

# Jenna Oberstaller

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3848104/publications.pdf>

Version: 2024-02-01

18  
papers

1,147  
citations

687363

13  
h-index

888059

17  
g-index

20  
all docs

20  
docs citations

20  
times ranked

1938  
citing authors

#	ARTICLE	IF	CITATIONS
1	Targeting Gametocytes of the Malaria Parasite <i>Plasmodium falciparum</i> in a Functional Genomics Era: Next Steps. <i>Pathogens</i> , 2021, 10, 346.	2.8	18
2	Essential Genes of the Parasitic Apicomplexa. <i>Trends in Parasitology</i> , 2021, 37, 304-316.	3.3	17
3	The apicoplast link to fever-survival and artemisinin-resistance in the malaria parasite. <i>Nature Communications</i> , 2021, 12, 4563.	12.8	26
4	Integration of population and functional genomics to understand mechanisms of artemisinin resistance in <i>Plasmodium falciparum</i> . <i>International Journal for Parasitology: Drugs and Drug Resistance</i> , 2021, 16, 119-128.	3.4	11
5	The human malaria parasite genome is configured into thousands of coexpressed linear regulatory units. <i>Journal of Genetics and Genomics</i> , 2020, 47, 513-521.	3.9	2
6	Light pollution increases West Nile virus competence of a ubiquitous passerine reservoir species. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20191051.	2.6	42
7	<i>Plasmodium</i> male gametocyte development and transmission are critically regulated by the two putative deadenylases of the CAF1/CCR4/NOT complex. <i>PLoS Pathogens</i> , 2019, 15, e1007164.	4.7	28
8	Iron Hack - A symposium/hackathon focused on porphyrias, Friedreich's ataxia, and other rare iron-related diseases. <i>F1000Research</i> , 2019, 8, 1135.	1.6	11
9	Blood flukes <i>Cardicola parvus</i> and <i>C. laruei</i> (Trematoda: Aporocotylidae): life cycles and cryptic infection in spotted seatrout, <i>Cynoscion nebulosus</i> (Teleost: Sciaenidae). <i>Parasitology International</i> , 2018, 67, 150-158.	1.3	15
10	Uncovering the essential genes of the human malaria parasite <i>Plasmodium falciparum</i> by saturation mutagenesis. <i>Science</i> , 2018, 360, .	12.6	687
11	First evidence of polychaete intermediate hosts for <i>Neosporichis</i> spp. marine turtle blood flukes (Trematoda: Spirorchiiidae). <i>International Journal for Parasitology</i> , 2018, 48, 1097-1106.	3.1	20
12	Phenotypic Screens Identify Parasite Genetic Factors Associated with Malarial Fever Response in <i>Plasmodium falciparum</i> piggyBac Mutants. <i>MSphere</i> , 2016, 1, .	2.9	18
13	The <i>Cryptosporidium parvum</i> ApiAP2 gene family: insights into the evolution of apicomplexan AP2 regulatory systems. <i>Nucleic Acids Research</i> , 2014, 42, 8271-8284.	14.5	40
14	Genome-wide upstream motif analysis of <i>Cryptosporidium parvum</i> genes clustered by expression profile. <i>BMC Genomics</i> , 2013, 14, 516.	2.8	18
15	Real-Time Loop-Mediated Isothermal Amplification (RealAmp) for the Species-Specific Identification of <i>Plasmodium vivax</i> . <i>PLoS ONE</i> , 2013, 8, e54986.	2.5	68
16	A New Single-Step PCR Assay for the Detection of the Zoonotic Malaria Parasite <i>Plasmodium knowlesi</i> . <i>PLoS ONE</i> , 2012, 7, e31848.	2.5	44
17	Applied Genomics: Data Mining Reveals Species-Specific Malaria Diagnostic Targets More Sensitive than 18S rRNA. <i>Journal of Clinical Microbiology</i> , 2011, 49, 2411-2418.	3.9	74
18	Uncovering host-microbiome interactions in global systems with collaborative programming: a novel approach integrating social and data sciences. <i>F1000Research</i> , 0, 9, 1478.	1.6	0