falciparum</i> PfArk1 and PfNek1 kinases. <i>Communications Biology</i> , 2020 , 3, 701	6.7	8
196	Genome-Wide Dynamic Evaluation of the UV-Induced DNA Damage Response. <i>G3: Genes, Genomes, Genetics</i> , 2020 , 10, 2981-2988	3.2	
195	A consensus-based and readable extension of near de for eaction ules (LiCoRR). <i>Beilstein Journal of Organic Chemistry</i> , 2020 , 16, 2645-2662	2.5	8
194	Synthesis and Structure-Activity Relationship of Dual-Stage Antimalarial Pyrazolo[3,4-]pyridines. <i>Journal of Medicinal Chemistry</i> , 2020 , 63, 11902-11919	8.3	8
193	Genomic Approaches to Drug Resistance in Malaria. <i>Annual Review of Microbiology</i> , 2020 , 74, 761-786	17.5	2
192	A Novel Antiparasitic Compound Kills Ring-Stage <i>Plasmodium falciparum</i> and Retains Activity Against Artemisinin-Resistant Parasites. <i>Journal of Infectious Diseases</i> , 2020 , 221, 956-962	7	5
191	Pan-active imidazolopiperazine antimalarials target the <i>Plasmodium falciparum</i> intracellular secretory pathway. <i>Nature Communications</i> , 2020 , 11, 1780	17.4	10
190	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
189	Validation of the protein kinase CLK3 as a multistage cross-species malarial drug target. <i>Science</i> , 2019 , 365,	33.3	29
188	A roadmap for malaria research. <i>Science</i> , 2019 , 365, 753-754	33.3	1
187	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
186	Dual RNA-seq identifies human mucosal immunity protein Mucin-13 as a hallmark of <i>Plasmodium</i> exoerythrocytic infection. <i>Nature Communications</i> , 2019 , 10, 488	17.4	27

185	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
184	Substituted Aminoacetamides as Novel Leads for Malaria Treatment. <i>ChemMedChem</i> , 2019 , 14, 1329-1335	3.7	3
183	The proteasome as a target: How not tidying up can have toxic consequences for parasitic protozoa. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 10198-10200	11.5	3
182	Cyclization-blocked proguanil as a strategy to improve the antimalarial activity of atovaquone. <i>Communications Biology</i> , 2019 , 2, 166	6.7	6
181	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
180	Optimal 10-Aminoartemisinins With Potent Transmission-Blocking Capabilities for New Artemisinin Combination Therapies-Activities Against Blood Stage Including K13 C580Y Mutants and Liver Stage Parasites. <i>Frontiers in Chemistry</i> , 2019 , 7, 901	5	6
179	Niemann-Pick type C1-related protein is a druggable target required for parasite membrane homeostasis. <i>ELife</i> , 2019 , 8,	8.9	31
178	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
177	The genomic architecture of antimalarial drug resistance. <i>Briefings in Functional Genomics</i> , 2019 , 18, 314-328	19.8	25
176	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
175	Synthesis, Profiling, and in Vivo Evaluation of Cyclopeptides Containing -Methyl Amino Acids as Antiplasmodial Agents. <i>ACS Medicinal Chemistry Letters</i> , 2019 , 10, 137-141	4.3	9
174	An improbable journey: Creativity helped me make the transition from art to curing malaria. <i>Journal of Biological Chemistry</i> , 2019 , 294, 405-409	5.4	
173	8-Aminoquinolines with an Aminoxyalkyl Side Chain Exert in vitro Dual-Stage Antiplasmodial Activity. <i>ChemMedChem</i> , 2019 , 14, 501-511	3.7	3
172	Continuous Supply of Plasmodium vivax Sporozoites from Colonized Anopheles darlingi in the Peruvian Amazon. <i>ACS Infectious Diseases</i> , 2018 , 4, 541-548	5.5	6
171	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
170	Mapping the malaria parasite druggable genome by using in vitro evolution and chemogenomics. <i>Science</i> , 2018 , 359, 191-199	33.3	124
169	A Sleeping Area of Malaria Research Awakes. <i>Cell Host and Microbe</i> , 2018 , 23, 292-295	23.4	1
168	Developing Plasmodium vivax Resources for Liver Stage Study in the Peruvian Amazon Region. <i>ACS Infectious Diseases</i> , 2018 , 4, 531-540	5.5	7

167	Common PIEZO1 Allele in African Populations Causes RBC Dehydration and Attenuates Plasmodium Infection. <i>Cell</i> , 2018 , 173, 443-455.e12	56.2	104
166	Exploration of Plasmodium vivax transmission dynamics and recurrent infections in the Peruvian Amazon using whole genome sequencing. <i>Genome Medicine</i> , 2018 , 10, 52	14.4	11
165	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. <i>Lancet Infectious Diseases</i> , 2018 , 18, 874-883	25.5	62
164	Open-source discovery of chemical leads for next-generation chemoprotective antimalarials. <i>Science</i> , 2018 , 362,	33.3	60
163	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
162	Accessible and distinct decoquininate derivatives active against Mycobacterium tuberculosis and apicomplexan parasites. <i>Communications Chemistry</i> , 2018 , 1,	6.3	14
161	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
160	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
159	A high throughput screen for next-generation leads targeting malaria parasite transmission. <i>Nature Communications</i> , 2018 , 9, 3805	17.4	61
158	Esterase mutation is a mechanism of resistance to antimalarial compounds. <i>Nature Communications</i> , 2017 , 8, 14240	17.4	18
157	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
156	A Variant PfCRT Isoform Can Contribute to Resistance to the First-Line Partner Drug Piperaquine. <i>MBio</i> , 2017 , 8,	7.8	58
155	Glycophorin alleles link to malaria protection. <i>Science</i> , 2017 , 356, 1122-1123	33.3	1
154	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
153	malERA: An updated research agenda for malaria elimination and eradication. <i>PLoS Medicine</i> , 2017 , 14, e1002456	11.6	148
152	Design and Synthesis of Terephthalic Acid-Based Histone Deacetylase Inhibitors with Dual-Stage Anti-Plasmodium Activity. <i>ChemMedChem</i> , 2017 , 12, 1627-1636	3.7	9
151	Development of a Potent Inhibitor of the Plasmodium Proteasome with Reduced Mammalian Toxicity. <i>Journal of Medicinal Chemistry</i> , 2017 , 60, 6721-6732	8.3	46
150	3-Hydroxy-NFarylidenopropanehydrazonamides with Halo-Substituted Phenanthrene Scaffolds Cure P. berghei Infected Mice When Administered Perorally. <i>Journal of Medicinal Chemistry</i> , 2017 , 60, 6036-6044	8.3	3

149	Longitudinal study of Plasmodium pathogens identifies new loci associated with artemisinin resistance. <i>Genome Biology</i> , 2017 , 18, 79	18.3	1
148	Hexahydroquinolines are antimalarial candidates with potent blood-stage and transmission-blocking activity. <i>Nature Microbiology</i> , 2017 , 2, 1403-1414	26.6	25
147	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
146	UDP-galactose and acetyl-CoA transporters as Plasmodium multidrug resistance genes. <i>Nature Microbiology</i> , 2016 , 1, 16166	26.6	67
145	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
144	A broad analysis of resistance development in the malaria parasite. <i>Nature Communications</i> , 2016 , 7, 11901	17.4	70
143	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
142	Phenotypic Screens in Antimalarial Drug Discovery. <i>Trends in Parasitology</i> , 2016 , 32, 697-707	6.4	31
141	Trisubstituted Pyrimidines as Efficacious and Fast-Acting Antimalarials. <i>Journal of Medicinal Chemistry</i> , 2016 , 59, 6101-20	8.3	7
140	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
139	Whole Genome Shotgun Sequencing Shows Selection on Leptospira Regulatory Proteins During in vitro Culture Attenuation. <i>American Journal of Tropical Medicine and Hygiene</i> , 2016 , 94, 302-313	3.2	8
138	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
137	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
136	Kalkipyronone B, a marine cyanobacterial Epyrone possessing cytotoxic and anti-fungal activities. <i>Phytochemistry</i> , 2016 , 122, 113-118	4	15
135	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
134	CRISPR-Cas9-modified pfmdr1 protects Plasmodium falciparum 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
133	Mutations in the Plasmodium falciparum Cyclic Amine Resistance Locus (PFCARL) Confer Multidrug Resistance. <i>MBio</i> , 2016 , 7,	7.8	32
132	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

131	Diversity-oriented synthesis yields novel multistage antimalarial inhibitors. <i>Nature</i> , 2016 , 538, 344-349	50.4	172
130	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
129	A novel multiple-stage antimalarial agent that inhibits protein synthesis. <i>Nature</i> , 2015 , 522, 315-20	50.4	250
128	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
127	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
126	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
125	Systems analysis of host-parasite interactions. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2015 , 7, 381-400	6.6	15
124	Bacterial genome reduction using the progressive clustering of deletions via yeast sexual cycling. <i>Genome Research</i> , 2015 , 25, 435-44	9.7	19
123	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
122	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
121	Identification of pathogen genomic variants through an integrated pipeline. <i>BMC Bioinformatics</i> , 2014 , 15, 63	3.6	37
120	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
119	A high resolution case study of a patient with recurrent Plasmodium vivax infections shows that relapses were caused by meiotic siblings. <i>PLoS Neglected Tropical Diseases</i> , 2014 , 8, e2882	4.8	52
118	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
117	KAI407, a potent non-8-aminoquinoline compound that kills Plasmodium cynomolgi early dormant liver stage parasites in vitro. <i>Antimicrobial Agents and Chemotherapy</i> , 2014 , 58, 1586-95	5.9	56
116	Targeted disruption of a ring-infected erythrocyte surface antigen (RESA)-like export protein gene in Plasmodium falciparum confers stable chondroitin 4-sulfate cytoadherence capacity. <i>Journal of Biological Chemistry</i> , 2014 , 289, 34408-21	5.4	12
115	Drug resistance genomics of the antimalarial drug artemisinin. <i>Genome Biology</i> , 2014 , 15, 544	18.3	53
114	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

113	Targeting Plasmodium PI(4)K to eliminate malaria. <i>Nature</i> , 2013 , 504, 248-253	50.4	291
112	Antimalarial drug discovery - approaches and progress towards new medicines. <i>Nature Reviews Microbiology</i> , 2013 , 11, 849-62	22.2	202
111	Identification of the Plasmodium berghei resistance locus 9 linked to survival on chromosome 9. <i>Malaria Journal</i> , 2013 , 12, 316	3.6	10
110	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
109	Direct transfer of whole genomes from bacteria to yeast. <i>Nature Methods</i> , 2013 , 10, 410-2	21.6	45
108	Genetic analysis of primaquine tolerance in a patient with relapsing vivax malaria. <i>Emerging Infectious Diseases</i> , 2013 , 19, 802-5	10.2	17
107	A key role for lipoic acid synthesis during Plasmodium liver stage development. <i>Cellular Microbiology</i> , 2013 , 15, 1585-604	3.9	22
106	Epidemiology: resistance mapping in malaria. <i>Nature</i> , 2013 , 498, 446-7	50.4	9
105	Experimentally induced blood-stage Plasmodium vivax infection in healthy volunteers. <i>Journal of Infectious Diseases</i> , 2013 , 208, 1688-94	7	71
104	Mitotic evolution of Plasmodium falciparum shows a stable core genome but recombination in antigen families. <i>PLoS Genetics</i> , 2013 , 9, e1003293	6	149
103	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
102	Synthesis and biological evaluation of epidithio-, epitetrathio-, and bis-(methylthio)diketopiperazines: synthetic methodology, enantioselective total synthesis of epicoccin G, 8,8Tepi-ent-rostratin B, gliotoxin, gliotoxin G, emethallicin E, and haematocin and their synthesis from the corresponding dihydroxy ketones. <i>Journal of the American Chemical Society</i> , 2012 , 134, 1211-21	16.4	101
101	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
100	Whole genome sequencing analysis of Plasmodium vivax using whole genome capture. <i>BMC Genomics</i> , 2012 , 13, 262	4.5	34
99	Perspectives: The missing pieces. <i>Nature</i> , 2012 , 484, S22-3	50.4	10
98	Imidazolopiperazines: lead optimization of the second-generation antimalarial agents. <i>Journal of Medicinal Chemistry</i> , 2012 , 55, 4244-73	8.3	75
97	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
96	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

95	Platypus - A Streamlined Pipeline to Identify Plasmodium Genomic Variants, with Drug Development Applications. <i>FASEB Journal</i> , 2012 , 26, lb239	0.9	
94	Chapter 4: Human Targets Repositioning and Cell-based Approaches for Antimalarial Discovery. <i>RSC Drug Discovery Series</i> , 2011 , 88-111	0.6	
93	Target identification and validation of novel antimalarials. <i>Future Microbiology</i> , 2011 , 6, 693-704	2.9	30
92	Identification of non-CSP antigens bearing CD8 epitopes in mice immunized with irradiated sporozoites. <i>Vaccine</i> , 2011 , 29, 7335-42	4.1	17
91	Imaging of Plasmodium liver stages to drive next-generation antimalarial drug discovery. <i>Science</i> , 2011 , 334, 1372-7	33.3	243
90	Imidazolopiperazines: hit to lead optimization of new antimalarial agents. <i>Journal of Medicinal Chemistry</i> , 2011 , 54, 5116-30	8.3	88
89	Noncoding RNA, antigenic variation, and the virulence genes of Plasmodium falciparum. <i>BMC Biology</i> , 2011 , 9, 50	7.3	8
88	A chemical genomic analysis of decoquinatone, a Plasmodium falciparum cytochrome b inhibitor. <i>ACS Chemical Biology</i> , 2011 , 6, 1214-22	4.9	72
87	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
86	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
85	Advances in Parasite Genomics 2011 , 198-205		
84	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
83	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
82	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
81	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
80	A plant-like kinase in Plasmodium falciparum regulates parasite egress from erythrocytes. <i>Science</i> , 2010 , 328, 910-2	33.3	221
79	Genome scanning of Amazonian Plasmodium falciparum shows subtelomeric instability and clindamycin-resistant parasites. <i>Genome Research</i> , 2010 , 20, 1534-44	9.7	48
78	Spiroindolones, a potent compound class for the treatment of malaria. <i>Science</i> , 2010 , 329, 1175-80	33.3	883

77	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
76	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
75	Advances in parasite genomics: from sequences to regulatory networks. <i>PLoS Pathogens</i> , 2009 , 5, e1000649	6.49	4
74	In vivo profiles in malaria are consistent with a novel physiological state. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, E70; author reply E71-2	11.5	6
73	Genome-wide nucleosome mapping of Plasmodium falciparum 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
72	Cell-based optimization of novel benzamides as potential antimalarial leads. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2009 , 19, 6970-4	2.9	15
71	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
70	Malaria research in the post-genomic era. <i>Nature</i> , 2008 , 455, 751-6	50.4	110
69	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
68	In silico discovery of transcription regulatory elements in Plasmodium falciparum. <i>BMC Genomics</i> , 2008 , 9, 70	4.5	88
67	A systematic approach to understand the mechanism of action of the bisthiazolium compound T4 on the human malaria parasite, Plasmodium falciparum. <i>BMC Genomics</i> , 2008 , 9, 513	4.5	51
66	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
65	Evidence-based annotation of the malaria parasite's genome using comparative expression profiling. <i>PLoS ONE</i> , 2008 , 3, e1570	3.7	70
64	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
63	Distinct physiological states of Plasmodium falciparum in malaria-infected patients. <i>Nature</i> , 2007 , 450, 1091-5	50.4	186
62	Plasmodium falciparum: genome wide perturbations in transcript profiles among mixed stage cultures after chloroquine treatment. <i>Experimental Parasitology</i> , 2007 , 117, 87-92	2.1	46
61	Regulatory motifs uncovered among gene expression clusters in Plasmodium falciparum. <i>Molecular and Biochemical Parasitology</i> , 2007 , 153, 19-30	1.9	29
60	Exposure of Plasmodium 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

59	Plasmodium circumsporozoite protein promotes the development of the liver stages of the parasite. <i>Cell</i> , 2007 , 131, 492-504	56.2	164
58	Genomics, systems biology and drug development for infectious diseases. <i>Molecular BioSystems</i> , 2007 , 3, 841-8		18
57	A systematic map of genetic variation in Plasmodium falciparum. <i>PLoS Pathogens</i> , 2006 , 2, e57	7.6	159
56	Using the genome to dissect the molecular basis of drug resistance. <i>Future Microbiology</i> , 2006 , 1, 185-99	2.9	3
55	Applied systems biology and malaria. <i>Nature Reviews Microbiology</i> , 2006 , 4, 145-51	22.2	31
54	A comparison of match-only algorithms for the analysis of Plasmodium falciparum oligonucleotide arrays. <i>International Journal for Parasitology</i> , 2005 , 35, 523-31	4.3	2
53	The Plasmodium falciparum sexual development transcriptome: a microarray analysis using ontology-based pattern identification. <i>Molecular and Biochemical Parasitology</i> , 2005 , 143, 67-79	1.9	258
52	Microarray-based comparative genomic analyses of the human malaria parasite Plasmodium falciparum using Affymetrix arrays. <i>Molecular and Biochemical Parasitology</i> , 2005 , 144, 177-86	1.9	45
51	Elucidating genetic diversity with oligonucleotide arrays. <i>Chromosome Research</i> , 2005 , 13, 225-35	4.4	13
50	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
49	Molecular mechanism for switching of P. falciparum invasion pathways into human erythrocytes. <i>Science</i> , 2005 , 309, 1384-7	33.3	224
48	Using expression information to discover new drug and vaccine targets in the malaria parasite Plasmodium falciparum. <i>Pharmacogenomics</i> , 2005 , 6, 17-26	2.6	18
47	In silico gene function prediction using ontology-based pattern identification. <i>Bioinformatics</i> , 2005 , 21, 1237-45	7.2	65
46	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
45	Global analysis of transcript and protein levels across the Plasmodium falciparum life cycle. <i>Genome Research</i> , 2004 , 14, 2308-18	9.7	354
44	Coordinated functions of WSS1, PSY2 and TOF1 in the DNA damage response. <i>Nucleic Acids Research</i> , 2004 , 32, 6519-30	20.1	26
43	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
42	In vivo transcriptional profiling of Plasmodium falciparum. <i>Malaria Journal</i> , 2004 , 3, 30	3.6	46

41	Genome-Wide Analysis of Gene Expression 2004 , 175-180		
40	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
39	Large-scale identification of single-feature polymorphisms in complex genomes. <i>Genome Research</i> , 2003 , 13, 513-23	9.7	307
38	Discovery of gene function by expression profiling of the malaria parasite life cycle. <i>Science</i> , 2003 , 301, 1503-8	33.3	1010
37	Genetic diversity in yeast assessed with whole-genome oligonucleotide arrays. <i>Genetics</i> , 2003 , 163, 79-89		148
36	The paradoxical population genetics of <i>Plasmodium falciparum</i> . <i>Trends in Parasitology</i> , 2002 , 18, 266-72	6.4	40
35	Large-scale mutagenesis and functional genomics in yeast. <i>Functional and Integrative Genomics</i> , 2002 , 2, 193-8	3.8	15
34	Functional profiling of the <i>Saccharomyces cerevisiae</i> genome. <i>Nature</i> , 2002 , 418, 387-91	50.4	3278
33	Treasures and traps in genome-wide data sets: case examples from yeast. <i>Nature Reviews Genetics</i> , 2002 , 3, 653-61	30.1	63
32	Parallel identification of new genes in <i>Saccharomyces cerevisiae</i> . <i>Genome Research</i> , 2002 , 12, 1210-20	9.7	53
31	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
30	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
29	Excess polymorphisms in genes for membrane proteins in <i>Plasmodium falciparum</i> . <i>Science</i> , 2002 , 298, 216-8	33.3	73
28	Further strategies for signature-tagged mutagenesis and the application of oligonucleotide microarrays for the quantification of DNA-tagged strains. <i>Methods in Microbiology</i> , 2002 , 33, 167-184	2.8	
27	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, 233-43	3.2	41
26	Application of high-density array-based signature-tagged mutagenesis to discover novel <i>Yersinia</i> virulence-associated genes. <i>Infection and Immunity</i> , 2001 , 69, 7810-9	3.7	80
25	Replication dynamics of the yeast genome. <i>Science</i> , 2001 , 294, 115-21	33.3	622
24	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

23	The core meiotic transcriptome in budding yeasts. <i>Nature Genetics</i> , 2000 , 26, 415-23	36.3	378
22	Genomics, gene expression and DNA arrays. <i>Nature</i> , 2000 , 405, 827-36	50.4	1695
21	Genomic profiling of drug sensitivities via induced haploinsufficiency. <i>Nature Genetics</i> , 1999 , 21, 278-83	36.3	472
20	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
19	Fluorescence-based expression monitoring using microarrays. <i>Methods in Enzymology</i> , 1999 , 306, 3-18	1.7	41
18	A genome-wide transcriptional analysis of the mitotic cell cycle. <i>Molecular Cell</i> , 1998 , 2, 65-73	17.6	1659
17	Direct allelic variation scanning of the yeast genome. <i>Science</i> , 1998 , 281, 1194-7	33.3	306
16	Transcriptional analysis of the <i>Caulobacter</i> 4.5 S RNA ffs gene and the physiological basis of an ffs mutant with a Ts phenotype. <i>Journal of Molecular Biology</i> , 1997 , 272, 665-76	6.5	4
15	Functional analysis of the yeast genome. <i>Current Opinion in Genetics and Development</i> , 1997 , 7, 771-6	4.9	52
14	Translation of the leaderless <i>Caulobacter</i> dnaX mRNA. <i>Journal of Bacteriology</i> , 1997 , 179, 3981-8	3.5	16
13	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
12	Use of flow cytometry to identify a <i>Caulobacter</i> 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
11	Fluorescence anisotropy decay of ethidium bound to nucleosome core particles. 2. The torsional motion of the DNA is highly constrained and sensitive to pH. <i>Biochemistry</i> , 1991 , 30, 5304-13	3.2	10
10	Flexing of DNA on the nucleosome core particle 1990 , 1204, 297		
9	The Transcriptome of the Malaria Parasite <i>Plasmodium falciparum</i> 68-84		2
8	Pan-active imidazolopiperazine antimalarials target the <i>Plasmodium falciparum</i> intracellular secretory pathway		1
7	Common Piezo1 allele in African populations causes xerocytosis and attenuates <i>Plasmodium</i> infection		3
6	Multistage and transmission-blocking targeted antimalarials discovered from the open-source MMV Pandemic Response Box		2

5	Failure of in vitro differentiation of <i>Plasmodium falciparum</i> gametocytes into ookinetes arises because of poor gamete fertilisation	1
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