

# Jane M Carlton

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2079162/publications.pdf>

Version: 2024-02-01

91  
papers

13,449  
citations

76294

40  
h-index

43868

91  
g-index

95  
all docs

95  
docs citations

95  
times ranked

11608  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome sequence of the human malaria parasite <i>Plasmodium falciparum</i> . <i>Nature</i> , 2002, 419, 498-511.	13.7	3,881
2	Comparative genomics of the neglected human malaria parasite <i>Plasmodium vivax</i> . <i>Nature</i> , 2008, 455, 757-763.	13.7	756
3	A Comprehensive Survey of the <i>Plasmodium</i> Life Cycle by Genomic, Transcriptomic, and Proteomic Analyses. <i>Science</i> , 2005, 307, 82-86.	6.0	743
4	Draft Genome Sequence of the Sexually Transmitted Pathogen <i>Trichomonas vaginalis</i> . <i>Science</i> , 2007, 315, 207-212.	6.0	731
5	Comparative Genomics of Trypanosomatid Parasitic Protozoa. <i>Science</i> , 2005, 309, 404-409.	6.0	713
6	Genome sequence and comparative analysis of the model rodent malaria parasite <i>Plasmodium yoelii yoelii</i> . <i>Nature</i> , 2002, 419, 512-519.	13.7	666
7	Macronuclear Genome Sequence of the Ciliate <i>Tetrahymena thermophila</i> , a Model Eukaryote. <i>PLoS Biology</i> , 2006, 4, e286.	2.6	657
8	Key gaps in the knowledge of <i>Plasmodium vivax</i> , a neglected human malaria parasite. <i>Lancet Infectious Diseases</i> , The, 2009, 9, 555-566.	4.6	565
9	Genome Sequence of <i>Theileria parva</i> , a Bovine Pathogen That Transforms Lymphocytes. <i>Science</i> , 2005, 309, 134-137.	6.0	309
10	The malaria parasite <i>Plasmodium vivax</i> exhibits greater genetic diversity than <i>Plasmodium falciparum</i> . <i>Nature Genetics</i> , 2012, 44, 1046-1050.	9.4	256
11	Geospatial Resolution of Human and Bacterial Diversity with City-Scale Metagenomics. <i>Cell Systems</i> , 2015, 1, 72-87.	2.9	241
12	The transcriptome of <i>Plasmodium vivax</i> reveals divergence and diversity of transcriptional regulation in malaria parasites. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 16290-16295.	3.3	234
13	Population genomics studies identify signatures of global dispersal and drug resistance in <i>Plasmodium vivax</i> . <i>Nature Genetics</i> , 2016, 48, 953-958.	9.4	194
14	Global phylogeography and ancient evolution of the widespread human gut virus crAssphage. <i>Nature Microbiology</i> , 2019, 4, 1727-1736.	5.9	184
15	<i>Plasmodium cynomolgi</i> genome sequences provide insight into <i>Plasmodium vivax</i> and the monkey malaria clade. <i>Nature Genetics</i> , 2012, 44, 1051-1055.	9.4	172
16	Sequence of <i>Plasmodium falciparum</i> chromosomes 2, 10, 11 and 14. <i>Nature</i> , 2002, 419, 531-534.	13.7	167
17	Contrasting genetic structure in <i>Plasmodium vivax</i> populations from Asia and South America. <i>International Journal for Parasitology</i> , 2007, 37, 1013-1022.	1.3	140
18	Association Between <i>Trichomonas vaginalis</i> and Vaginal Bacterial Community Composition Among Reproductive-Age Women. <i>Sexually Transmitted Diseases</i> , 2012, 39, 807-812.	0.8	138

#	ARTICLE	IF	CITATIONS
19	A Plasmodium Whole-Genome Synteny Map: Indels and Synteny Breakpoints as Foci for Species-Specific Genes. PLoS Pathogens, 2005, 1, e44.	2.1	131
20	Local Adaptation and Vector-Mediated Population Structure in Plasmodium vivax Malaria. Molecular Biology and Evolution, 2008, 25, 1245-1252.	3.5	115
21	Malaria in India: The Center for the Study of Complex Malaria in India. Acta Tropica, 2012, 121, 267-273.	0.9	115
22	A Systems-Based Analysis of Plasmodium vivax Lifecycle Transcription from Human to Mosquito. PLoS Neglected Tropical Diseases, 2010, 4, e653.	1.3	96
23	What is the importance of zoonotic trichomonads for human health?. Trends in Parasitology, 2014, 30, 333-341.	1.5	92
24	Single-nucleotide polymorphisms and genome diversity in Plasmodium vivax. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 8502-8507.	3.3	91
25	Spliceosomal introns in the deep-branching eukaryote Trichomonas vaginalis. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 4430-4435.	3.3	86
26	Why Is Plasmodium vivax a Neglected Tropical Disease?. PLoS Neglected Tropical Diseases, 2011, 5, e1160.	1.3	84
27	Extensive Genetic Diversity, Unique Population Structure and Evidence of Genetic Exchange in the Sexually Transmitted Parasite Trichomonas vaginalis. PLoS Neglected Tropical Diseases, 2012, 6, e1573.	1.3	81
28	Malaria Molecular Epidemiology: Lessons from the International Centers of Excellence for Malaria Research Network. American Journal of Tropical Medicine and Hygiene, 2015, 93, 79-86.	0.6	80
29	Carotenoid Biosynthesis in Intraerythrocytic Stages of Plasmodium falciparum. Journal of Biological Chemistry, 2009, 284, 9974-9985.	1.6	73
30	Plasmepsin 4, the food vacuole aspartic proteinase found in all Plasmodium spp. infecting man. Molecular and Biochemical Parasitology, 2003, 130, 1-12.	0.5	72
31	Plasmodium vivax in India. Trends in Parasitology, 2008, 24, 228-235.	1.5	67
32	Overlapping Community Compositions of Gut and Fecal Microbiomes in Lab-Reared and Field-Collected German Cockroaches. Applied and Environmental Microbiology, 2018, 84, .	1.4	67
33	Single-dose versus 7-day-dose metronidazole for the treatment of trichomoniasis in women: an open-label, randomised controlled trial. Lancet Infectious Diseases, The, 2018, 18, 1251-1259.	4.6	61
34	Comparative evolutionary genomics of human malaria parasites. Trends in Parasitology, 2008, 24, 545-550.	1.5	57
35	Identification of a very large Rab GTPase family in the parasitic protozoan Trichomonas vaginalis. Molecular and Biochemical Parasitology, 2005, 143, 226-235.	0.5	55
36	What is the value of reactive case detection in malaria control? A case-study in India and a systematic review. Malaria Journal, 2016, 15, 67.	0.8	54

#	ARTICLE	IF	CITATIONS
37	Genome sequences reveal divergence times of malaria parasite lineages. <i>Parasitology</i> , 2011, 138, 1737-1749.	0.7	50
38	Microsatellite polymorphism in the sexually transmitted human pathogen <i>Trichomonas vaginalis</i> indicates a genetically diverse parasite. <i>Molecular and Biochemical Parasitology</i> , 2011, 175, 30-38.	0.5	48
39	Linkage maps from multiple genetic crosses and loci linked to growth-related virulent phenotype in <i>Plasmodium yoelii</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, E374-E382.	3.3	45
40	The origin and diversification of the merozoite surface protein 3 (msp3) multi-gene family in <i>Plasmodium vivax</i> and related parasites. <i>Molecular Phylogenetics and Evolution</i> , 2014, 78, 172-184.	1.2	44
41	Genetic Indicators of Drug Resistance in the Highly Repetitive Genome of <i>Trichomonas vaginalis</i> . <i>Genome Biology and Evolution</i> , 2017, 9, 1658-1672.	1.1	44
42	The burden of submicroscopic and asymptomatic malaria in India revealed from epidemiology studies at three varied transmission sites in India. <i>Scientific Reports</i> , 2019, 9, 17095.	1.6	44
43	Genomics, Population Genetics and Evolutionary History of <i>Plasmodium vivax</i> . <i>Advances in Parasitology</i> , 2013, 81, 203-222.	1.4	42
44	Getting trichy: tools and approaches to interrogating <i>Trichomonas vaginalis</i> in a post-genome world. <i>Trends in Parasitology</i> , 2013, 29, 17-25.	1.5	41
45	A Method for Amplicon Deep Sequencing of Drug Resistance Genes in <i>Plasmodium falciparum</i> Clinical Isolates from India. <i>Journal of Clinical Microbiology</i> , 2016, 54, 1500-1511.	1.8	41
46	A Potentially Functional Mariner Transposable Element in the Protist <i>Trichomonas vaginalis</i> . <i>Molecular Biology and Evolution</i> , 2004, 22, 126-134.	3.5	40
47	Phylogeny of Parasitic Parabasalia and Free-Living Relatives Inferred from Conventional Markers vs. <i>Rpb1</i> , a Single-Copy Gene. <i>PLoS ONE</i> , 2011, 6, e20774.	1.1	37
48	An 18S rRNA Workflow for Characterizing Protists in Sewage, with a Focus on Zoonotic Trichomonads. <i>Microbial Ecology</i> , 2017, 74, 923-936.	1.4	36
49	Characterizing Antibody Responses to <i>Plasmodium vivax</i> and <i>Plasmodium falciparum</i> Antigens in India Using Genome-Scale Protein Microarrays. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005323.	1.3	33
50	Patterns of protist diversity associated with raw sewage in New York City. <i>ISME Journal</i> , 2019, 13, 2750-2763.	4.4	33
51	Chloroquine efficacy studies confirm drug susceptibility of <i>Plasmodium vivax</i> in Chennai, India. <i>Malaria Journal</i> , 2014, 13, 129.	0.8	29
52	Novel Antigen Identification Method for Discovery of Protective Malaria Antigens by Rapid Testing of DNA Vaccines Encoding Exons from the Parasite Genome. <i>Infection and Immunity</i> , 2004, 72, 1594-1602.	1.0	28
53	Microbial Community Patterns Associated with Automated Teller Machine Keypads in New York City. <i>MSphere</i> , 2016, 1, .	1.3	28
54	The use of mosquito repellents at three sites in India with declining malaria transmission: surveys in the community and clinic. <i>Parasites and Vectors</i> , 2016, 9, 418.	1.0	27

#	ARTICLE	IF	CITATIONS
55	Immune responses to <i>Plasmodium vivax</i> pre-erythrocytic stage antigens in naturally exposed Duffy-negative humans: a potential model for identification of liver-stage antigens. <i>European Journal of Immunology</i> , 2005, 35, 1859-1868.	1.6	25
56	The biology of <i>Plasmodium vivax</i> explored through genomics. <i>Annals of the New York Academy of Sciences</i> , 2015, 1342, 53-61.	1.8	25
57	Gene discovery in <i>Plasmodium vivax</i> through sequencing of ESTs from mixed blood stages. <i>Molecular and Biochemical Parasitology</i> , 2005, 144, 1-9.	0.5	24
58	Dengue, chikungunya, and scrub typhus are important etiologies of non-malarial febrile illness in Rourkela, Odisha, India. <i>BMC Infectious Diseases</i> , 2019, 19, 572.	1.3	24
59	Characterizing the genetic diversity of the monkey malaria parasite <i>Plasmodium cynomolgi</i> . <i>Infection, Genetics and Evolution</i> , 2016, 40, 243-252.	1.0	23
60	Population Genetics, Evolutionary Genomics, and Genome-Wide Studies of Malaria: A View Across the International Centers of Excellence for Malaria Research. <i>American Journal of Tropical Medicine and Hygiene</i> , 2015, 93, 87-98.	0.6	22
61	Ahead of the curve: next generation estimators of drug resistance in malaria infections. <i>Trends in Parasitology</i> , 2013, 29, 321-328.	1.5	21
62	The Tc1/mariner transposable element family shapes genetic variation and gene expression in the protist <i>Trichomonas vaginalis</i> . <i>Mobile DNA</i> , 2014, 5, 12.	1.3	20
63	Longitudinal Comparison of Bacterial Diversity and Antibiotic Resistance Genes in New York City Sewage. <i>MSystems</i> , 2019, 4, .	1.7	19
64	Clinical and epidemiological characterization of severe <i>Plasmodium vivax</i> malaria in Gujarat, India. <i>Virulence</i> , 2020, 11, 730-738.	1.8	19
65	Identification of a polymorphic <i>Plasmodium vivax</i> microsatellite marker. <i>American Journal of Tropical Medicine and Hygiene</i> , 2003, 69, 377-9.	0.6	19
66	Filthy lucre: A metagenomic pilot study of microbes found on circulating currency in New York City. <i>PLoS ONE</i> , 2017, 12, e0175527.	1.1	18
67	Genetic diversity in <i>Trichomonas vaginalis</i> . <i>Sexually Transmitted Infections</i> , 2013, 89, 444-448.	0.8	17
68	The impact of genomics on population genetics of parasitic diseases. <i>Current Opinion in Microbiology</i> , 2015, 23, 49-54.	2.3	16
69	Malaria in Meghalaya: a systematic literature review and analysis of data from the National Vector-Borne Disease Control Programme. <i>Malaria Journal</i> , 2018, 17, 411.	0.8	15
70	Antibody responses within two leading <i>Plasmodium vivax</i> vaccine candidate antigens in three geographically diverse malaria-endemic regions of India. <i>Malaria Journal</i> , 2019, 18, 425.	0.8	15
71	Toward a malaria haplotype map. <i>Nature Genetics</i> , 2007, 39, 5-6.	9.4	14
72	Comparative assessment on the prevalence of mutations in the <i>Plasmodium falciparum</i> drug-resistant genes in two different ecotypes of Odisha state, India. <i>Infection, Genetics and Evolution</i> , 2016, 41, 47-55.	1.0	14

#	ARTICLE	IF	CITATIONS
73	Genome Sequencing and Comparative Genomics of Tropical Disease Pathogens. <i>Cellular Microbiology</i> , 2003, 5, 861-873.	1.1	13
74	Microsatellite analysis of chloroquine resistance associated alleles and neutral loci reveal genetic structure of Indian <i>Plasmodium falciparum</i> . <i>Infection, Genetics and Evolution</i> , 2013, 19, 164-175.	1.0	13
75	A Systematic Review of the Evidence on the Effectiveness and Cost-Effectiveness of Mass Screen-and-Treat Interventions for Malaria Control. <i>American Journal of Tropical Medicine and Hygiene</i> , 2021, 105, 1722-1731.	0.6	12
76	Household and individual level risk factors associated with declining malaria incidence in Meghalaya, India: implications for malaria elimination in low-endemic settings. <i>Malaria Journal</i> , 2021, 20, 460.	0.8	12
77	Spatial and temporal village-level prevalence of <i>Plasmodium</i> infection and associated risk factors in two districts of Meghalaya, India. <i>Malaria Journal</i> , 2021, 20, 70.	0.8	11
78	Malaria parasite evolution in a test tube. <i>Science</i> , 2018, 359, 159-160.	6.0	10
79	Malaria in Sundargarh district, Odisha, India: Epidemiological and behavioral aspects from surveys. <i>Acta Tropica</i> , 2020, 211, 105647.	0.9	9
80	Does the common sexually transmitted parasite <i>Trichomonas vaginalis</i> have sex?. <i>PLoS Pathogens</i> , 2018, 14, e1006831.	2.1	8
81	OUP accepted manuscript. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	1.4	8
82	Implementation and acceptance of government-sponsored malaria control interventions in Meghalaya, India. <i>Malaria Journal</i> , 2022, 21, .	0.8	8
83	Glycophorins, Blood Groups, and Protection from Severe Malaria. <i>Trends in Parasitology</i> , 2016, 32, 5-7.	1.5	7
84	Defining symptoms of malaria in India in an era of asymptomatic infections. <i>Malaria Journal</i> , 2020, 19, 237.	0.8	7
85	The effectiveness of malaria camps as part of the Durgama Anchalare Malaria Nirakaran (DAMaN) program in Odisha, India: study protocol for a cluster-assigned quasi-experimental study. <i>Global Health Action</i> , 2021, 14, 1886458.	0.7	7
86	Genetic diversity of <i>Trichomonas vaginalis</i> reinfection in HIV-positive women. <i>Sexually Transmitted Infections</i> , 2013, 89, 473-478.	0.8	5
87	A Feast of Malaria Parasite Genomes. <i>Cell Host and Microbe</i> , 2017, 21, 310-312.	5.1	4
88	Evolution of human malaria. <i>Nature Microbiology</i> , 2018, 3, 642-643.	5.9	4
89	Small RNAs Are Implicated in Regulation of Gene and Transposable Element Expression in the Protist <i>Trichomonas vaginalis</i> . <i>MSphere</i> , 2021, 6, .	1.3	4
90	Genetic diversity in two leading <i>Plasmodium vivax</i> malaria vaccine candidates AMA1 and MSP119 at three sites in India. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0009652.	1.3	3

#	ARTICLE	IF	CITATIONS
91	A cornucopia of research resources for the fourth rodent malaria parasite species. BMC Biology, 2021, 19, 82.	1.7	0