

Theo Sanderson

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9181320/publications.pdf>

Version: 2024-02-01

22
papers

1,289
citations

840776

11
h-index

940533

16
g-index

44
all docs

44
docs citations

44
times ranked

2468
citing authors

#	ARTICLE	IF	CITATIONS
1	Using deep learning to annotate the protein universe. <i>Nature Biotechnology</i> , 2022, 40, 932-937.	17.5	133
2	CRISPR/Cas9 and genetic screens in malaria parasites: small genomes, big impact. <i>Biochemical Society Transactions</i> , 2022, 50, 1069-1079.	3.4	7
3	An apicoplast-resident folate transporter is essential for sporogony of malaria parasites. <i>Cellular Microbiology</i> , 2021, 23, e13266.	2.1	5
4	Clinical outcomes of COVID-19 in long-term care facilities for people with epilepsy. <i>Epilepsy and Behavior</i> , 2021, 115, 107602.	1.7	11
5	Mixology: a tool for calculating required masses and volumes for laboratory solutions. <i>Wellcome Open Research</i> , 2021, 6, 128.	1.8	0
6	Using <i>Plasmodium knowlesi</i> as a model for screening <i>Plasmodium vivax</i> blood-stage malaria vaccine targets reveals new candidates. <i>PLoS Pathogens</i> , 2021, 17, e1008864.	4.7	17
7	Defining multiplicity of vector uptake in transfected <i>Plasmodium</i> parasites. <i>Scientific Reports</i> , 2020, 10, 10894.	3.3	9
8	Genomic and transcriptomic evidence for descent from <i>Plasmodium</i> and loss of blood schizogony in <i>Hepaticystis</i> parasites from naturally infected red colobus monkeys. <i>PLoS Pathogens</i> , 2020, 16, e1008717.	4.7	18
9	Pandemic peak SARS-CoV-2 infection and seroconversion rates in London frontline health-care workers. <i>Lancet</i> , The, 2020, 396, e6-e7.	13.7	196
10	Critiquing Protein Family Classification Models Using Sufficient Input Subsets. <i>Journal of Computational Biology</i> , 2020, 27, 1219-1231.	1.6	7
11	Title is missing!. , 2020, 16, e1008717.		0
12	Title is missing!. , 2020, 16, e1008717.		0
13	Title is missing!. , 2020, 16, e1008717.		0
14	Title is missing!. , 2020, 16, e1008717.		0
15	Landscape of the <i>Plasmodium</i> Interactome Reveals Both Conserved and Species-Specific Functionality. <i>Cell Reports</i> , 2019, 28, 1635-1647.e5.	6.4	49
16	Genome-Scale Identification of Essential Metabolic Processes for Targeting the <i>Plasmodium</i> Liver Stage. <i>Cell</i> , 2019, 179, 1112-1128.e26.	28.9	92
17	<i>Plasmodium knowlesi</i> as a model system for characterising <i>Plasmodium vivax</i> drug resistance candidate genes. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007470.	3.0	17
18	Synergistic malaria vaccine combinations identified by systematic antigen screening. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 12045-12050.	7.1	49

#	ARTICLE	IF	CITATIONS
19	Functional Profiling of a Plasmodium Genome Reveals an Abundance of Essential Genes. Cell, 2017, 170, 260-272.e8.	28.9	471
20	PhenoPlasm: a database of disruption phenotypes for malaria parasite genes. Wellcome Open Research, 2017, 2, 45.	1.8	23
21	Plasmodium knowlesi Genome Sequences from Clinical Isolates Reveal Extensive Genomic Dimorphism. PLoS ONE, 2015, 10, e0121303.	2.5	54
22	PhenoPlasm: a database of disruption phenotypes for malaria parasite genes. Wellcome Open Research, 0, 2, 45.	1.8	10