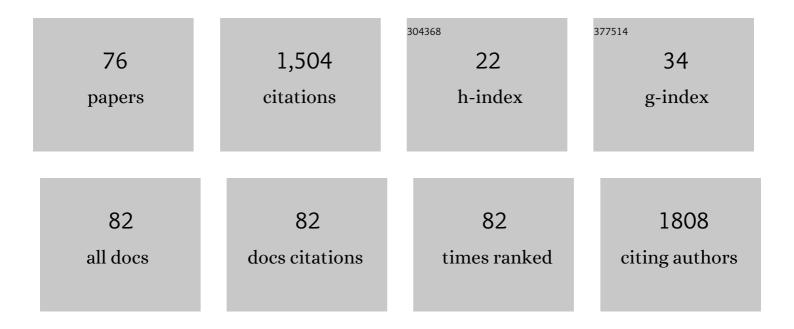
## **Om Prakash Singh**

List of Publications by Year in descending order

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OM PRAKASH SINCH

#	Article	IF	CITATIONS
1	Malaria in India: The Center for the Study of Complex Malaria in India. Acta Tropica, 2012, 121, 267-273.	0.9	115
2	A review of malaria transmission dynamics in forest ecosystems. Parasites and Vectors, 2014, 7, 265.	1.0	97
3	Pyrethroid-Resistance and Presence of Two Knockdown Resistance (kdr) Mutations, F1534C and a Novel Mutation T1520I, in Indian Aedes aegypti. PLoS Neglected Tropical Diseases, 2015, 9, e3332.	1.3	87
4	DIFFERENTIATION OF MEMBERS OF THE ANOPHELES FLUVIATILIS SPECIES COMPLEX BY AN ALLELE-SPECIFIC POLYMERASE CHAIN REACTION BASED ON 28S RIBOSOMAL DNA SEQUENCES. American Journal of Tropical Medicine and Hygiene, 2004, 70, 27-32.	0.6	57
5	Emerging polymorphisms in falciparum Kelch 13 gene in Northeastern region of India. Malaria Journal, 2016, 15, 583.	0.8	51
6	Comparative susceptibility of different members of the Anopheles culicifacies complex to Plasmodium vivax. Transactions of the Royal Society of Tropical Medicine and Hygiene, 1999, 93, 573-577.	0.7	47
7	The burden of submicroscopic and asymptomatic malaria in India revealed from epidemiology studies at three varied transmission sites in India. Scientific Reports, 2019, 9, 17095.	1.6	44
8	IDENTIFICATION OF ALL MEMBERS OF THE ANOPHELES CULICIFACIES COMPLEX USING ALLELE-SPECIFIC POLYMERASE CHAIN REACTION ASSAYS. American Journal of Tropical Medicine and Hygiene, 2006, 75, 454-460.	0.6	42
9	Presence of two alternative kdr-like mutations, L1014F and L1014S, and a novel mutation, V1010L, in the voltage gated Na+ channel of Anopheles culicifacies from Orissa, India. Malaria Journal, 2010, 9, 146.	0.8	41
10	A Method for Amplicon Deep Sequencing of Drug Resistance Genes in Plasmodium falciparum Clinical Isolates from India. Journal of Clinical Microbiology, 2016, 54, 1500-1511.	1.8	41
11	Knockdown resistance (kdr)-like mutations in the voltage-gated sodium channel of a malaria vector Anopheles stephensi and PCR assays for their detection. Malaria Journal, 2011, 10, 59.	0.8	40
12	Genetic evidence for malaria vectors of the Anopheles sundaicus complex in Sri Lanka with morphological characteristics attributed to Anopheles subpictus species B. Malaria Journal, 2010, 9, 343.	0.8	37
13	Gut microbes influence fitness and malaria transmission potential of Asian malaria vector Anopheles stephensi. Acta Tropica, 2013, 128, 41-47.	0.9	37
14	Molecular evidence of misidentification of Anopheles minimus as Anopheles fluviatilis in Assam (India). Acta Tropica, 2010, 113, 241-244.	0.9	35
15	Responsiveness in Parentâ€Adolescent Relationships: Are Influences Conditional? Does the Reporter Matter?. Journal of Marriage and Family, 2008, 70, 1015-1029.	1.6	34
16	PCR-based methods for the detection of L1014 kdr mutation in Anopheles culicifacies sensu lato. Malaria Journal, 2009, 8, 154.	0.8	32
17	COMPARATIVE SUSCEPTIBILITY OF THREE IMPORTANT MALARIA VECTORS ANOPHELES STEPHENSI, ANOPHELES FLUVIATILIS, AND ANOPHELES SUNDAICUS TO PLASMODIUM VIVAX. Journal of Parasitology, 2005, 91, 79-82.	0.3	30
18	An allele-specific polymerase chain reaction assay for the differentiation of members of theAnopheles culicifacies complex. Journal of Biosciences, 2004, 29, 275-280.	0.5	29

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19	Evidence for natural vertical transmission of chikungunya viruses in field populations of Aedes aegypti in Delhi and Haryana states in India—a preliminary report. Acta Tropica, 2016, 162, 46-55.	0.9	28
20	Alleles â^'308A and â^'1031C in the TNF-α gene promoter do not increase the risk but associated with circulating levels of TNF-α and clinical features of vivax malaria in Indian patients. Molecular Immunology, 2008, 45, 1682-1692.	1.0	27
21	On the conspecificity ofAnopheles fluviatilis species S withAnopheles minimus species C. Journal of Biosciences, 2006, 31, 671-677.	0.5	25
22	iNOS polymorphism modulates iNOS/NO expression via impaired antioxidant and ROS content in P. vivax and P. falciparum infection. Redox Biology, 2018, 15, 192-206.	3.9	25
23	Numerical evaluation of the Hankel transform by using linear Legendre multi-wavelets. Computer Physics Communications, 2008, 179, 424-429.	3.0	24
24	Differentiation of members of the Anopheles fluviatilis species complex by an allele-specific polymerase chain reaction based on 28S ribosomal DNA sequences. American Journal of Tropical Medicine and Hygiene, 2004, 70, 27-32.	0.6	23
25	Population Genetics, Evolutionary Genomics, and Genome-Wide Studies of Malaria: A View Across the International Centers of Excellence for Malaria Research. American Journal of Tropical Medicine and Hygiene, 2015, 93, 87-98.	0.6	22
26	Evaluation of SYBR green I based visual loop-mediated isothermal amplification (LAMP) assay for genus and species-specific diagnosis of malaria in and endemic regions. Journal of Vector Borne Diseases, 2017, 54, 54-60.	0.1	22
27	Isolation of a Plasmodium vivax refractory Anopheles culicifacies strain from India. Tropical Medicine and International Health, 2006, 11, 197-203.	1.0	21
28	A new knockdown resistance (kdr) mutation, F1534L, in the voltage-gated sodium channel of Aedes aegypti, co-occurring with F1534C, S989P and V1016C. Parasites and Vectors, 2020, 13, 327.	1.0	20
29	Comparison of three PCR-based assays for the non-invasive diagnosis of malaria: detection of Plasmodium parasites in blood and saliva. European Journal of Clinical Microbiology and Infectious Diseases, 2014, 33, 1631-1639.	1.3	19
30	Knockdown resistance (kdr) mutations in Indian Anopheles culicifacies populations. Parasites and Vectors, 2015, 8, 333.	1.0	18
31	First report on the transmission of Zika virus by Aedes (Stegomyia) aegypti (L.) (Diptera: Culicidae) during the 2018 Zika outbreak in India. Acta Tropica, 2019, 199, 105114.	0.9	17
32	Remodeling of human red cells infected with Plasmodium falciparum and the impact of PHIST proteins. Blood Cells, Molecules, and Diseases, 2013, 51, 195-202.	0.6	16
33	Role of IL-1β, IL-6 and TNF-α cytokines and TNF-α promoter variability in Plasmodium vivax infection during pregnancy in endemic population of Jharkhand, India. Molecular Immunology, 2018, 97, 82-93.	1.0	16
34	Knockdown Resistance ( <i>kdr</i> ) Mutations in Indian <i>Anopheles stephensi</i> (Diptera: Culicidae) Populations. Journal of Medical Entomology, 2016, 53, 315-320.	0.9	15
35	Antibody responses within two leading Plasmodium vivax vaccine candidate antigens in three geographically diverse malaria-endemic regions of India. Malaria Journal, 2019, 18, 425.	0.8	15
36	Analysis of population genetic structure of Indian Anopheles culicifacies species A using microsatellite markers. Parasites and Vectors, 2013, 6, 166.	1.0	14

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37	Microsatellite analysis of chloroquine resistance associated alleles and neutral loci reveal genetic structure of Indian Plasmodium falciparum. Infection, Genetics and Evolution, 2013, 19, 164-175.	1.0	13
38	L1014F-kdr Mutation in Indian Anopheles subpictus (Diptera: Culicidae) Arising From Two Alternative Transversions in the Voltage-Gated Sodium Channel and a Single PIRA-PCR for Their Detection. Journal of Medical Entomology, 2015, 52, 24-27.	0.9	13
39	Intragenomic sequence variations in the second internal transcribed spacer (ITS2) ribosomal DNA of the malaria vector Anopheles stephensi. PLoS ONE, 2021, 16, e0253173.	1.1	13
40	Polymorphism in drug resistance genes dihydrofolate reductase and dihydropteroate synthase in Plasmodium falciparum in some states of India. Parasites and Vectors, 2015, 8, 471.	1.0	12
41	Malaria transmission in Tripura: Disease distribution & determinants. Indian Journal of Medical Research, 2015, 142, 12.	0.4	12
42	Insights into the invasion biology of Plasmodium vivax. Frontiers in Cellular and Infection Microbiology, 2013, 3, 8.	1.8	11
43	Disagreement in genotyping results of drug resistance alleles of the Plasmodium falciparum dihydrofolate reductase (Pfdhfr) gene by allele-specific PCR (ASPCR) assays and Sanger sequencing. Parasitology Research, 2016, 115, 323-328.	0.6	11
44	Species B of Anopheles culicifacies (Diptera: Culicidae) is reproductively less fit than species A and C of the complex. Acta Tropica, 2009, 112, 316-319.	0.9	10
45	Assessing the genetic diversity of the vir genes in Indian Plasmodium vivax population. Acta Tropica, 2012, 124, 133-139.	0.9	10
46	Population cytogenetic and molecular evidence for existence of a new species in Anopheles fluviatilis complex (Diptera: Culicidae). Infection, Genetics and Evolution, 2013, 13, 218-223.	1.0	10
47	MERA India: Malaria Elimination Research Alliance India. Journal of Vector Borne Diseases, 2019, 56, 1.	0.1	10
48	Pathogenic involvement of Mallophaga. Zeitschrift Für Angewandte Entomologie, 1985, 99, 294-301.	0.0	9
49	Phylogenetic inference of Indian malaria vectors from multilocus DNA sequences. Infection, Genetics and Evolution, 2010, 10, 755-763.	1.0	9
50	Relative Abundance and Plasmodium Infection Rates of Malaria Vectors in and around Jabalpur, a Malaria Endemic Region in Madhya Pradesh State, Central India. PLoS ONE, 2015, 10, e0126932.	1.1	9
51	Molecular forms of Anopheles subpictus and Anopheles sundaicus in the Indian subcontinent. Malaria Journal, 2020, 19, 417.	0.8	9
52	Multilocus nuclear DNA markers and genetic parameters in an Indian Anopheles minimus population. Infection, Genetics and Evolution, 2011, 11, 572-579.	1.0	8
53	Molecular characterization and expression profile of an alternate proliferating cell nuclear antigen homolog PbPCNA2 in <i>Plasmodium berghei</i> . IUBMB Life, 2019, 71, 1293-1301.	1.5	8
54	Dissecting The role of <i>Plasmodium</i> metacaspase-2 in malaria gametogenesis and sporogony. Emerging Microbes and Infections, 2022, 11, 938-955.	3.0	8

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55	Modified PCR-based assay for the differentiation of members of Anopheles fluviatilis complex in consequence of the discovery of a new cryptic species (species V). Malaria Journal, 2020, 19, 96.	0.8	6
56	Molecular analysis of reticulocyte binding protein-2 gene in Plasmodium vivax isolates from India. BMC Microbiology, 2012, 12, 243.	1.3	5
57	Reduced heterozygosity at intragenic and flanking microsatellites of pfcrt gene establishes natural selection based molecular evolution of chloroquine-resistant Plasmodium falciparum in India. Infection, Genetics and Evolution, 2013, 20, 407-412.	1.0	5
58	Genetic diversity and allelic variation in MSP3α gene of paired clinical Plasmodium vivax isolates from Delhi, India. Journal of Infection and Public Health, 2019, 12, 576-584.	1.9	5
59	Isolation and characterization of microsatellite markers from malaria vector, Anopheles culicifacies. Molecular Ecology Notes, 2004, 4, 440-442.	1.7	4
60	kdr-like mutations in the voltage gated sodium channel of a malaria vector Anopheles stephensi and development of PCR-based assays for their detection. Malaria Journal, 2010, 9, .	0.8	3
61	Laboratory Colonization of Anopheles fluviatilis Species T and U. Journal of Medical Entomology, 2011, 48, 395-397.	0.9	3
62	Identification of avir-orthologous immune evasion gene family from primate malaria parasites. Parasitology, 2014, 141, 641-645.	0.7	3
63	<scp><i>Aedes aegypti</i></scp> lachesin protein binds to the domain III of envelop protein of Dengue virusâ€2 and inhibits viral replication. Cellular Microbiology, 2020, 22, e13200.	1.1	3
64	Genetic diversity in two leading Plasmodium vivax malaria vaccine candidates AMA1 and MSP119 at three sites in India. PLoS Neglected Tropical Diseases, 2021, 15, e0009652.	1.3	3
65	Are members of the Anopheles fluviatilis complex conspecific?. Acta Tropica, 2021, 224, 106149.	0.9	3
66	Protein trafficking in Plasmodium falciparum-infected red cells and impact of the expansion of exported protein families. Parasitology, 2014, 141, 1533-1543.	0.7	2
67	Isolation and Characterization of Polymorphic Microsatellite Markers from the Malaria Vector Anopheles fluviatilis Species T (Diptera: Culicidae). Journal of Medical Entomology, 2015, 52, 408-412.	0.9	2
68	Susceptibility of Species A, B, and C of Anopheles culicifacies Complex to Plasmodium yoelii yoelii and Plasmodium vinckei petteri Infections. Journal of Parasitology, 2000, 86, 1345.	0.3	1
69	Case study of misdiagnosis of malaria in primary care set-up leading to rapid complications and death in a high malaria endemic district of India. Journal of Vector Borne Diseases, 2020, 57, 378.	0.1	1
70	Morphological and odorantâ€binding protein 1 gene intron 1 sequence variations in <i>Anopheles stephensi</i> from Jaffna city in northern Sri Lanka. Medical and Veterinary Entomology, 2022, 36, 496-502.	0.7	1
71	The repertoire diversity of the Plasmodium falciparum stevor multigene family in complicated and uncomplicated malaria in India. Malaria Journal, 2012, 11, .	0.8	0
72	Comparative Susceptibilities of Species T and U of theAnopheles fluviatilisComplex toPlasmodium vinckei petteriSporogony. Journal of Medical Entomology, 2013, 50, 594-597.	0.9	0

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73	Studies on Plasmodium Falciparum Drug Resistance in Endemic Regions of India. Indo Global Journal of Pharmaceutical Sciences, 2014, 04, .	0.3	0
74	Isolation and Characterization of Microsatellite Markers from the Malaria Vector Anopheles Fluviatilis Species T. Indo Global Journal of Pharmaceutical Sciences, 2014, 04, .	0.3	0
75	Population genetic structure of the malaria vector <i>Anopheles fluviatilis</i> species T (Diptera:) Tj ETQq1 1 0.7	'84314 rgE 0.7	BT /Overlock
76	First report of classical knockdown resistance ( <i>kdr</i> ) mutation, <scp>L1014F</scp> , in human head louse <i>Pediculus humanus capitis</i> (Phthiraptera: Anoplura). Medical and Veterinary Entomology, 2023, 37, 209-212.	0.7	0