

Priya Duggal

List of Publications by Year in descending order

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Version: 2024-02-01

116
papers

5,042
citations

81900

39
h-index

102487

66
g-index

132
all docs

132
docs citations

132
times ranked

8788
citing authors

#	ARTICLE	IF	CITATIONS
1	Analysis of antibody binding specificities in twin and SNP-genotyped cohorts reveals that antiviral antibody epitope selection is a heritable trait. <i>Immunity</i> , 2022, 55, 174-184.e5.	14.3	22
2	Postâ€sequelae symptoms and comorbidities after COVIDâ€19. <i>Journal of Medical Virology</i> , 2022, 94, 2060-2066.	5.0	14
3	Trans-ancestral fine-mapping of MHC reveals key amino acids associated with spontaneous clearance of hepatitis C in HLA-DQ ²¹ . <i>American Journal of Human Genetics</i> , 2022, 109, 299-310.	6.2	6
4	Genome-Wide Association Study of Campylobacter <i>-</i> Positive Diarrhea Identifies Genes Involved in Toxin Processing and Inflammatory Response. <i>MBio</i> , 2022, 13, e0055622.	4.1	5
5	Benchmarking statistical methods for analyzing parentâ€child dyads in genetic association studies. <i>Genetic Epidemiology</i> , 2022, 46, 266-284.	1.3	2
6	A Multiancestry Sex-Stratified Genome-Wide Association Study of Spontaneous Clearance of Hepatitis C Virus. <i>Journal of Infectious Diseases</i> , 2021, 223, 2090-2098.	4.0	5
7	Acute flaccid myelitis: cause, diagnosis, and management. <i>Lancet, The</i> , 2021, 397, 334-346.	13.7	88
8	Enterovirus D68 molecular and cellular biology and pathogenesis. <i>Journal of Biological Chemistry</i> , 2021, 296, 100317.	3.4	19
9	Genetic association of ERAP1 and ERAP2 with eclampsia and preeclampsia in northeastern Brazilian women. <i>Scientific Reports</i> , 2021, 11, 6764.	3.3	9
10	APOL1 variant alleles associate with reduced risk for opportunistic infections in HIV infection. <i>Communications Biology</i> , 2021, 4, 284.	4.4	4
11	Host Genome-Wide Association Study of Infant Susceptibility to <i>Shigella</i>-Associated Diarrhea. <i>Infection and Immunity</i> , 2021, 89, .	2.2	12
12	Role of direct and indirect social and spatial ties in the diffusion of HIV and HCV among people who inject drugs: a cross-sectional community-based network analysis in New Delhi, India. <i>ELife</i> , 2021, 10, .	6.0	3
13	Spatiotemporal Phylodynamics of Hepatitis C Among People Who Inject Drugs in India. <i>Hepatology</i> , 2021, 74, 1782-1794.	7.3	6
14	Increased Rate of Epigenetic Aging in Men Living With HIV Prior to Treatment. <i>Frontiers in Genetics</i> , 2021, 12, 796547.	2.3	9
15	Prevalence and Phylogenetic Characterization of Hepatitis C Virus Among Indian Men Who Have Sex With Men: Limited Evidence for Sexual Transmission. <i>Journal of Infectious Diseases</i> , 2020, 221, 1875-1883.	4.0	4
16	The Ethics of Precision Rationing: Human Genetics and the Need for Debate on Stratifying Access to Medication. <i>Public Health Genomics</i> , 2020, 23, 149-154.	1.0	2
17	HLA tapasin independence: broader peptide repertoire and HIV control. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 28232-28238.	7.1	51
18	Multi-ancestry fine mapping of interferon lambda and the outcome of acute hepatitis C virus infection. <i>Genes and Immunity</i> , 2020, 21, 348-359.	4.1	5

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19	Mendelian Randomization Analysis of n-6 Polyunsaturated Fatty Acid Levels and Pancreatic Cancer Risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2020, 29, 2735-2739.	2.5	6
20	The Role of Host Genetic Factors in Coronavirus Susceptibility: Review of Animal and Systematic Review of Human Literature. <i>American Journal of Human Genetics</i> , 2020, 107, 381-402.	6.2	51
21	Genomics in the era of COVID-19: ethical implications for clinical practice and public health. <i>Genome Medicine</i> , 2020, 12, 95.	8.2	9
22	Obesity could shift severe COVID-19 disease to younger ages. <i>Lancet</i> , The, 2020, 395, 1544-1545.	13.7	364
23	Genome-Wide Association Study of Cryptosporidiosis in Infants Implicates <i>PRKCA</i> . <i>MBio</i> , 2020, 11, .	4.1	20
24	Genomics and Infectious Diseases: Expert Perspectives on Public Health Considerations regarding Actionability and Privacy. <i>Ethics & Human Research</i> , 2020, 42, 30-40.	0.9	5
25	Perspectives on the Future of Epidemiology: A Framework for Training. <i>American Journal of Epidemiology</i> , 2020, 189, 634-639.	3.4	7
26	The Evolving Field of Genetic Epidemiology: From Familial Aggregation to Genomic Sequencing. <i>American Journal of Epidemiology</i> , 2019, 188, 2069-2077.	3.4	6
27	Personal Genetic Information about HIV: Research Participants' Views of Ethical, Social, and Behavioral Implications. <i>Public Health Genomics</i> , 2019, 22, 36-45.	1.0	3
28	Heritability analysis of nontraditional glycemc biomarkers in the Atherosclerosis Risk in Communities Study. <i>Genetic Epidemiology</i> , 2019, 43, 776-785.	1.3	8
29	Analysis of Heritability and Genetic Architecture of Pancreatic Cancer: A PanC4 Study. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2019, 28, 1238-1245.	2.5	48
30	Association of <i>FMO3</i> Variants with Blood Pressure in the Atherosclerosis Risk in Communities Study. <i>International Journal of Hypertension</i> , 2019, 2019, 1-8.	1.3	3
31	Multi-Ancestry Genome-Wide Association Study of Spontaneous Clearance of Hepatitis C Virus. <i>Gastroenterology</i> , 2019, 156, 1496-1507.e7.	1.3	32
32	Rare variants in <i>SLC5A10</i> are associated with serum 1,5-anhydroglucitol (1,5-AG) in the Atherosclerosis Risk in Communities (ARIC) Study. <i>Scientific Reports</i> , 2019, 9, 5941.	3.3	9
33	Case-Control Study of <i>Cryptosporidium</i> Transmission in Bangladeshi Households. <i>Clinical Infectious Diseases</i> , 2019, 68, 1073-1079.	5.8	28
34	Clinical Subpopulations in a Sample of North American Children Diagnosed With Acute Flaccid Myelitis, 2012-2016. <i>JAMA Pediatrics</i> , 2019, 173, 134.	6.2	51
35	Genotype imputation performance of three reference panels using African ancestry individuals. <i>Human Genetics</i> , 2018, 137, 281-292.	3.8	38
36	Epidemiology and Risk Factors for Cryptosporidiosis in Children From 8 Low-income Sites: Results From the MAL-ED Study. <i>Clinical Infectious Diseases</i> , 2018, 67, 1660-1669.	5.8	41

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37	Exome Array Analysis of Nuclear Lens Opacity. <i>Ophthalmic Epidemiology</i> , 2018, 25, 215-219.	1.7	3
38	Refraction and Change in Refraction Over a 20-Year Period in the Beaver Dam Eye Study. , 2018, 59, 4518.		18
39	Genome-Wide Association Study Reveals Genetic Link between Diarrhea-Associated <i>Entamoeba histolytica</i> Infection and Inflammatory Bowel Disease. <i>MBio</i> , 2018, 9, .	4.1	23
40	A high-throughput sequencing assay to comprehensively detect and characterize unicellular eukaryotes and helminths from biological and environmental samples. <i>Microbiome</i> , 2018, 6, 195.	11.1	21
41	Association analysis of exome variants and refraction, axial length, and corneal curvature in a European-American population. <i>Human Mutation</i> , 2018, 39, 1973-1979.	2.5	3
42	Genome-Wide Association Study of Serum Fructosamine and Glycated Albumin in Adults Without Diagnosed Diabetes: Results From the Atherosclerosis Risk in Communities Study. <i>Diabetes</i> , 2018, 67, 1684-1696.	0.6	16
43	Epidemiology at a time for unity. <i>International Journal of Epidemiology</i> , 2018, 47, 1366-1371.	1.9	6
44	Does Malnutrition Have a Genetic Component?. <i>Annual Review of Genomics and Human Genetics</i> , 2018, 19, 247-262.	6.2	17
45	Comprehensive candidate gene analysis for symptomatic or asymptomatic outcomes of <i>Leishmania infantum</i> infection in Brazil. <i>Annals of Human Genetics</i> , 2017, 81, 41-48.	0.8	8
46	Whole-Exome Sequencing Identifies the 6q12-q16 Linkage Region and a Candidate Gene, <i>TTK</i> , for Pulmonary Nontuberculous Mycobacterial Disease. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2017, 196, 1599-1604.	5.6	28
47	Fine-mapping of genetic loci driving spontaneous clearance of hepatitis C virus infection. <i>Scientific Reports</i> , 2017, 7, 15843.	3.3	6
48	Natural History of Cryptosporidiosis in a Longitudinal Study of Slum-Dwelling Bangladeshi Children: Association with Severe Malnutrition. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004564.	3.0	78
49	Fine mapping under linkage peaks for symptomatic or asymptomatic outcomes of <i>Leishmania infantum</i> infection in Brazil. <i>Infection, Genetics and Evolution</i> , 2016, 43, 1-5.	2.3	6
50	MicroRNA-related polymorphisms and non-Hodgkin lymphoma susceptibility in the Multicenter AIDS Cohort Study. <i>Cancer Epidemiology</i> , 2016, 45, 47-57.	1.9	21
51	Role of nucleotide-binding oligomerization domain 1 (NOD1) and its variants in human cytomegalovirus control in vitro and in vivo. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E7818-E7827.	7.1	30
52	Polymorphisms in melanoma differentiation-associated gene 5 are not associated with clearance of hepatitis C virus in a European American population. <i>Hepatology</i> , 2016, 63, 1061-1062.	7.3	3
53	Genetic Epidemiology and Public Health: The Evolution From Theory to Technology. <i>American Journal of Epidemiology</i> , 2016, 183, 387-393.	3.4	12
54	Variation in PTCHD2, CRISP3, NAP1L4, FSCB, and AP3B2 associated with spherical equivalent. <i>Molecular Vision</i> , 2016, 22, 783-96.	1.1	8

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55	Lipid levels in HIV-positive men receiving anti-retroviral therapy are not associated with copy number variation of reverse cholesterol transport pathway genes. <i>BMC Research Notes</i> , 2015, 8, 697.	1.4	0
56	Exome Array Analysis Identifies CAV1/CAV2 as a Susceptibility Locus for Intraocular Pressure. <i>Investigative Ophthalmology and Visual Science</i> , 2015, 56, 544-551.	3.3	43
57	Pulmonary Nontuberculous Mycobacterial Infection. A Multisystem, Multigenic Disease. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2015, 192, 618-628.	5.6	136
58	Gene-Gene Interaction Among <i>WNT</i> Genes for Oral Cleft in Trios. <i>Genetic Epidemiology</i> , 2015, 39, 385-394.	1.3	30
59	Relative performance of gene- and pathway-level methods as secondary analyses for genome-wide association studies. <i>BMC Genetics</i> , 2015, 16, 34.	2.7	34
60	Variants in HAVCR1 Gene Region Contribute to Hepatitis C Persistence in African Americans. <i>Journal of Infectious Diseases</i> , 2014, 209, 355-359.	4.0	13
61	LILRB2 Interaction with HLA Class I Correlates with Control of HIV-1 Infection. <i>PLoS Genetics</i> , 2014, 10, e1004196.	3.5	83
62	Genomics and infectious disease: a call to identify the ethical, legal and social implications for public health and clinical practice. <i>Genome Medicine</i> , 2014, 6, 106.	8.2	31
63	Role of Leptin-Mediated Colonic Inflammation in Defense against <i>Clostridium difficile</i> Colitis. <i>Infection and Immunity</i> , 2014, 82, 341-349.	2.2	46
64	Distinct Assembly Profiles of HLA-B Molecules. <i>Journal of Immunology</i> , 2014, 192, 4967-4976.	0.8	85
65	Preeclampsia is associated with increased maternal body weight in a northeastern Brazilian population. <i>BMC Pregnancy and Childbirth</i> , 2013, 13, 159.	2.4	17
66	Genome-Wide Association Study of Spontaneous Resolution of Hepatitis C Virus Infection: Data From Multiple Cohorts. <i>Annals of Internal Medicine</i> , 2013, 158, 235.	3.9	187
67	Large scale international replication and meta-analysis study confirms association of the 15q14 locus with myopia. The CREAM consortium. <i>Human Genetics</i> , 2012, 131, 1467-1480.	3.8	67
68	Polymorphisms in Toll-like receptor genes influence antibody responses to cytomegalovirus glycoprotein B vaccine. <i>BMC Research Notes</i> , 2012, 5, 140.	1.4	24
69	The expression of REG 1A and REG 1B is increased during acute amebic colitis. <i>Parasitology International</i> , 2011, 60, 296-300.	1.3	45
70	A mutation in the leptin receptor is associated with <i>Entamoeba histolytica</i> infection in children. <i>Journal of Clinical Investigation</i> , 2011, 121, 1191-1198.	8.2	127
71	Current Gene Discovery Strategies for Ocular Conditions. , 2011, 52, 7761.		4
72	Identification of functional genetic variation in exome sequence analysis. <i>BMC Proceedings</i> , 2011, 5, S13.	1.6	9

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73	Gene-environment interplay in common complex diseases: forging an integrative model—recommendations from an NIH workshop. <i>Genetic Epidemiology</i> , 2011, 35, 217-225.	1.3	95
74	Decreased dyskerin levels as a mechanism of telomere shortening in X-linked dyskeratosis congenita. <i>Journal of Medical Genetics</i> , 2011, 48, 327-333.	3.2	55
75	Linkage Analysis of Quantitative Refraction and Refractive Errors in the Beaver Dam Eye Study. , 2011, 52, 5220.		18
76	Leptin signaling in intestinal epithelium mediates resistance to enteric infection by <i>Entamoeba histolytica</i> . <i>Mucosal Immunology</i> , 2011, 4, 294-303.	6.0	102
77	Genome-wide Linkage Analysis of Multiple Metabolic Factors: Evidence of Genetic Heterogeneity. <i>Obesity</i> , 2010, 18, 146-152.	3.0	6
78	Association between TNF- α and <i>Entamoeba histolytica</i> Diarrhea. <i>American Journal of Tropical Medicine and Hygiene</i> , 2010, 82, 620-625.	1.4	37
79	Large-scale Candidate Gene Analysis of Spontaneous Clearance of Hepatitis C Virus. <i>Journal of Infectious Diseases</i> , 2010, 201, 1371-1380.	4.0	56
80	Deficient Serum Mannose-binding Lectin Levels and MBL2 Polymorphisms Increase the Risk of Single and Recurrent <i>Cryptosporidium</i> Infections in Young Children. <i>Journal of Infectious Diseases</i> , 2009, 200, 1540-1547.	4.0	33
81	Association of malnutrition with amebiasis. <i>Nutrition Reviews</i> , 2009, 67, S207-S215.	5.8	44
82	Genetic Admixture in Brazilians Exposed to Infection with <i>Leishmania chagasi</i> . <i>Annals of Human Genetics</i> , 2009, 73, 304-313.	0.8	21
83	Heritability Analysis of Spherical Equivalent, Axial Length, Corneal Curvature, and Anterior Chamber Depth in the Beaver Dam Eye Study. <i>JAMA Ophthalmology</i> , 2009, 127, 649.	2.4	91
84	Examining the effect of linkage disequilibrium between markers on the Type I error rate and power of nonparametric multipoint linkage analysis of two-generation and multigenerational pedigrees in the presence of missing genotype data. <i>Genetic Epidemiology</i> , 2008, 32, 41-51.	1.3	7
85	Establishing an adjusted p-value threshold to control the family-wide type 1 error in genome wide association studies. <i>BMC Genomics</i> , 2008, 9, 516.	2.8	287
86	Association between <i>Cryptosporidium</i> Infection and Human Leukocyte Antigen Class I and Class II Alleles. <i>Journal of Infectious Diseases</i> , 2008, 197, 474-478.	4.0	40
87	Genes Influencing Susceptibility to Infection. <i>Journal of Infectious Diseases</i> , 2008, 197, 4-6.	4.0	13
88	Polymorphisms of CUL5 Are Associated with CD4+ T Cell Loss in HIV-1 Infected Individuals. <i>PLoS Genetics</i> , 2007, 3, e19.	3.5	47
89	Genetic Predisposition to Self-curing Infection with the Protozoan <i>Leishmania chagasi</i> : A Genomewide Scan. <i>Journal of Infectious Diseases</i> , 2007, 196, 1261-1269.	4.0	52
90	The GLC1H Glaucoma Locus May Reflect Glaucoma With Elevated Intraocular Pressure. <i>JAMA Ophthalmology</i> , 2007, 125, 1716.	2.4	3

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91	Confirmation of Linkage to Ocular Refraction on Chromosome 22q and Identification of a Novel Linkage Region on 1q. <i>JAMA Ophthalmology</i> , 2007, 125, 80.	2.4	47
92	Identification of Novel Genetic Loci for Intraocular Pressure. <i>JAMA Ophthalmology</i> , 2007, 125, 74.	2.4	47
93	KLF6 IVS1 -27G>A Variant and the Risk of Prostate Cancer in Finland. <i>European Urology</i> , 2007, 52, 1076-1081.	1.9	14
94	CORRELATION OF INTERFERON- γ PRODUCTION BY PERIPHERAL BLOOD MONONUCLEAR CELLS WITH CHILDHOOD MALNUTRITION AND SUSCEPTIBILITY TO AMEBIASIS. <i>American Journal of Tropical Medicine and Hygiene</i> , 2007, 76, 340-344.	1.4	79
95	Correlation of interferon-gamma production by peripheral blood mononuclear cells with childhood malnutrition and susceptibility to amebiasis. <i>American Journal of Tropical Medicine and Hygiene</i> , 2007, 76, 340-4.	1.4	43
96	Comparison of SNP tagging methods using empirical data: association study of 713 SNPs on chromosome 12q14.3â€“12q24.21 for asthma and total serum IgE in an African Caribbean population. <i>Genetic Epidemiology</i> , 2006, 30, 609-619.	1.3	37
97	Profiling Genetic Variation along the Androgen Biosynthesis and Metabolism Pathways Implicates Several Single Nucleotide Polymorphisms and Their Combinations as Prostate Cancer Risk Factors. <i>Cancer Research</i> , 2006, 66, 743-747.	0.9	54
98	IL6 γ 174 G/C Promoter Polymorphism Influences Susceptibility to Mucosal but Not Localized Cutaneous Leishmaniasis in Brazil. <i>Journal of Infectious Diseases</i> , 2006, 194, 519-527.	4.0	87
99	<i>Entamoeba histolytica</i> Infection in Children and Protection from Subsequent Amebiasis. <i>Infection and Immunity</i> , 2006, 74, 904-909.	2.2	166
100	Haplotypes and haplotype-tagging single-nucleotide polymorphism: Presentation Group 8 of Genetic Analysis Workshop 14. <i>Genetic Epidemiology</i> , 2005, 29, S59-S71.	1.3	11
101	Investigation of altering single-nucleotide polymorphism density on the power to detect trait loci and frequency of false positive in nonparametric linkage analyses of qualitative traits. <i>BMC Genetics</i> , 2005, 6, S20.	2.7	5
102	Identification of tag single-nucleotide polymorphisms in regions with varying linkage disequilibrium. <i>BMC Genetics</i> , 2005, 6, S73.	2.7	7
103	A Genetic Contribution to Intraocular Pressure: The Beaver Dam Eye Study. , 2005, 46, 555.		50
104	Support for Polygenic Influences on Ocular Refractive Error. , 2005, 46, 442.		51
105	Polygenic Effects and Cigarette Smoking Account for a Portion of the Familial Aggregation of Nuclear Sclerosis. <i>American Journal of Epidemiology</i> , 2005, 161, 707-713.	3.4	17
106	The Effect of RANTES Chemokine Genetic Variants on Early HIV-1 Plasma RNA Among African American Injection Drug Users. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2005, 38, 584-589.	2.1	24
107	An Emerging Peri-Urban Pattern of Infection with <i>Leishmania chagasi</i> , the Protozoan Causing Visceral Leishmaniasis in Northeast Brazil. <i>Scandinavian Journal of Infectious Diseases</i> , 2004, 36, 443-449.	1.5	77
108	Influence of Human Leukocyte Antigen Class II Alleles on Susceptibility to <i>Entamoeba histolytica</i> Infection in Bangladeshi Children. <i>Journal of Infectious Diseases</i> , 2004, 189, 520-526.	4.0	85

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109	APOBEC3G Genetic Variants and Their Influence on the Progression to AIDS. Journal of Virology, 2004, 78, 11070-11076.	3.4	178
110	High prevalence of V37I genetic variant in the connexin-26 (GJB2) gene among non-syndromic hearing-impaired and control Thai individuals. Clinical Genetics, 2004, 66, 452-460.	2.0	75
111	GeneLink: a database to facilitate genetic studies of complex traits. BMC Genomics, 2004, 5, 81.	2.8	7
112	Comprehensive Analysis of Class I and Class II HLA Antigens and Chronic Hepatitis B Virus Infection. Journal of Virology, 2003, 77, 12083-12087.	3.4	133
113	Innate and Acquired Resistance to Amebiasis in Bangladeshi Children. Journal of Infectious Diseases, 2002, 186, 547-552.	4.0	140
114	Sodium channel abnormalities are infrequent in patients with long QT Syndrome: Identification of two novel SCN5A mutations. , 1999, 86, 470-476.		48
115	Multiple different missense mutations in the pore region of HERG in patients with long QT syndrome. Human Genetics, 1998, 102, 265-272.	3.8	57
116	Mutation of the Gene for I sK Associated With Both Jervell and Lange-Nielsen and Romano-Ward Forms of Long-QT Syndrome. Circulation, 1998, 97, 142-146.	1.6	205