

# Sebastian Baumgarten

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8448193/publications.pdf>

Version: 2024-02-01

25  
papers

1,720  
citations

361296

20  
h-index

610775

24  
g-index

27  
all docs

27  
docs citations

27  
times ranked

2213  
citing authors

#	ARTICLE	IF	CITATIONS
1	The genome of <i>Aiptasia</i> , a sea anemone model for coral symbiosis. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 11893-11898.	3.3	359
2	Comparative genomics explains the evolutionary success of reef-forming corals. ELife, 2016, 5, .	2.8	169
3	Gene Expression Variation Resolves Species and Individual Strains among Coral-Associated Dinoflagellates within the Genus <i>Symbiodinium</i> . Genome Biology and Evolution, 2016, 8, 665-680.	1.1	144
4	Comparative analysis of the genomes of <i>Stylophora pistillata</i> and <i>Acropora digitifera</i> provides evidence for extensive differences between species of corals. Scientific Reports, 2017, 7, 17583.	1.6	121
5	Integrating microRNA and mRNA expression profiling in <i>Symbiodinium microadriaticum</i> , a dinoflagellate symbiont of reef-building corals. BMC Genomics, 2013, 14, 704.	1.2	109
6	A Specific PfEMP1 Is Expressed in <i>P. falciparum</i> Sporozoites and Plays a Role in Hepatocyte Infection. Cell Reports, 2018, 22, 2951-2963.	2.9	99
7	<i>Aiptasia</i> sp. larvae as a model to reveal mechanisms of symbiont selection in cnidarians. Scientific Reports, 2016, 6, 32366.	1.6	85
8	Distinct Bacterial Communities Associated with the Coral Model <i>Aiptasia</i> in Aposymbiotic and Symbiotic States with <i>Symbiodinium</i> . Frontiers in Marine Science, 2016, 3, .	1.2	67
9	Transcriptome-wide dynamics of extensive m6A mRNA methylation during <i>Plasmodium falciparum</i> blood-stage development. Nature Microbiology, 2019, 4, 2246-2259.	5.9	66
10	Metatranscriptome analysis of the reef-building coral <i>Orbicella faveolata</i> indicates holobiont response to coral disease. Frontiers in Marine Science, 2015, 2, .	1.2	61
11	Hologenome analysis of two marine sponges with different microbiomes. BMC Genomics, 2016, 17, 158.	1.2	60
12	Condition-specific RNA editing in the coral symbiont <i>Symbiodinium microadriaticum</i> . PLoS Genetics, 2017, 13, e1006619.	1.5	57
13	Identification of MicroRNAs in the Coral <i>Stylophora pistillata</i> . PLoS ONE, 2014, 9, e91101.	1.1	49
14	A Novel Tool for the Generation of Conditional Knockouts To Study Gene Function across the <i>Plasmodium falciparum</i> Life Cycle. MBio, 2019, 10, .	1.8	45
15	CRISPR in Parasitology: Not Exactly Cut and Dried!. Trends in Parasitology, 2019, 35, 409-422.	1.5	43
16	Evidence for miRNA-mediated modulation of the host transcriptome in cnidarian-dinoflagellate symbiosis. Molecular Ecology, 2018, 27, 403-418.	2.0	35
17	Exploring the virulence gene interactome with CRISPR-dCas9 in the human malaria parasite. Molecular Systems Biology, 2020, 16, e9569.	3.2	32
18	Population structure, growth and production of a recent brachiopod from the Chilean fjord region. Marine Ecology, 2014, 35, 401-413.	0.4	24

#	ARTICLE	IF	CITATIONS
19	Transcriptomes and expression profiling of deep-sea corals from the Red Sea provide insight into the biology of azooxanthellate corals. <i>Scientific Reports</i> , 2017, 7, 6442.	1.6	21
20	CRISPR/Cas9 Genome Editing Reveals That the Intron Is Not Essential for <i>var2csa</i> Gene Activation or Silencing in <i>Plasmodium falciparum</i> . <i>MBio</i> , 2017, 8, .	1.8	20
21	Malaria Parasite Stress Tolerance Is Regulated by DNMT2-Mediated tRNA Cytosine Methylation. <i>MBio</i> , 2021, 12, e0255821.	1.8	18
22	Disruption of the RNA exosome reveals the hidden face of the malaria parasite transcriptome. <i>RNA Biology</i> , 2018, 15, 1206-1214.	1.5	16
23	Functional Characterization of the m <sup>6</sup> A-Dependent Translational Modulator PfYTH.2 in the Human Malaria Parasite. <i>MBio</i> , 2021, 12, .	1.8	11
24	Rapid activation of distinct members of multigene families in <i>Plasmodium</i> spp. <i>Communications Biology</i> , 2020, 3, 351.	2.0	8
25	Chromatin structure can introduce systematic biases in genome-wide analyses of <i>Plasmodium falciparum</i> . <i>Open Research Europe</i> , 0, 2, 75.	2.0	0