

# Adam J Reid

## List of Publications by Year in descending order

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Version: 2024-02-01

47  
papers

3,278  
citations

331670

21  
h-index

276875

41  
g-index

60  
all docs

60  
docs citations

60  
times ranked

4187  
citing authors

#	ARTICLE	IF	CITATIONS
1	Defining the early stages of intestinal colonisation by whipworms. Nature Communications, 2022, 13, 1725.	12.8	18
2	Individual-level variations in malaria susceptibility and acquisition of clinical protection. Wellcome Open Research, 2021, 6, 22.	1.8	6
3	Mapping immune variation and var gene switching in naive hosts infected with Plasmodium falciparum. ELife, 2021, 10, .	6.0	22
4	10-year longitudinal study of malaria in children: Insights into acquisition and maintenance of naturally acquired immunity. Wellcome Open Research, 2021, 6, 79.	1.8	7
5	A single-cell atlas of Plasmodium falciparum transmission through the mosquito. Nature Communications, 2021, 12, 3196.	12.8	54
6	The complete genome sequence of Eimeria tenella (Tyzzer 1929), a common gut parasite of chickens. Wellcome Open Research, 2021, 6, 225.	1.8	14
7	Controlled human malaria infection with a clone of Plasmodium vivax with high-quality genome assembly. JCI Insight, 2021, 6, .	5.0	22
8	Analysis of pir gene expression across the Plasmodium life cycle. Malaria Journal, 2021, 20, 445.	2.3	9
9	Daily rhythms in gene expression of the human parasite Schistosoma mansoni. BMC Biology, 2021, 19, 255.	3.8	12
10	Structural basis for RIFIN-mediated activation of LILRB1 in malaria. Nature, 2020, 587, 309-312.	27.8	30
11	Structure of the <i>Plasmodium</i> -interspersed repeat proteins of the malaria parasite. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 32098-32104.	7.1	10
12	Genomic and transcriptomic evidence for descent from Plasmodium and loss of blood schizogony in Hepatocystis parasites from naturally infected red colobus monkeys. PLoS Pathogens, 2020, 16, e1008717.	4.7	18
13	Title is missing!. , 2020, 16, e1008717.		0
14	Title is missing!. , 2020, 16, e1008717.		0
15	Title is missing!. , 2020, 16, e1008717.		0
16	Title is missing!. , 2020, 16, e1008717.		0
17	The Malaria Cell Atlas: Single parasite transcriptomes across the complete <i>Plasmodium</i> life cycle. Science, 2019, 365, .	12.6	198
18	Repeated clinical malaria episodes are associated with modification of the immune system in children. BMC Medicine, 2019, 17, 60.	5.5	37

#	ARTICLE	IF	CITATIONS
19	Single-cell RNA-seq reveals hidden transcriptional variation in malaria parasites. <i>ELife</i> , 2018, 7, .	6.0	171
20	Long read assemblies of geographically dispersed <i>Plasmodium falciparum</i> isolates reveal highly structured subtelomeres. <i>Wellcome Open Research</i> , 2018, 3, 52.	1.8	114
21	Genomic and transcriptomic comparisons of closely related malaria parasites differing in virulence and sequestration pattern. <i>Wellcome Open Research</i> , 2018, 3, 142.	1.8	13
22	Genomic and transcriptomic comparisons of closely related malaria parasites differing in virulence and sequestration pattern. <i>Wellcome Open Research</i> , 2018, 3, 142.	1.8	11
23	<i>Plasmodium malariae</i> and <i>P. ovale</i> genomes provide insights into malaria parasite evolution. <i>Nature</i> , 2017, 542, 101-104.	27.8	150
24	The genomic basis of parasitism in the <i>Strongyloides</i> clade of nematodes. <i>Nature Genetics</i> , 2016, 48, 299-307.	21.4	226
25	Large, rapidly evolving gene families are at the forefront of host-parasite interactions in <i>Apicomplexa</i> . <i>Parasitology</i> , 2015, 142, S57-S70.	1.5	36
26	The evolutionary dynamics of variant antigen genes in <i>Babesia</i> reveal a history of genomic innovation underlying host-parasite interaction. <i>Nucleic Acids Research</i> , 2014, 42, 7113-7131.	14.5	90
27	Genomic characterisation of the effector complement of the potato cyst nematode <i>Globodera pallida</i> . <i>BMC Genomics</i> , 2014, 15, 923.	2.8	81
28	The genome and life-stage specific transcriptomes of <i>Globodera pallida</i> elucidate key aspects of plant parasitism by a cyst nematode. <i>Genome Biology</i> , 2014, 15, R43.	9.6	212
29	Genomic analysis of the causative agents of coccidiosis in domestic chickens. <i>Genome Research</i> , 2014, 24, 1676-1685.	5.5	176
30	Whipworm genome and dual-species transcriptome analyses provide molecular insights into an intimate host-parasite interaction. <i>Nature Genetics</i> , 2014, 46, 693-700.	21.4	139
31	Bioinformatic Analysis of Expression Data to Identify Effector Candidates. <i>Methods in Molecular Biology</i> , 2014, 1127, 17-27.	0.9	1
32	The genome and transcriptome of <i>Haemonchus contortus</i> , a key model parasite for drug and vaccine discovery. <i>Genome Biology</i> , 2013, 14, R88.	9.6	293
33	Vector transmission regulates immune control of <i>Plasmodium</i> virulence. <i>Nature</i> , 2013, 498, 228-231.	27.8	168
34	Genes involved in host-parasite interactions can be revealed by their correlated expression. <i>Nucleic Acids Research</i> , 2013, 41, 1508-1518.	14.5	38
35	Characterization and gene expression analysis of the <i>cir</i> multi-gene family of <i>plasmodium chabaudi</i> ( <i>AS</i> ). <i>BMC Genomics</i> , 2012, 13, 125.	2.8	26
36	Uncovering the Molecular Machinery of the Human Spindle—An Integration of Wet and Dry Systems Biology. <i>PLoS ONE</i> , 2012, 7, e31813.	2.5	14

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37	Genomic Insights into the Origin of Parasitism in the Emerging Plant Pathogen <i>Bursaphelenchus xylophilus</i> . <i>PLoS Pathogens</i> , 2011, 7, e1002219.	4.7	351
38	Comparative evolutionary analysis of protein complexes in <i>E. coli</i> and yeast. <i>BMC Genomics</i> , 2010, 11, 79.	2.8	18
39	Assessment of protein domain fusions in human protein interaction networks prediction: Application to the human kinetochore model. <i>New Biotechnology</i> , 2010, 27, 755-765.	4.4	9
40	CODA: Accurate Detection of Functional Associations between Proteins in Eukaryotic Genomes Using Domain Fusion. <i>PLoS ONE</i> , 2010, 5, e10908.	2.5	10
41	Finding the "Dark Matter" in Human and Yeast Protein Network Prediction and Modelling. <i>PLoS Computational Biology</i> , 2010, 6, e1000945.	3.2	21
42	The CATH Hierarchy Revisited" Structural Divergence in Domain Superfamilies and the Continuity of Fold Space. <i>Structure</i> , 2009, 17, 1051-1062.	3.3	58
43	The evolution of protein functions and networks: a family-centric approach. <i>Biochemical Society Transactions</i> , 2009, 37, 745-750.	3.4	3
44	Gene3D: comprehensive structural and functional annotation of genomes. <i>Nucleic Acids Research</i> , 2007, 36, D414-D418.	14.5	68
45	The CATH domain structure database: new protocols and classification levels give a more comprehensive resource for exploring evolution. <i>Nucleic Acids Research</i> , 2007, 35, D291-D297.	14.5	274
46	Individual-level variations in malaria susceptibility and acquisition of clinical protection. <i>Wellcome Open Research</i> , 0, 6, 22.	1.8	4
47	10-year longitudinal study of malaria in children: Insights into acquisition and maintenance of naturally acquired immunity. <i>Wellcome Open Research</i> , 0, 6, 79.	1.8	4