Karine G Le Roch

List of Publications by Year in descending order

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85 papers 10,001 citations

36 h-index 84 g-index

97 all docs 97
docs citations

97 times ranked 18555 citing authors

#	Article	IF	CITATIONS
1	Guidelines for the use and interpretation of assays for monitoring autophagy (3rd edition). Autophagy, 2016, 12, 1-222.	9.1	4,701
2	Discovery of Gene Function by Expression Profiling of the Malaria Parasite Life Cycle. Science, 2003, 301, 1503-1508.	12.6	1,122
3	Global analysis of transcript and protein levels across the Plasmodium falciparum life cycle. Genome Research, 2004, 14, 2308-2318.	5.5	394
4	Gene expression signatures and small-molecule compounds link a protein kinase to Plasmodium falciparum motility. Nature Chemical Biology, 2008, 4, 347-356.	8.0	203
5	Three-dimensional modeling of the <i>P. falciparum</i> genome during the erythrocytic cycle reveals a strong connection between genome architecture and gene expression. Genome Research, 2014, 24, 974-988.	5.5	193
6	Recent advances in malaria drug discovery. Bioorganic and Medicinal Chemistry Letters, 2013, 23, 2829-2843.	2.2	182
7	Marine Actinomycetes: A New Source of Compounds against the Human Malaria Parasite. PLoS ONE, 2008, 3, e2335.	2.5	160
8	High content live cell imaging for the discovery of new antimalarial marine natural products. BMC Infectious Diseases, 2012, 12, 1.	2.9	137
9	Polysome profiling reveals translational control of gene expression in the human malaria parasite Plasmodium falciparum. Genome Biology, 2013, 14, R128.	9.6	131
10	Nucleosome landscape and control of transcription in the human malaria parasite. Genome Research, 2010, 20, 228-238.	5.5	126
11	In silico discovery of transcription regulatory elements in Plasmodium falciparum. BMC Genomics, 2008, 9, 70.	2.8	104
12	Pfnek-1, a NIMA-related kinase from the human malaria parasitePlasmodium falciparum. FEBS Journal, 2001, 268, 2600-2608.	0.2	103
13	Activation of a Plasmodium falciparum cdc2-related Kinase by Heterologous p25 and Cyclin H. Journal of Biological Chemistry, 2000, 275, 8952-8958.	3.4	91
14	The mRNA-bound proteome of the human malaria parasite Plasmodium falciparum. Genome Biology, 2016, 17, 147.	8.8	87
15	Changes in genome organization of parasite-specific gene families during the Plasmodium transmission stages. Nature Communications, 2018, 9, 1910.	12.8	82
16	Deciphering the Ubiquitin-Mediated Pathway in Apicomplexan Parasites: A Potential Strategy to Interfere with Parasite Virulence. PLoS ONE, 2008, 3, e2386.	2.5	80
17	Genome-wide Mapping of DNA Methylation in the Human Malaria Parasite Plasmodium falciparum. Cell Host and Microbe, 2013, 14, 696-706.	11.0	79
18	Antimalarial Bromophycolides Jâ^'Q from the Fijian Red Alga <i>Callophycus serratus</i> . Journal of Organic Chemistry, 2009, 74, 2736-2742.	3.2	77

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19	The multifunctional autophagy pathway in the human malaria parasite, <i>Plasmodium falciparum</i> Autophagy, 2014, 10, 80-92.	9.1	77
20	Nascent RNA sequencing reveals mechanisms of gene regulation in the human malaria parasite Plasmodium falciparum. Nucleic Acids Research, 2017, 45, 7825-7840.	14.5	70
21	Identification and Initial Characterization of Three Novel Cyclin-related Proteins of the Human Malaria Parasite Plasmodium falciparum. Journal of Biological Chemistry, 2003, 278, 39839-39850.	3.4	69
22	Unraveling the Ubiquitome of the Human Malaria Parasite. Journal of Biological Chemistry, 2011, 286, 40320-40330.	3.4	66
23	BRAT: bisulfite-treated reads analysis tool. Bioinformatics, 2010, 26, 572-573.	4.1	65
24	Comparative 3D genome organization in apicomplexan parasites. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 3183-3192.	7.1	65
25	An Apicoplast Localized Ubiquitylation System Is Required for the Import of Nuclear-encoded Plastid Proteins. PLoS Pathogens, 2013, 9, e1003426.	4.7	63
26	A systematic approach to understand the mechanism of action of the bisthiazolium compound T4 on the human malaria parasite, Plasmodium falciparum. BMC Genomics, 2008, 9, 513.	2.8	58
27	Multiple dimensions of epigenetic gene regulation in the malaria parasite <i>Plasmodium falciparum</i> . BioEssays, 2015, 37, 182-194.	2.5	54
28	Bioactive Bromophycolides Râ^'U from the Fijian Red Alga <i>Callophycus serratus</i> . Journal of Natural Products, 2010, 73, 275-278.	3.0	53
29	Callophycoic Acids and Callophycols from the Fijian Red Alga <i>Callophycus serratus</i> . Journal of Organic Chemistry, 2007, 72, 7343-7351.	3.2	52
30	DNA-encoded nucleosome occupancy is associated with transcription levels in the human malaria parasite Plasmodium falciparum. BMC Genomics, 2014, 15, 347.	2.8	52
31	Real-time dynamics of <i>Plasmodium</i> NDC80 reveals unusual modes of chromosome segregation during parasite proliferation. Journal of Cell Science, 2020, 134, .	2.0	51
32	Dynamic and Combinatorial Landscape of Histone Modifications during the Intraerythrocytic Developmental Cycle of the Malaria Parasite. Journal of Proteome Research, 2016, 15, 2787-2801.	3.7	49
33	The Role of Chromatin Structure in Gene Regulation of the Human Malaria Parasite. Trends in Parasitology, 2017, 33, 364-377.	3.3	46
34	Monitoring the chromosome 2 intraerythrocytic transcriptome of Plasmodium falciparum using oligonucleotide arrays American Journal of Tropical Medicine and Hygiene, 2002, 67, 233-243.	1.4	46
35	An Introduction to Functional Genomics and Systems Biology. Advances in Wound Care, 2013, 2, 490-498.	5.1	45
36	Plasmodium kinesin-8X associates with mitotic spindles and is essential for oocyst development during parasite proliferation and transmission. PLoS Pathogens, 2019, 15, e1008048.	4.7	43

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37	Synthesis and Potent Antimalarial Activity of Kalihinol B. Journal of the American Chemical Society, 2015, 137, 4912-4915.	13.7	42
38	Post-translational modifications in Plasmodium: More than you think!. Molecular and Biochemical Parasitology, 2009, 168, 123-134.	1.1	39
39	Nucleosome occupancy at transcription start sites in the human malaria parasite: A hard-wired evolution of virulence?. Infection, Genetics and Evolution, 2011, 11, 716-724.	2.3	38
40	Unusual antimalarial meroditerpenes from tropical red macroalgae. Bioorganic and Medicinal Chemistry Letters, 2010, 20, 5662-5665.	2.2	34
41	The Arabidopsis PHD-finger protein EDM2 has multiple roles in balancing NLR immune receptor gene expression. PLoS Genetics, 2020, 16, e1008993.	3.5	33
42	Characterization of the Ubiquitylating Components of the Human Malaria Parasite's Protein Degradation Pathway. PLoS ONE, 2012, 7, e43477.	2.5	33
43	Kinesin-8B controls basal body function and flagellum formation and is key to malaria transmission. Life Science Alliance, 2019, 2, e201900488.	2.8	33
44	High-content live cell imaging with RNA probes: advancements in high-throughput antimalarial drug discovery. BMC Cell Biology, 2009, 10, 45.	3.0	31
45	Bromophycoic Acids: Bioactive Natural Products from a Fijian Red Alga <i>Callophycus</i> sp Journal of Organic Chemistry, 2012, 77, 8000-8006.	3.2	31
46	NO <scp>r</scp> MAL: accurate nucleosome positioning using a modified Gaussian mixture model. Bioinformatics, 2012, 28, i242-i249.	4.1	30
47	Influence of Human p16INK4 and p21CIP1 on the in Vitro Activity of Recombinant Plasmodium falciparum Cyclin-Dependent Protein Kinases. Biochemical and Biophysical Research Communications, 2001, 288, 1207-1211.	2.1	29
48	From Genes to Transcripts, a Tightly Regulated Journey in Plasmodium. Frontiers in Cellular and Infection Microbiology, 2020, 10, 618454.	3.9	29
49	Mechanisms of gene regulation in Plasmodium. American Journal of Tropical Medicine and Hygiene, 2007, 77, 201-8.	1.4	29
50	The ubiquitin system: an essential component to unlocking the secrets of malaria parasite biology. Molecular BioSystems, 2014, 10, 715-723.	2.9	26
51	Structures, semisyntheses, and absolute configurations ofÂtheÂantiplasmodial α-substituted β-lactam monamphilectines BÂand C from the sponge Svenzea flava. Tetrahedron, 2015, 71, 487-494.	1.9	26
52	Antimalarial Properties of Simplified Kalihinol Analogues. ACS Medicinal Chemistry Letters, 2017, 8, 355-360.	2.8	25
53	The role of epigenetics and chromatin structure in transcriptional regulation in malaria parasites. Briefings in Functional Genomics, 2019, 18, 302-313.	2.7	25
54	The Arabidopsis <scp>RRM</scp> domain protein <scp>EDM</scp> 3 mediates raceâ€specific disease resistance by controlling H3K9me2â€dependent alternative polyadenylation of <i><scp>RPP</scp>7</i> immune receptor transcripts. Plant Journal, 2019, 97, 646-660.	5.7	24

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55	Predicting gene expression in the human malaria parasite Plasmodium falciparum using histone modification, nucleosome positioning, and 3D localization features. PLoS Computational Biology, 2019, 15, e1007329.	3.2	23
56	Plasmodium Condensin Core Subunits SMC2/SMC4 Mediate Atypical Mitosis and Are Essential for Parasite Proliferation and Transmission. Cell Reports, 2020, 30, 1883-1897.e6.	6.4	22
57	Bromophycolideâ€A Targets Heme Crystallization in the Human Malaria Parasite <i>Plasmodium falciparum</i>). ChemMedChem, 2011, 6, 1572-1577.	3.2	21
58	Synthesis and preliminary biological evaluation of a small library of hybrid compounds based on Ugi isocyanide multicomponent reactions with a marine natural product scaffold. Bioorganic and Medicinal Chemistry Letters, 2015, 25, 5339-5343.	2.2	21
59	Exploratory analysis of genomic segmentations with Segtools. BMC Bioinformatics, 2011, 12, 415.	2.6	20
60	Natural product-based synthesis of novel anti-infective isothiocyanate- and isoselenocyanate-functionalized amphilectane diterpenes. Bioorganic and Medicinal Chemistry Letters, 2016, 26, 854-857.	2.2	20
61	Third-generation sequencing revises the molecular karyotype for <i>Toxoplasma gondii</i> and identifies emerging copy number variants in sexual recombinants. Genome Research, 2021, 31, 834-851.	5.5	19
62	Dynamic Chromatin Structure and Epigenetics Control the Fate of Malaria Parasites. Trends in Genetics, 2021, 37, 73-85.	6.7	18
63	The transcriptional regulator HDP1 controls expansion of the inner membrane complex during early sexual differentiation of malaria parasites. Nature Microbiology, 2022, 7, 289-299.	13.3	15
64	Attacking COVID-19 Progression Using Multi-Drug Therapy for Synergetic Target Engagement. Biomolecules, 2021, 11, 787.	4.0	14
65	Structures and Bioactivities of Dihydrochalcones from <i>Metrodorea stipularis</i> Natural Products, 2014, 77, 2418-2422.	3.0	13
66	Insights into the evolution and drug susceptibility of Babesia duncani from the sequence of its mitochondrial and apicoplast genomes. International Journal for Parasitology, 2019, 49, 105-113.	3.1	13
67	The chromatin bound proteome of the human malaria parasite. Microbial Genomics, 2020, 6, .	2.0	13
68	Concise Synthesis of the Antiplasmodial Isocyanoterpene 7,20â€Diisocyanoadociane. Angewandte Chemie - International Edition, 2019, 58, 13749-13752.	13.8	12
69	Functional genomics of RAP proteins and their role in mitoribosome regulation in Plasmodium falciparum. Nature Communications, 2022, 13, 1275.	12.8	12
70	Chromatin-driven de novo discovery of DNA binding motifs in the human malaria parasite. BMC Genomics, 2011, 12, 601.	2.8	10
71	Homopolymer tract organization in the human malarial parasite Plasmodium falciparum and related Apicomplexan parasites. BMC Genomics, 2014, 15, 848.	2.8	10
72	Pharmacokinetics, Metabolism, and in Vivo Efficacy of the Antimalarial Natural Product Bromophycolide A. ACS Medicinal Chemistry Letters, 2013, 4, 989-993.	2.8	9

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73	Sex in Plasmodium falciparum: Silence Play between GDV1 and HP1. Trends in Parasitology, 2018, 34, 450-452.	3.3	8
74	Unraveling the 3D genome of human malaria parasites. Seminars in Cell and Developmental Biology, 2019, 90, 144-153.	5.0	6
75	Design and tests of prospective property predictions for novel antimalarial 2-aminopropylaminoquinolones. Journal of Computer-Aided Molecular Design, 2020, 34, 1117-1132.	2.9	6
76	Analysis of nucleosome positioning landscapes enables gene discovery in the human malaria parasite Plasmodium falciparum. BMC Genomics, 2015, 16, 1005.	2.8	5
77	Genome-Wide Analysis of RNA–Protein Interactions in Plasmodium falciparum Using eCLIP-Seq. Methods in Molecular Biology, 2021, 2369, 139-164.	0.9	5
78	Three-dimensional chromatin in infectious diseaseâ€"A role for gene regulation and pathogenicity?. PLoS Pathogens, 2021, 17, e1009207.	4.7	5
79	Identification and phylogenetic analysis of RNA binding domain abundant in apicomplexans or RAP proteins. Microbial Genomics, 2021, 7, .	2.0	5
80	PfAlba1: master regulator of translation in the malaria parasite. Genome Biology, 2015, 16, 221.	8.8	4
81	Chromosomes Conformation Capture Coupled with Next-Generation Sequencing (Hi-C) in Plasmodium falciparum. Methods in Molecular Biology, 2021, 2369, 15-25.	0.9	4
82	Three-Dimensional Genome Organization and Virulence in Apicomplexan Parasites. Epigenetics Insights, 2019, 12, 251686571987943.	2.0	3
83	Strand-Specific RNA-Seq Applied to Malaria Samples. Methods in Molecular Biology, 2021, 2170, 19-33.	0.9	3
84	A newly characterized malaria antigen on erythrocyte and merozoite surfaces induces parasite inhibitory antibodies. Journal of Experimental Medicine, 2021, 218, .	8.5	2
85	Epigenetics of Malaria Parasites. Epigenetics and Human Health, 2017, , 243-264.	0.2	O