Priya Duggal

List of Publications by Year
in descending order

116	5,042	81900	102487
papers	citations	39 h-index	66 g-index

132	132	132	8788
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Obesity could shift severe COVID-19 disease to younger ages. Lancet, The, 2020, 395, 1544-1545.	13.7	364
2	Establishing an adjusted p-value threshold to control the family-wide type 1 error in genome wide association studies. BMC Genomics, 2008, 9, 516.	2.8	287
3	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
4	Genome-Wide Association Study of Spontaneous Resolution of Hepatitis C Virus Infection: Data From Multiple Cohorts. Annals of Internal Medicine, 2013, 158, 235.	3.9	187
5	APOBEC3G Genetic Variants and Their Influence on the Progression to AIDS. Journal of Virology, 2004, 78, 11070-11076.	3.4	178
6	Entamoeba histolytica Infection in Children and Protection from Subsequent Amebiasis. Infection and Immunity, 2006, 74, 904-909.	2.2	166
7	Innate and Acquired Resistance to Amebiasis in Bangladeshi Children. Journal of Infectious Diseases, 2002, 186, 547-552.	4.0	140
8	Pulmonary Nontuberculous Mycobacterial Infection. A Multisystem, Multigenic Disease. American Journal of Respiratory and Critical Care Medicine, 2015, 192, 618-628.	5.6	136
9	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
10	A mutation in the leptin receptor is associated with Entamoeba histolytica infection in children. Journal of Clinical Investigation, 2011, 121, 1191-1198.	8.2	127
11	Leptin signaling in intestinal epithelium mediates resistance to enteric infection by Entamoeba histolytica. Mucosal Immunology, 2011, 4, 294-303.	6.0	102
12	Geneâ€environment interplay in common complex diseases: forging an integrative modelâ€"recommendations from an NIH workshop. Genetic Epidemiology, 2011, 35, 217-225.	1.3	95
13	Heritability Analysis of Spherical Equivalent, Axial Length, Corneal Curvature, and Anterior Chamber Depth in the Beaver Dam Eye Study. JAMA Ophthalmology, 2009, 127, 649.	2.4	91
14	Acute flaccid myelitis: cause, diagnosis, and management. Lancet, The, 2021, 397, 334-346.	13.7	88
15	IL6â^'174 G/C Promoter Polymorphism Influences Susceptibility to Mucosal but Not Localized Cutaneous Leishmaniasis in Brazil. Journal of Infectious Diseases, 2006, 194, 519-527.	4.0	87
16	Influence of Human Leukocyte Antigen Class II Alleles on Susceptibility toEntamoeba histolyticaInfection in Bangladeshi Children. Journal of Infectious Diseases, 2004, 189, 520-526.	4.0	85
17	Distinct Assembly Profiles of HLA-B Molecules. Journal of Immunology, 2014, 192, 4967-4976.	0.8	85
18	LILRB2 Interaction with HLA Class I Correlates with Control of HIV-1 Infection. PLoS Genetics, 2014, 10, e1004196.	3.5	83

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19	CORRELATION OF INTERFERON-Î³ PRODUCTION BY PERIPHERAL BLOOD MONONUCLEAR CELLS WITH CHILDHOOD MALNUTRITION AND SUSCEPTIBILITY TO AMEBIASIS. American Journal of Tropical Medicine and Hygiene, 2007, 76, 340-344.	1.4	79
20	Natural History of Cryptosporidiosis in a Longitudinal Study of Slum-Dwelling Bangladeshi Children: Association with Severe Malnutrition. PLoS Neglected Tropical Diseases, 2016, 10, e0004564.	3.0	78
21	An Emerging Peri-Urban Pattern of Infection with Leishmania chagasi, the Protozoan Causing Visceral Leishmaniasis in Northeast Brazil. Scandinavian Journal of Infectious Diseases, 2004, 36, 443-449.	1.5	77
22	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
23	Large scale international replication and meta-analysis study confirms association of the 15q14 locus with myopia. The CREAM consortium. Human Genetics, 2012, 131, 1467-1480.	3.8	67
24	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
25	Largeâ€Scale Candidate Gene Analysis of Spontaneous Clearance of Hepatitis C Virus. Journal of Infectious Diseases, 2010, 201, 1371-1380.	4.0	56
26	Decreased dyskerin levels as a mechanism of telomere shortening in X-linked dyskeratosis congenita. Journal of Medical Genetics, 2011, 48, 327-333.	3.2	55
27	Profiling Genetic Variation along the Androgen Biosynthesis and Metabolism Pathways Implicates Several Single Nucleotide Polymorphisms and Their Combinations as Prostate Cancer Risk Factors. Cancer Research, 2006, 66, 743-747.	0.9	54
28	Genetic Predisposition to Selfâ€Curing Infection with the ProtozoanLeishmania chagasi:A Genomewide Scan. Journal of Infectious Diseases, 2007, 196, 1261-1269.	4.0	52
29	Support for Polygenic Influences on Ocular Refractive Error. , 2005, 46, 442.		51
30	Clinical Subpopulations in a Sample of North American Children Diagnosed With Acute Flaccid Myelitis, 2012-2016. JAMA Pediatrics, 2019, 173, 134.	6.2	51
31	HLA tapasin independence: broader peptide repertoire and HIV control. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 28232-28238.	7.1	51
32	The Role of Host Genetic Factors in Coronavirus Susceptibility: Review of Animal and Systematic Review of Human Literature. American Journal of Human Genetics, 2020, 107, 381-402.	6.2	51
33	A Genetic Contribution to Intraocular Pressure: The Beaver Dam Eye Study. , 2005, 46, 555.		50
34	Sodium channel abnormalities are infrequent in patients with long QT Syndrome: Identification of two novelSCN5A mutations. , 1999, 86, 470-476.		48
35	Analysis of Heritability and Genetic Architecture of Pancreatic Cancer: A PanC4 Study. Cancer Epidemiology Biomarkers and Prevention, 2019, 28, 1238-1245.	2.5	48
36	Polymorphisms of CUL5 Are Associated with CD4+ T Cell Loss in HIV-1 Infected Individuals. PLoS Genetics, 2007, 3, e19.	3.5	47

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37	Confirmation of Linkage to Ocular Refraction on Chromosome 22q and Identification of a Novel Linkage Region on 1q. JAMA Ophthalmology, 2007, 125, 80.	2.4	47
38	Identification of Novel Genetic Loci for Intraocular Pressure. JAMA Ophthalmology, 2007, 125, 74.	2.4	47
39	Role of Leptin-Mediated Colonic Inflammation in Defense against Clostridium difficile Colitis. Infection and Immunity, 2014, 82, 341-349.	2.2	46
40	The expression of REG 1A and REG 1B is increased during acute amebic colitis. Parasitology International, 2011, 60, 296-300.	1.3	45
41	Association of malnutrition with amebiasis. Nutrition Reviews, 2009, 67, S207-S215.	5.8	44
42	Exome Array Analysis Identifies CAV1/CAV2 as a Susceptibility Locus for Intraocular Pressure. Investigative Ophthalmology and Visual Science, 2015, 56, 544-551.	3.3	43
43	Correlation of interferon-gamma production by peripheral blood mononuclear cells with childhood malnutrition and susceptibility to amebiasis. American Journal of Tropical Medicine and Hygiene, 2007, 76, 340-4.	1.4	43
44	Epidemiology and Risk Factors for Cryptosporidiosis in Children From 8 Low-income Sites: Results From the MAL-ED Study. Clinical Infectious Diseases, 2018, 67, 1660-1669.	5.8	41
45	Association betweenCryptosporidiumInfection and Human Leukocyte Antigen Class I and Class II Alleles. Journal of Infectious Diseases, 2008, 197, 474-478.	4.0	40
46	Genotype imputation performance of three reference panels using African ancestry individuals. Human Genetics, 2018, 137, 281-292.	3.8	38
47	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. Genetic Epidemiology, 2006, 30, 609-619.	1.3	37
48	Association between TNF-Î± and Entamoeba histolytica Diarrhea. American Journal of Tropical Medicine and Hygiene, 2010, 82, 620-625.	1.4	37
49	Relative performance of gene- and pathway-level methods as secondary analyses for genome-wide association studies. BMC Genetics, 2015, 16, 34.	2.7	34
50	Deficient Serum Mannoseâ€Binding Lectin Levels andMBL2Polymorphisms Increase the Risk of Single and RecurrentCryptosporidiumInfections in Young Children. Journal of Infectious Diseases, 2009, 200, 1540-1547.	4.0	33
51	Multi-Ancestry Genome-Wide Association Study of Spontaneous Clearance of Hepatitis C Virus. Gastroenterology, 2019, 156, 1496-1507.e7.	1.3	32
52	Genomics and infectious disease: a call to identify the ethical, legal and social implications for public health and clinical practice. Genome Medicine, 2014, 6, 106.	8.2	31
53	Geneâ€Gene Interaction Among WNT Genes for Oral Cleft in Trios. Genetic Epidemiology, 2015, 39, 385-394.	1.3	30
54	Role of nucleotide-binding oligomerization domain 1 (NOD1) and its variants in human cytomegalovirus control in vitro and in vivo. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E7818-E7827.	7.1	30

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55	Whole-Exome Sequencing Identifies the 6q12-q16 Linkage Region and a Candidate Gene, TTK, for Pulmonary Nontuberculous Mycobacterial Disease. American Journal of Respiratory and Critical Care Medicine, 2017, 196, 1599-1604.	5.6	28
56	Case-Control Study of Cryptosporidium Transmission in Bangladeshi Households. Clinical Infectious Diseases, 2019, 68, 1073-1079.	5.8	28
57	The Effect of RANTES Chemokine Genetic Variants on Early HIV-1 Plasma RNA Among African American Injection Drug Users. Journal of Acquired Immune Deficiency Syndromes (1999), 2005, 38, 584-589.	2.1	24
58	Polymorphisms in Toll-like receptor genes influence antibody responses to cytomegalovirus glycoprotein B vaccine. BMC Research Notes, 2012, 5, 140.	1.4	24
59	Genome-Wide Association Study Reveals Genetic Link between Diarrhea-Associated Entamoeba histolytica Infection and Inflammatory Bowel Disease. MBio, 2018, 9, .	4.1	23
60	Analysis of antibody binding specificities in twin and SNP-genotyped cohorts reveals that antiviral antibody epitope selection is a heritable trait. Immunity, 2022, 55, 174-184.e5.	14.3	22
61	Genetic Admixture in Brazilians Exposed to Infection with Leishmania chagasi. Annals of Human Genetics, 2009, 73, 304-313.	0.8	21
62	MicroRNA-related polymorphisms and non-Hodgkin lymphoma susceptibility in the Multicenter AIDS Cohort Study. Cancer Epidemiology, 2016, 45, 47-57.	1.9	21
63	A high-throughput sequencing assay to comprehensively detect and characterize unicellular eukaryotes and helminths from biological and environmental samples. Microbiome, 2018, 6, 195.	11.1	21
64	Genome-Wide Association Study of Cryptosporidiosis in Infants Implicates PRKCA. MBio, 2020, 11, .	4.1	20
65	Enterovirus D68 molecular and cellular biology and pathogenesis. Journal of Biological Chemistry, 2021, 296, 100317.	3.4	19
66	Linkage Analysis of Quantitative Refraction and Refractive Errors in the Beaver Dam Eye Study. , 2011, 52, 5220.		18
67	Refraction and Change in Refraction Over a 20-Year Period in the Beaver Dam Eye Study. , 2018, 59, 4518.		18
68	Polygenic Effects and Cigarette Smoking Account for a Portion of the Familial Aggregation of Nuclear Sclerosis. American Journal of Epidemiology, 2005, 161, 707-713.	3.4	17
69	Preeclampsia is associated with increased maternal body weight in a northeastern Brazilian population. BMC Pregnancy and Childbirth, 2013, 13, 159.	2.4	17
70	Does Malnutrition Have a Genetic Component?. Annual Review of Genomics and Human Genetics, 2018, 19, 247-262.	6.2	17
71	Genome-Wide Association Study of Serum Fructosamine and Glycated Albumin in Adults Without Diagnosed Diabetes: Results From the Atherosclerosis Risk in Communities Study. Diabetes, 2018, 67, 1684-1696.	0.6	16
72	KLF6 IVS1 -27G>A Variant and the Risk of Prostate Cancer in Finland. European Urology, 2007, 52, 1076-1081.	1.9	14

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73	Postâ€sequelae symptoms and comorbidities after COVIDâ€19. Journal of Medical Virology, 2022, 94, 2060-2066.	5.0	14
74	Genes Influencing Susceptibility to Infection. Journal of Infectious Diseases, 2008, 197, 4-6.	4.0	13
75	Variants in HAVCR1 Gene Region Contribute to Hepatitis C Persistence in African Americans. Journal of Infectious Diseases, 2014, 209, 355-359.	4.0	13
76	Genetic Epidemiology and Public Health: The Evolution From Theory to Technology. American Journal of Epidemiology, 2016, 183, 387-393.	3.4	12
77	Host Genome-Wide Association Study of Infant Susceptibility toShigella-Associated Diarrhea. Infection and Immunity, 2021, 89, .	2.2	12
78	Haplotypes and haplotype-tagging single-nucleotide polymorphism: Presentation Group 8 of Genetic Analysis Workshop 14. Genetic Epidemiology, 2005, 29, S59-S71.	1.3	11
79	Identification of functional genetic variation in exome sequence analysis. BMC Proceedings, 2011, 5, S13.	1.6	9
80	Rare variants in SLC5A10 are associated with serum 1,5-anhydroglucitol (1,5-AG) in the Atherosclerosis Risk in Communities (ARIC) Study. Scientific Reports, 2019, 9, 5941.	3.3	9
81	Genomics in the era of COVID-19: ethical implications for clinical practice and public health. Genome Medicine, 2020, 12, 95.	8.2	9
82	Genetic association of ERAP1 and ERAP2 with eclampsia and preeclampsia in northeastern Brazilian women. Scientific Reports, 2021, 11, 6764.	3.3	9
83	Increased Rate of Epigenetic Aging in Men Living With HIV Prior to Treatment. Frontiers in Genetics, 2021, 12, 796547.	2.3	9
84	Comprehensive candidate gene analysis for symptomatic or asymptomatic outcomes of Leishmania infantum infection in Brazil. Annals of Human Genetics, 2017, 81, 41-48.	0.8	8
85	Heritability analysis of nontraditional glycemic biomarkers in the Atherosclerosis Risk in Communities Study. Genetic Epidemiology, 2019, 43, 776-785.	1.3	8
86	Variation in PTCHD2, CRISP3, NAP1L4, FSCB, and AP3B2 associated with spherical equivalent. Molecular Vision, 2016, 22, 783-96.	1.1	8
87	GeneLink: a database to facilitate genetic studies of complex traits. BMC Genomics, 2004, 5, 81.	2.8	7
88	Identification of tag single-nucleotide polymorphisms in regions with varying linkage disequilibrium. BMC Genetics, 2005, 6, S73.	2.7	7
89	Examining the effect of linkage disequilibrium between markers on the Type I error rate and power of nonparametric multipoint linkage analysis of twoâ€generation and multigenerational pedigrees in the presence of missing genotype data. Genetic Epidemiology, 2008, 32, 41-51.	1.3	7
90	Perspectives on the Future of Epidemiology: A Framework for Training. American Journal of Epidemiology, 2020, 189, 634-639.	3.4	7

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91	Genomeâ€wide Linkage Analysis of Multiple Metabolic Factors: Evidence of Genetic Heterogeneity. Obesity, 2010, 18, 146-152.	3.0	6
92	Fine mapping under linkage peaks for symptomatic or asymptomatic outcomes of Leishmania infantum infection in Brazil. Infection, Genetics and Evolution, 2016, 43, 1-5.	2.3	6
93	Fine-mapping of genetic loci driving spontaneous clearance of hepatitis C virus infection. Scientific Reports, 2017, 7, 15843.	3.3	6
94	Epidemiology at a time for unity. International Journal of Epidemiology, 2018, 47, 1366-1371.	1.9	6
95	The Evolving Field of Genetic Epidemiology: From Familial Aggregation to Genomic Sequencing. American Journal of Epidemiology, 2019, 188, 2069-2077.	3.4	6
96	Mendelian Randomization Analysis of n-6 Polyunsaturated Fatty Acid Levels and Pancreatic Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 2735-2739.	2.5	6
97	Spatiotemporal Phylodynamics of Hepatitis C Among People Who Inject Drugs in India. Hepatology, 2021, 74, 1782-1794.	7.3	6
98	Trans-ancestral fine-mapping of MHC reveals key amino acids associated with spontaneous clearance of hepatitis C in HLA-DQβ1. American Journal of Human Genetics, 2022, 109, 299-310.	6.2	6
99	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. BMC Genetics, 2005, 6, S20.	2.7	5
100	A Multiancestry Sex-Stratified Genome-Wide Association Study of Spontaneous Clearance of Hepatitis C Virus. Journal of Infectious Diseases, 2021, 223, 2090-2098.	4.0	5
101	Multi-ancestry fine mapping of interferon lambda and the outcome of acute hepatitis C virus infection. Genes and Immunity, 2020, 21, 348-359.	4.1	5
102	Genomics and Infectious Diseases: Expert Perspectives on Public Health Considerations regarding Actionability and Privacy. Ethics & Human Research, 2020, 42, 30-40.	0.9	5
103	Genome-Wide Association Study of Campylobacter - Positive Diarrhea Identifies Genes Involved in Toxin Processing and Inflammatory Response. MBio, 2022, 13, e0055622.	4.1	5
104	Current Gene Discovery Strategies for Ocular Conditions. , 2011, 52, 7761.		4
105	Prevalence and Phylogenetic Characterization of Hepatitis C Virus Among Indian Men Who Have Sex With Men: Limited Evidence for Sexual Transmission. Journal of Infectious Diseases, 2020, 221, 1875-1883.	4.0	4
106	APOL1 variant alleles associate with reduced risk for opportunistic infections in HIV infection. Communications Biology, 2021, 4, 284.	4.4	4
107	The GLC1H Glaucoma Locus May Reflect Glaucoma With Elevated Intraocular Pressure. JAMA Ophthalmology, 2007, 125, 1716.	2.4	3
108	Polymorphisms in melanoma differentiationâ€associated gene 5 are not associated with clearance of hepatitis C virus in a European American population. Hepatology, 2016, 63, 1061-1062.	7.3	3

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109	Exome Array Analysis of Nuclear Lens Opacity. Ophthalmic Epidemiology, 2018, 25, 215-219.	1.7	3
110	Association analysis of exome variants and refraction, axial length, and corneal curvature in a European-American population. Human Mutation, 2018, 39, 1973-1979.	2.5	3
111	Personal Genetic Information about HIV: Research Participantsâ€™ Views of Ethical, Social, and Behavioral Implications. Public Health Genomics, 2019, 22, 36-45.	1.0	3
112	Association of FMO3 Variants with Blood Pressure in the Atherosclerosis Risk in Communities Study. International Journal of Hypertension, 2019, 2019, 1-8.	1.3	3
113	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. ELife, 2021, 10, .	6.0	3
114	The Ethics of Precision Rationing: Human Genetics and the Need for Debate on Stratifying Access to Medication. Public Health Genomics, 2020, 23, 149-154.	1.0	2
115	Benchmarking statistical methods for analyzing parentâ€“child dyads in genetic association studies. Genetic Epidemiology, 2022, 46, 266-284.	1.3	2
116	Lipid levels in HIV-positive men receiving anti-retroviral therapy are not associated with copy number variation of reverse cholesterol transport pathway genes. BMC Research Notes, 2015, 8, 697.	1.4	0