

# 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	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
2	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
3	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
4	The genomic basis of parasitism in the <i>Strongyloides</i> clade of nematodes. <i>Nature Genetics</i> , 2016, 48, 299-307.	21.4	226
5	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
6	The Malaria Cell Atlas: Single parasite transcriptomes across the complete <i>Plasmodium</i> life cycle. <i>Science</i> , 2019, 365, .	12.6	198
7	Genomic analysis of the causative agents of coccidiosis in domestic chickens. <i>Genome Research</i> , 2014, 24, 1676-1685.	5.5	176
8	Single-cell RNA-seq reveals hidden transcriptional variation in malaria parasites. <i>ELife</i> , 2018, 7, .	6.0	171
9	Vector transmission regulates immune control of <i>Plasmodium</i> virulence. <i>Nature</i> , 2013, 498, 228-231.	27.8	168
10	<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
11	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
12	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
13	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
14	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
15	Gene3D: comprehensive structural and functional annotation of genomes. <i>Nucleic Acids Research</i> , 2007, 36, D414-D418.	14.5	68
16	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
17	A single-cell atlas of <i>Plasmodium falciparum</i> transmission through the mosquito. <i>Nature Communications</i> , 2021, 12, 3196.	12.8	54
18	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

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19	Repeated clinical malaria episodes are associated with modification of the immune system in children. BMC Medicine, 2019, 17, 60.	5.5	37
20	Large, rapidly evolving gene families are at the forefront of host-parasite interactions in Apicomplexa. Parasitology, 2015, 142, S57-S70.	1.5	36
21	Structural basis for RIFIN-mediated activation of LILRB1 in malaria. Nature, 2020, 587, 309-312.	27.8	30
22	Characterization and gene expression analysis of the cir multi-gene family of Plasmodium chabaudi chabaudi (AS). BMC Genomics, 2012, 13, 125.	2.8	26
23	Mapping immune variation and var gene switching in naive hosts infected with Plasmodium falciparum. ELife, 2021, 10, .	6.0	22
24	Controlled human malaria infection with a clone of Plasmodium vivax with high-quality genome assembly. JCI Insight, 2021, 6, .	5.0	22
25	Finding the "Dark Matter" in Human and Yeast Protein Network Prediction and Modelling. PLoS Computational Biology, 2010, 6, e1000945.	3.2	21
26	Comparative evolutionary analysis of protein complexes in E. coli and yeast. BMC Genomics, 2010, 11, 79.	2.8	18
27	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
28	Defining the early stages of intestinal colonisation by whipworms. Nature Communications, 2022, 13, 1725.	12.8	18
29	Uncovering the Molecular Machinery of the Human Spindle"An Integration of Wet and Dry Systems Biology. PLoS ONE, 2012, 7, e31813.	2.5	14
30	The complete genome sequence of Eimeria tenella (Tyzzer 1929), a common gut parasite of chickens. Wellcome Open Research, 2021, 6, 225.	1.8	14
31	Genomic and transcriptomic comparisons of closely related malaria parasites differing in virulence and sequestration pattern. Wellcome Open Research, 2018, 3, 142.	1.8	13
32	Daily rhythms in gene expression of the human parasite Schistosoma mansoni. BMC Biology, 2021, 19, 255.	3.8	12
33	Genomic and transcriptomic comparisons of closely related malaria parasites differing in virulence and sequestration pattern. Wellcome Open Research, 2018, 3, 142.	1.8	11
34	CODA: Accurate Detection of Functional Associations between Proteins in Eukaryotic Genomes Using Domain Fusion. PLoS ONE, 2010, 5, e10908.	2.5	10
35	Structure of the Plasmodium-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
36	Assessment of protein domain fusions in human protein interaction networks prediction: Application to the human kinetochore model. New Biotechnology, 2010, 27, 755-765.	4.4	9

#	ARTICLE	IF	CITATIONS
37	Analysis of pir gene expression across the Plasmodium life cycle. Malaria Journal, 2021, 20, 445.	2.3	9
38	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
39	Individual-level variations in malaria susceptibility and acquisition of clinical protection. Wellcome Open Research, 2021, 6, 22.	1.8	6
40	Individual-level variations in malaria susceptibility and acquisition of clinical protection. Wellcome Open Research, 0, 6, 22.	1.8	4
41	10-year longitudinal study of malaria in children: Insights into acquisition and maintenance of naturally acquired immunity. Wellcome Open Research, 0, 6, 79.	1.8	4
42	The evolution of protein functions and networks: a family-centric approach. Biochemical Society Transactions, 2009, 37, 745-750.	3.4	3
43	Bioinformatic Analysis of Expression Data to Identify Effector Candidates. Methods in Molecular Biology, 2014, 1127, 17-27.	0.9	1
44	Title is missing!. , 2020, 16, e1008717.		0
45	Title is missing!. , 2020, 16, e1008717.		0
46	Title is missing!. , 2020, 16, e1008717.		0
47	Title is missing!. , 2020, 16, e1008717.		0