

# Jane M Carlton

## List of Publications by Year in descending order

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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	Implementation and acceptance of government-sponsored malaria control interventions in Meghalaya, India. <i>Malaria Journal</i> , 2022, 21, .	0.8	8
2	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
3	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
4	A cornucopia of research resources for the fourth rodent malaria parasite species. <i>BMC Biology</i> , 2021, 19, 82.	1.7	0
5	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
6	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
7	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
8	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
9	Malaria in Sundargarh district, Odisha, India: Epidemiological and behavioral aspects from surveys. <i>Acta Tropica</i> , 2020, 211, 105647.	0.9	9
10	Clinical and epidemiological characterization of severe <i>Plasmodium vivax</i> malaria in Gujarat, India. <i>Virulence</i> , 2020, 11, 730-738.	1.8	19
11	Defining symptoms of malaria in India in an era of asymptomatic infections. <i>Malaria Journal</i> , 2020, 19, 237.	0.8	7
12	OUP accepted manuscript. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	1.4	8
13	Longitudinal Comparison of Bacterial Diversity and Antibiotic Resistance Genes in New York City Sewage. <i>MSystems</i> , 2019, 4, .	1.7	19
14	Patterns of protist diversity associated with raw sewage in New York City. <i>ISME Journal</i> , 2019, 13, 2750-2763.	4.4	33
15	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
16	Global phylogeography and ancient evolution of the widespread human gut virus crAssphage. <i>Nature Microbiology</i> , 2019, 4, 1727-1736.	5.9	184
17	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
18	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

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19	Malaria parasite evolution in a test tube. <i>Science</i> , 2018, 359, 159-160.	6.0	10
20	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
21	Single-dose versus 7-day-dose metronidazole for the treatment of trichomoniasis in women: an open-label, randomised controlled trial. <i>Lancet Infectious Diseases</i> , The, 2018, 18, 1251-1259.	4.6	61
22	Evolution of human malaria. <i>Nature Microbiology</i> , 2018, 3, 642-643.	5.9	4
23	Overlapping Community Compositions of Gut and Fecal Microbiomes in Lab-Reared and Field-Collected German Cockroaches. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	67
24	Does the common sexually transmitted parasite <i>Trichomonas vaginalis</i> have sex?. <i>PLoS Pathogens</i> , 2018, 14, e1006831.	2.1	8
25	A Feast of Malaria Parasite Genomes. <i>Cell Host and Microbe</i> , 2017, 21, 310-312.	5.1	4
26	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
27	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
28	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
29	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
30	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
31	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
32	Microbial Community Patterns Associated with Automated Teller Machine Keypads in New York City. <i>MSphere</i> , 2016, 1, .	1.3	28
33	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
34	What is the value of reactive case detection in malaria control? A case-study in India and a systematic review. <i>Malaria Journal</i> , 2016, 15, 67.	0.8	54
35	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
36	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

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37	Glycophorins, Blood Groups, and Protection from Severe Malaria. <i>Trends in Parasitology</i> , 2016, 32, 5-7.	1.5	7
38	Geospatial Resolution of Human and Bacterial Diversity with City-Scale Metagenomics. <i>Cell Systems</i> , 2015, 1, 72-87.	2.9	241
39	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
40	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
41	Malaria Molecular Epidemiology: Lessons from the International Centers of Excellence for Malaria Research Network. <i>American Journal of Tropical Medicine and Hygiene</i> , 2015, 93, 79-86.	0.6	80
42	The impact of genomics on population genetics of parasitic diseases. <i>Current Opinion in Microbiology</i> , 2015, 23, 49-54.	2.3	16
43	What is the importance of zoonotic trichomonads for human health?. <i>Trends in Parasitology</i> , 2014, 30, 333-341.	1.5	92
44	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
45	Chloroquine efficacy studies confirm drug susceptibility of <i>Plasmodium vivax</i> in Chennai, India. <i>Malaria Journal</i> , 2014, 13, 129.	0.8	29
46	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
47	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
48	Genetic diversity in <i>Trichomonas vaginalis</i> . <i>Sexually Transmitted Infections</i> , 2013, 89, 444-448.	0.8	17
49	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
50	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
51	Genomics, Population Genetics and Evolutionary History of <i>Plasmodium vivax</i> . <i>Advances in Parasitology</i> , 2013, 81, 203-222.	1.4	42
52	Genetic diversity of <i>Trichomonas vaginalis</i> reinfection in HIV-positive women. <i>Sexually Transmitted Infections</i> , 2013, 89, 473-478.	0.8	5
53	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
54	Extensive Genetic Diversity, Unique Population Structure and Evidence of Genetic Exchange in the Sexually Transmitted Parasite <i>Trichomonas vaginalis</i> . <i>PLoS Neglected Tropical Diseases</i> , 2012, 6, e1573.	1.3	81

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55	<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
56	Malaria in India: The Center for the Study of Complex Malaria in India. <i>Acta Tropica</i> , 2012, 121, 267-273.	0.9	115
57	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
58	Genome sequences reveal divergence times of malaria parasite lineages. <i>Parasitology</i> , 2011, 138, 1737-1749.	0.7	50
59	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
60	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
61	Why Is <i>Plasmodium vivax</i> a Neglected Tropical Disease?. <i>PLoS Neglected Tropical Diseases</i> , 2011, 5, e1160.	1.3	84
62	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
63	A Systems-Based Analysis of <i>Plasmodium vivax</i> Lifecycle Transcription from Human to Mosquito. <i>PLoS Neglected Tropical Diseases</i> , 2010, 4, e653.	1.3	96
64	Carotenoid Biosynthesis in Intraerythrocytic Stages of <i>Plasmodium falciparum</i> . <i>Journal of Biological Chemistry</i> , 2009, 284, 9974-9985.	1.6	73
65	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
66	Comparative genomics of the neglected human malaria parasite <i>Plasmodium vivax</i> . <i>Nature</i> , 2008, 455, 757-763.	13.7	756
67	<i>Plasmodium vivax</i> in India. <i>Trends in Parasitology</i> , 2008, 24, 228-235.	1.5	67
68	Comparative evolutionary genomics of human malaria parasites. <i>Trends in Parasitology</i> , 2008, 24, 545-550.	1.5	57
69	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
70	Local Adaptation and Vector-Mediated Population Structure in <i>Plasmodium vivax</i> Malaria. <i>Molecular Biology and Evolution</i> , 2008, 25, 1245-1252.	3.5	115
71	Draft Genome Sequence of the Sexually Transmitted Pathogen <i>Trichomonas vaginalis</i> . <i>Science</i> , 2007, 315, 207-212.	6.0	731
72	Toward a malaria haplotype map. <i>Nature Genetics</i> , 2007, 39, 5-6.	9.4	14

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73	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
74	Macronuclear Genome Sequence of the Ciliate <i>Tetrahymena thermophila</i> , a Model Eukaryote. <i>PLoS Biology</i> , 2006, 4, e286.	2.6	657
75	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
76	Identification of a very large Rab GTPase family in the parasitic protozoan <i>Trichomonas vaginalis</i> . <i>Molecular and Biochemical Parasitology</i> , 2005, 143, 226-235.	0.5	55
77	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
78	A <i>Plasmodium</i> Whole-Genome Synteny Map: Indels and Synteny Breakpoints as Foci for Species-Specific Genes. <i>PLoS Pathogens</i> , 2005, 1, e44.	2.1	131
79	Spliceosomal introns in the deep-branching eukaryote <i>Trichomonas vaginalis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 4430-4435.	3.3	86
80	Comparative Genomics of Trypanosomatid Parasitic Protozoa. <i>Science</i> , 2005, 309, 404-409.	6.0	713
81	Genome Sequence of <i>Theileria parva</i> , a Bovine Pathogen That Transforms Lymphocytes. <i>Science</i> , 2005, 309, 134-137.	6.0	309
82	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
83	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
84	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
85	Plasmepsin 4, the food vacuole aspartic proteinase found in all <i>Plasmodium</i> spp. infecting man. <i>Molecular and Biochemical Parasitology</i> , 2003, 130, 1-12.	0.5	72
86	Genome Sequencing and Comparative Genomics of Tropical Disease Pathogens. <i>Cellular Microbiology</i> , 2003, 5, 861-873.	1.1	13
87	Single-nucleotide polymorphisms and genome diversity in <i>Plasmodium vivax</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 8502-8507.	3.3	91
88	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
89	Sequence of <i>Plasmodium falciparum</i> chromosomes 2, 10, 11 and 14. <i>Nature</i> , 2002, 419, 531-534.	13.7	167
90	Genome sequence of the human malaria parasite <i>Plasmodium falciparum</i> . <i>Nature</i> , 2002, 419, 498-511.	13.7	3,881

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91	Genome sequence and comparative analysis of the model rodent malaria parasite <i>Plasmodium yoelii</i> . <i>Nature</i> , 2002, 419, 512-519.	13.7	666