

Manuel Llinas

List of Publications by Year in descending order

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105
papers

9,521
citations

44069

48
h-index

45317

90
g-index

121
all docs

121
docs citations

121
times ranked

7134
citing authors

#	ARTICLE	IF	CITATIONS
1	Chemogenomics identifies acetyl-coenzyme A synthetase as a target for malaria treatment and prevention. <i>Cell Chemical Biology</i> , 2022, 29, 191-201.e8.	5.2	39
2	Anti-inflammation and antimalarial profile of 5-pyridin-2-yl-1H-[1,2,4]triazole-3-carboxylic acid ethyl ester as a low molecular intermediate for hybrid drug synthesis. <i>Research on Chemical Intermediates</i> , 2022, 48, 885-898.	2.7	6
3	The transcriptional regulator HDP1 controls expansion of the inner membrane complex during early sexual differentiation of malaria parasites. <i>Nature Microbiology</i> , 2022, 7, 289-299.	13.3	15
4	Preclinical characterization and target validation of the antimalarial pantothenamide MMV693183. <i>Nature Communications</i> , 2022, 13, 2158.	12.8	13
5	Multistage and transmission-blocking targeted antimalarials discovered from the open-source MMV Pandemic Response Box. <i>Nature Communications</i> , 2021, 12, 269.	12.8	61
6	Atypical Molecular Basis for Drug Resistance to Mitochondrial Function Inhibitors in <i>Plasmodium falciparum</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, .	3.2	7
7	The PfAP2-2 transcription factor is a critical regulator of gametocyte maturation. <i>Molecular Microbiology</i> , 2021, 115, 1005-1024.	2.5	36
8	PfMFR3: A Multidrug-Resistant Modulator in <i>Plasmodium falciparum</i> . <i>ACS Infectious Diseases</i> , 2021, 7, 811-825.	3.8	16
9	H3K36 methylation reprograms gene expression to drive early gametocyte development in <i>Plasmodium falciparum</i> . <i>Epigenetics and Chromatin</i> , 2021, 14, 19.	3.9	11
10	The Kringle of Life. <i>Protein Journal</i> , 2021, 40, 454-456.	1.6	0
11	MalDA, Accelerating Malaria Drug Discovery. <i>Trends in Parasitology</i> , 2021, 37, 493-507.	3.3	51
12	Re-Envisioning Anti-Apicomplexan Parasite Drug Discovery Approaches. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 691121.	3.9	4
13	A heat-shock response regulated by the PfAP2-HS transcription factor protects human malaria parasites from febrile temperatures. <i>Nature Microbiology</i> , 2021, 6, 1163-1174.	13.3	30
14	Chemogenomic Fingerprints Associated with Stage-Specific Gametocytocidal Compound Action against Human Malaria Parasites. <i>ACS Infectious Diseases</i> , 2021, 7, 2904-2916.	3.8	1
15	Artemisinin-resistant K13 mutations rewire <i>Plasmodium falciparum</i> 's intra-erythrocytic metabolic program to enhance survival. <i>Nature Communications</i> , 2021, 12, 530.	12.8	82
16	Combining Stage Specificity and Metabolomic Profiling to Advance Antimalarial Drug Discovery. <i>Cell Chemical Biology</i> , 2020, 27, 158-171.e3.	5.2	54
17	The natural function of the malaria parasite's chloroquine resistance transporter. <i>Nature Communications</i> , 2020, 11, 3922.	12.8	53
18	Increased circulation time of <i>Plasmodium falciparum</i> underlies persistent asymptomatic infection in the dry season. <i>Nature Medicine</i> , 2020, 26, 1929-1940.	30.7	91

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19	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.	5.2	56
20	Refining the transcriptome of the human malaria parasite <i>Plasmodium falciparum</i> using amplification-free RNA-seq. <i>BMC Genomics</i> , 2020, 21, 395.	2.8	71
21	Dissecting the role of PfAP2-G in malaria gametocytogenesis. <i>Nature Communications</i> , 2020, 11, 1503.	12.8	108
22	A single-nucleotide polymorphism in a <i>Plasmodium berghei</i> ApiAP2 transcription factor alters the development of host immunity. <i>Science Advances</i> , 2020, 6, eaaw6957.	10.3	10
23	Genetic ablation of the mitoribosome in the malaria parasite <i>Plasmodium falciparum</i> sensitizes it to antimalarials that target mitochondrial functions. <i>Journal of Biological Chemistry</i> , 2020, 295, 7235-7248.	3.4	23
24	Cutting back malaria: CRISPR/Cas9 genome editing of <i>Plasmodium</i> . <i>Briefings in Functional Genomics</i> , 2019, 18, 281-289.	2.7	38
25	The G9a Histone Methyltransferase Inhibitor BIX-01294 Modulates Gene Expression during <i>Plasmodium falciparum</i> Gametocyte Development and Transmission. <i>International Journal of Molecular Sciences</i> , 2019, 20, 5087.	4.1	19
26	Antimalarial pantothenamide metabolites target acetyl-coenzyme A biosynthesis in <i>Plasmodium falciparum</i> . <i>Science Translational Medicine</i> , 2019, 11, .	12.4	59
27	Commitment Isn't for Everyone. <i>Trends in Parasitology</i> , 2019, 35, 381-383.	3.3	3
28	Hierarchical transcriptional control regulates <i>Plasmodium falciparum</i> sexual differentiation. <i>BMC Genomics</i> , 2019, 20, 920.	2.8	62
29	<i>Plasmodium</i> Niemann-Pick type C1-related protein is a druggable target required for parasite membrane homeostasis. <i>ELife</i> , 2019, 8, .	6.0	51
30	Specific Inhibition of the Bifunctional Farnesyl/Geranylgeranyl Diphosphate Synthase in Malaria Parasites via a New Small-Molecule Binding Site. <i>Cell Chemical Biology</i> , 2018, 25, 185-193.e5.	5.2	32
31	Mapping the malaria parasite druggable genome by using in vitro evolution and chemogenomics. <i>Science</i> , 2018, 359, 191-199.	12.6	194
32	Inducing controlled cell cycle arrest and re-entry during asexual proliferation of <i>Plasmodium falciparum</i> malaria parasites. <i>Scientific Reports</i> , 2018, 8, 16581.	3.3	31
33	Open-source discovery of chemical leads for next-generation chemoprotective antimalarials. <i>Science</i> , 2018, 362, .	12.6	99
34	Lipopeptisomes: Anticancer peptide-assembled particles for fusolytic oncotherapy. <i>Acta Biomaterialia</i> , 2018, 80, 269-277.	8.3	20
35	Evidence for Regulation of Hemoglobin Metabolism and Intracellular Ionic Flux by the <i>Plasmodium falciparum</i> Chloroquine Resistance Transporter. <i>Scientific Reports</i> , 2018, 8, 13578.	3.3	24
36	Glycolysis is important for optimal asexual growth and formation of mature tissue cysts by <i>Toxoplasma gondii</i> . <i>International Journal for Parasitology</i> , 2018, 48, 955-968.	3.1	45

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37	Regulation of Sexual Commitment and Gametocytogenesis in Malaria Parasites. Annual Review of Microbiology, 2018, 72, 501-519.	7.3	96
38	Genome-wide real-time in vivo transcriptional dynamics during Plasmodium falciparum blood-stage development. Nature Communications, 2018, 9, 2656.	12.8	73
39	A seven-helix protein constitutes stress granules crucial for regulating translation during human-to-mosquito transmission of Plasmodium falciparum. PLoS Pathogens, 2018, 14, e1007249.	4.7	22
40	Characterization of the <i>Plasmodium falciparum</i> and <i>P. berghei</i> glycerol 3-phosphate acyltransferase involved in FASII fatty acid utilization in the malaria parasite apicoplast. Cellular Microbiology, 2017, 19, e12633.	2.1	25
41	Capturing in vivo RNA transcriptional dynamics from the malaria parasite <i>Plasmodium falciparum</i> . Genome Research, 2017, 27, 1074-1086.	5.5	46
42	Red Blood Cell Invasion by the Malaria Parasite Is Coordinated by the PfAP2-I Transcription Factor. Cell Host and Microbe, 2017, 21, 731-741.e10.	11.0	106
43	Quantitative chromatin proteomics reveals a dynamic histone post-translational modification landscape that defines asexual and sexual Plasmodium falciparum parasites. Scientific Reports, 2017, 7, 607.	3.3	60
44	Less Lipid, More Commitment. Cell, 2017, 171, 1474-1476.	28.9	8
45	Nutrient sensing modulates malaria parasite virulence. Nature, 2017, 547, 213-216.	27.8	146
46	Transcriptional Profiling Defines Histone Acetylation as a Regulator of Gene Expression during Human-to-Mosquito Transmission of the Malaria Parasite Plasmodium falciparum. Frontiers in Cellular and Infection Microbiology, 2017, 7, 320.	3.9	40
47	Simultaneous genome-wide gene expression and transcript isoform profiling in the human malaria parasite. PLoS ONE, 2017, 12, e0187595.	2.5	9
48	Open Source Drug Discovery with the Malaria Box Compound Collection for Neglected Diseases and Beyond. PLoS Pathogens, 2016, 12, e1005763.	4.7	244
49	Sequestration and metabolism of host cell arginine by the intraerythrocytic malaria parasite <i>Plasmodium falciparum</i> . Cellular Microbiology, 2016, 18, 820-830.	2.1	19
50	Metabolomic Profiling of the Malaria Box Reveals Antimalarial Target Pathways. Antimicrobial Agents and Chemotherapy, 2016, 60, 6635-6649.	3.2	121
51	Proteome-wide analysis reveals widespread lysine acetylation of major protein complexes in the malaria parasite. Scientific Reports, 2016, 6, 19722.	3.3	70
52	Evolution of Fitness Cost-Neutral Mutant PfCRT Conferring P. falciparum 4-Aminoquinoline Drug Resistance Is Accompanied by Altered Parasite Metabolism and Digestive Vacuole Physiology. PLoS Pathogens, 2016, 12, e1005976.	4.7	34
53	Mutations in the Plasmodium falciparum chloroquine resistance transporter, PfCRT, enlarge the parasite's food vacuole and alter drug sensitivities. Scientific Reports, 2015, 5, 14552.	3.3	59
54	Genome-wide transcriptome profiling reveals functional networks involving the Plasmodium falciparum drug resistance transporters PfCRT and PfMDR1. BMC Genomics, 2015, 16, 1090.	2.8	20

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55	<i>PfPR</i> 1 controls alternative splicing and steady-state <i>RNA</i> levels in <i>Plasmodium falciparum</i> through preferential recognition of specific <i>RNA</i> motifs. <i>Molecular Microbiology</i> , 2015, 96, 1283-1297.	2.5	20
56	Beyond the E-Value: Stratified Statistics for Protein Domain Prediction. <i>PLoS Computational Biology</i> , 2015, 11, e1004509.	3.2	19
57	Sexual development in <i>Plasmodium</i> parasites: knowing when it's time to commit. <i>Nature Reviews Microbiology</i> , 2015, 13, 573-587.	28.6	172
58	Genetic Investigation of Tricarboxylic Acid Metabolism during the <i>Plasmodium falciparum</i> Life Cycle. <i>Cell Reports</i> , 2015, 11, 164-174.	6.4	134
59	Targeting NAD ⁺ Metabolism in the Human Malaria Parasite <i>Plasmodium falciparum</i> . <i>PLoS ONE</i> , 2014, 9, e94061.	2.5	39
60	The <i>Cryptosporidium parvum</i> <i>ApiAP2</i> gene family: insights into the evolution of apicomplexan AP2 regulatory systems. <i>Nucleic Acids Research</i> , 2014, 42, 8271-8284.	14.5	40
61	Metabolic QTL Analysis Links Chloroquine Resistance in <i>Plasmodium falciparum</i> to Impaired Hemoglobin Catabolism. <i>PLoS Genetics</i> , 2014, 10, e1004085.	3.5	73
62	Cross-Reactive Immune Responses as Primary Drivers of Malaria Chronicity. <i>Infection and Immunity</i> , 2014, 82, 140-151.	2.2	17
63	A cascade of DNA-binding proteins for sexual commitment and development in <i>Plasmodium</i> . <i>Nature</i> , 2014, 507, 253-257.	27.8	366
64	Supragenomic Network Compression and the Discovery of EXP1 as a Glutathione Transferase Inhibited by Artesunate. <i>Cell</i> , 2014, 158, 916-928.	28.9	113
65	A <i>Plasmodium falciparum</i> Histone Deacetylase Regulates Antigenic Variation and Gametocyte Conversion. <i>Cell Host and Microbe</i> , 2014, 16, 177-186.	11.0	192
66	A transcriptional switch underlies commitment to sexual development in malaria parasites. <i>Nature</i> , 2014, 507, 248-252.	27.8	430
67	Epigenetic switches in <i>clag3</i> genes mediate blasticidin S resistance in malaria parasites. <i>Cellular Microbiology</i> , 2013, 15, n/a-n/a.	2.1	56
68	Kinetic Flux Profiling Elucidates Two Independent Acetyl-CoA Biosynthetic Pathways in <i>Plasmodium falciparum</i> . <i>Journal of Biological Chemistry</i> , 2013, 288, 36338-36350.	3.4	79
69	A New System for Comparative Functional Genomics of <i>Saccharomyces</i> Yeasts. <i>Genetics</i> , 2013, 195, 275-287.	2.9	27
70	Stress and sex in malaria parasites. <i>Evolution, Medicine and Public Health</i> , 2013, 2013, 135-147.	2.5	74
71	<i>ApiAP2</i> transcription factor restricts development of the <i>Toxoplasma</i> tissue cyst. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 6871-6876.	7.1	120
72	<i>Plasmodium falciparum</i> responds to amino acid starvation by entering into a hibernatory state. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E3278-87.	7.1	147

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73	A Tetracycline-Repressible Transactivator System to Study Essential Genes in Malaria Parasites. <i>Cell Host and Microbe</i> , 2012, 12, 824-834.	11.0	94
74	Site-specific genome editing in <i>Plasmodium falciparum</i> using engineered zinc-finger nucleases. <i>Nature Methods</i> , 2012, 9, 993-998.	19.0	149
75	Whole-Genome Analysis of <i>Plasmodium</i> spp. Utilizing a New Agilent Technologies DNA Microarray Platform. <i>Methods in Molecular Biology</i> , 2012, 923, 213-219.	0.9	32
76	Extraction of Hydrophilic Metabolites from <i>Plasmodium falciparum</i> -Infected Erythrocytes for Metabolomic Analysis. <i>Methods in Molecular Biology</i> , 2012, 923, 259-266.	0.9	10
77	New Agilent platform DNA microarrays for transcriptome analysis of <i>Plasmodium falciparum</i> and <i>Plasmodium berghei</i> for the malaria research community. <i>Malaria Journal</i> , 2012, 11, 187.	2.3	27
78	Central carbon metabolism of <i>Plasmodium</i> parasites. <i>Molecular and Biochemical Parasitology</i> , 2011, 175, 95-103.	1.1	85
79	The Apicomplexan AP2 family: Integral factors regulating <i>Plasmodium</i> development. <i>Molecular and Biochemical Parasitology</i> , 2011, 176, 1-7.	1.1	195
80	The primase domain of PfPrex is a proteolytically matured, essential enzyme of the apicoplast. <i>Molecular and Biochemical Parasitology</i> , 2011, 180, 69-75.	1.1	21
81	Reconstruction and flux balance analysis of the <i>Plasmodium falciparum</i> metabolic network. <i>Molecular Systems Biology</i> , 2010, 6, 408.	7.2	120
82	New insights into the blood-stage transcriptome of <i>Plasmodium falciparum</i> using RNA-seq. <i>Molecular Microbiology</i> , 2010, 76, 12-24.	2.5	374
83	Branched tricarboxylic acid metabolism in <i>Plasmodium falciparum</i> . <i>Nature</i> , 2010, 466, 774-778.	27.8	111
84	Identification and Genome-Wide Prediction of DNA Binding Specificities for the ApiAP2 Family of Regulators from the Malaria Parasite. <i>PLoS Pathogens</i> , 2010, 6, e1001165.	4.7	226
85	Structural Determinants of DNA Binding by a <i>P. falciparum</i> ApiAP2 Transcriptional Regulator. <i>Journal of Molecular Biology</i> , 2010, 395, 558-567.	4.2	59
86	Eating at the Table of Another: Metabolomics of Host-Parasite Interactions. <i>Cell Host and Microbe</i> , 2010, 7, 90-99.	11.0	91
87	Identification and Characterization of a Liver Stage-Specific Promoter Region of the Malaria Parasite <i>Plasmodium</i> . <i>PLoS ONE</i> , 2010, 5, e13653.	2.5	35
88	Co-inhibition of <i>Plasmodium falciparum</i> S-Adenosylmethionine Decarboxylase/Ornithine Decarboxylase Reveals Perturbation-specific Compensatory Mechanisms by Transcriptome, Proteome, and Metabolome Analyses. <i>Journal of Biological Chemistry</i> , 2009, 284, 4635-4646.	3.4	73
89	Clonally variant gene families in <i>Plasmodium falciparum</i> share a common activation factor. <i>Molecular Microbiology</i> , 2009, 73, 1171-1185.	2.5	53
90	Host-Parasite Interactions Revealed by <i>Plasmodium falciparum</i> Metabolomics. <i>Cell Host and Microbe</i> , 2009, 5, 191-199.	11.0	290

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91	Quantitative determination of urea concentrations in cell culture medium. <i>Biochemistry and Cell Biology</i> , 2009, 87, 541-544.	2.0	45
92	Plasmodium gene regulation: far more to factor in. <i>Trends in Parasitology</i> , 2008, 24, 551-556.	3.3	24
93	Specific DNA-binding by Apicomplexan AP2 transcription factors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 8393-8398.	7.1	216
94	An Erythrocyte Vesicle Protein Exported by the Malaria Parasite Promotes Tubovesicular Lipid Import from the Host Cell Surface. <i>PLoS Pathogens</i> , 2008, 4, e1000118.	4.7	53
95	Exploring subdomain cooperativity in T4 lysozyme I: Structural and energetic studies of a circular permutant and protein fragment. <i>Protein Science</i> , 2007, 16, 842-851.	7.6	35
96	Mechanisms of gene regulation in Plasmodium. <i>American Journal of Tropical Medicine and Hygiene</i> , 2007, 77, 201-8.	1.4	29
97	Comparative whole genome transcriptome analysis of three Plasmodium falciparum strains. <i>Nucleic Acids Research</i> , 2006, 34, 1166-1173.	14.5	289
98	Mining the malaria transcriptome. <i>Trends in Parasitology</i> , 2005, 21, 350-352.	3.3	10
99	Genomic dissection of the cell-type-specification circuit in Saccharomyces cerevisiae. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 18069-18074.	7.1	98
100	Pernicious plans revealed: Plasmodium falciparum genome wide expression analysis. <i>Current Opinion in Microbiology</i> , 2004, 7, 382-387.	5.1	28
101	The Transcriptome of the Intraerythrocytic Developmental Cycle of Plasmodium falciparum. <i>PLoS Biology</i> , 2003, 1, e5.	5.6	1,433
102	The energetics of T4 lysozyme reveal a hierarchy of conformations. <i>Nature Structural Biology</i> , 1999, 6, 1072-1078.	9.7	100
103	Solution Structure of Syrian Hamster Prion Protein rPrP(90~231). <i>Biochemistry</i> , 1999, 38, 5362-5377.	2.5	186
104	Subdomain interactions as a determinant in the folding and stability of T4 lysozyme. <i>Protein Science</i> , 1998, 7, 96-104.	7.6	61
105	Active site labeling with dansyl-glutamyl-glycyl-arginyl chloromethyl ketone demonstrates the full activity of the refolded and purified tissue-type plasminogen activator variant BM 06.022. <i>Applied Biochemistry and Biotechnology</i> , 1995, 55, 157-166.	2.9	2