Saurabh Ghosh

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/7689112/publications.pdf

Version: 2024-02-01

57 papers	1,067 citations	471509 17 h-index	434195 31 g-index
58 all docs	58 docs citations	58 times ranked	1660 citing authors

#	Article	IF	Citations
1	Impact of Common Variants of PPARG, KCNJ11, TCF7L2, SLC30A8, HHEX, CDKN2A, IGF2BP2, and CDKAL1 on the Risk of Type 2 Diabetes in 5,164 Indians. Diabetes, 2010, 59, 2068-2074.	0.6	163
2	EGLN1 involvement in high-altitude adaptation revealed through genetic analysis of extreme constitution types defined in Ayurveda. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 18961-18966.	7.1	152
3	Genetic association of ADIPOQ gene variants with type 2 diabetes, obesity and serum adiponectin levels in south Indian population. Gene, 2013, 532, 253-262.	2.2	103
4	Polymorphisms in CaSR and CLDN14 Genes Associated with Increased Risk of Kidney Stone Disease in Patients from the Eastern Part of India. PLoS ONE, 2015, 10, e0130790.	2.5	53
5	Myeloidâ€derived suppressor cells induce regulatory T cells in chronically HBV infected patients with high levels of hepatitis B surface antigen and persist after antiviral therapy. Alimentary Pharmacology and Therapeutics, 2019, 49, 1346-1359.	3.7	52
6	Sexual dimorphic effect in the genetic association of monoamine oxidase A (MAOA) markers with autism spectrum disorder. Progress in Neuro-Psychopharmacology and Biological Psychiatry, 2014, 50, 11-20.	4.8	39
7	Combined genetic effects of EGLN1 and VWF modulate thrombotic outcome in hypoxia revealed by Ayurgenomics approach. Journal of Translational Medicine, 2015, 13, 184.	4.4	38
8	Genome wide association study of uric acid in Indian population and interaction of identified variants with Type 2 diabetes. Scientific Reports, 2016, 6, 21440.	3.3	36
9	Recapitulation of Ayurveda constitution types by machine learning of phenotypic traits. PLoS ONE, 2017, 12, e0185380.	2.5	35
10	Common Variants in CLDN2 and MORC4 Genes Confer Disease Susceptibility in Patients with Chronic Pancreatitis. PLoS ONE, 2016, 11, e0147345.	2.5	34
11	Linkage mapping of beta 2 EEG waves via non-parametric regression. American Journal of Medical Genetics Part A, 2003, 118B, 66-71.	2.4	31
12	SLC6A4 markers modulate platelet 5-HT level and specific behaviors of autism: A study from an Indian population. Progress in Neuro-Psychopharmacology and Biological Psychiatry, 2015, 56, 196-206.	4.8	30
13	Mapping quantitative trait loci in humans: achievements and limitations. Journal of Clinical Investigation, 2005, 115, 1419-1424.	8.2	27
14	Increased Risk of Psoriasis due to combined effect of HLA-Cw6 and LCE3 risk alleles in Indian population. Scientific Reports, 2016, 6, 24059.	3.3	25
15	Smokeless tobacco consumption impedes metabolic, cellular, apoptotic and systemic stress pattern: A study on Government employees in Kolkata, India. Scientific Reports, 2016, 5, 18284.	3.3	24
16	Genetic variants of MAOB affect serotonin level and specific behavioral attributes to increase autism spectrum disorder (ASD) susceptibility in males. Progress in Neuro-Psychopharmacology and Biological Psychiatry, 2016, 71, 123-136.	4.8	20
17	Effect of Population Stratification on False Positive Rates of Populationâ€Based Association Analyses of Quantitative Traits. Annals of Human Genetics, 2012, 76, 237-245.	0.8	19
18	A Two-Stage Variable-Stringency Semiparametric Method for Mapping Quantitative-Trait Loci with the Use of Genomewide-Scan Data on Sib Pairs. American Journal of Human Genetics, 2000, 66, 1046-1061.	6.2	16

#	Article	IF	Citations
19	Semiparametric Allelic Tests for Mapping Multiple Phenotypes: Binomial Regression and Mahalanobis Distance. Genetic Epidemiology, 2015, 39, 635-650.	1.3	16
20	Analysis of metabolic syndrome phenotypes in Framingham Heart Study families from Genetic Analysis Workshop 13. Genetic Epidemiology, 2003, 25, S78-S89.	1.3	14
21	Gender-Specific Effect of 5-HT and 5-HIAA on Threshold Level of Behavioral Symptoms and Sex-Bias in Prevalence of Autism Spectrum Disorder. Frontiers in Neuroscience, 2019, 13, 1375.	2.8	13
22	A novel hotspot and rare somatic mutation p.A138V, at TP53 is associated with poor survival of pancreatic ductal and periampullary adenocarcinoma patients. Molecular Medicine, 2020, 26, 59.	4.4	12
23	Power comparison between population-based case-control studies and family-based transmission-disequilibrium tests: An empirical study. Indian Journal of Human Genetics, 2011, 17, 27.	0.7	10
24	Sequence and expression variations in 23 genes involved in mitochondrial and non-mitochondrial apoptotic pathways and risk of oral leukoplakia and cancer. Mitochondrion, 2015, 25, 28-33.	3.4	9
25	Influence of age, body weight, parity and morphometric traits on litter size in prolific Black Bengal goats. Journal of Applied Animal Research, 2015, 43, 104-111.	1.2	8
26	Introduction to genetic analysis workshop 17 summaries. Genetic Epidemiology, 2011, 35, S1-4.	1.3	7
27	Statistical equivalent of the classical TDT for quantitative traits and multivariate phenotypes. Journal of Genetics, 2015, 94, 619-628.	0.7	7
28	Association of IL12B risk haplotype and lack of interaction with HLA-Cw6 among the psoriasis patients in India. Journal of Human Genetics, 2017, 62, 389-395.	2.3	7
29	Identifying rare variants from exome scans: the GAW17 experience. BMC Proceedings, 2011, 5, S1.	1.6	6
30	HBV quasispecies composition in Lamivudine-failed chronic hepatitis B patients and its influence on virological response to Tenofovir-based rescue therapy. Scientific Reports, 2017, 7, 44742.	3.3	6
31	An association study of severity of intellectual disability with peripheral biomarkers of disabled children in a rehabilitation home, Kolkata, India. Scientific Reports, 2019, 9, 13652.	3.3	6
32	A novel nonâ€parametric regression reveals linkage on chromosome 4 for the number of externalizing symptoms in sibâ€pairs. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2008, 147B, 1301-1305.	1.7	5
33	A Novel Bayesian Semiparametric Algorithm for Inferring Population Structure and Adjusting for Caseâ€Control Association Tests. Biometrics, 2013, 69, 164-173.	1.4	5
34	Mapping a quantitative trait locus via the EM algorithm and Bayesian classification. Genetic Epidemiology, 2000, 19, 97-126.	1.3	4
35	Association Analysis of Population-Based Quantitative Trait Data: An Assessment of ANOVA. Human Heredity, 2007, 64, 82-88.	0.8	4
36	A quantile-based method for association mapping of quantitative phenotypes: an application to rheumatoid arthritis phenotypes. BMC Proceedings, 2009, 3, S18.	1.6	4

#	Article	IF	Citations
37	Integrating binary traits with quantitative phenotypes for association mapping of multivariate phenotypes. BMC Proceedings, 2011, 5, S73.	1.6	3
38	The Sib TDT Adjusted For Age Of Disease Onset. Annals of Human Genetics, 2004, 68, 249-256.	0.8	2
39	Linkage mapping of a complex trait in the New York population of the GAW14 simulated dataset: a multivariate phenotype approach. BMC Genetics, 2005, 6, S19.	2.7	2
40	A nonparametric regression-based linkage scan of rheumatoid factor-IgM using sib-pair squared sums and differences. BMC Proceedings, 2007, 1, S99.	1.6	2
41	Multivariate Analyses of Blood Pressure Related Phenotypes in a Longitudinal Framework: Insights From Genetic Analysis Workshop 18. Genetic Epidemiology, 2014, 38, S63-7.	1.3	2
42	A novel transmission-based test of association for multivariate phenotypes: an application to systolic and diastolic blood pressure levels. BMC Proceedings, 2014, 8, S71.	1.6	2
43	Association mapping of blood pressure levels in a longitudinal framework using binomial regression. BMC Proceedings, 2014, 8, S74.	1.6	2
44	Interpreting a genetic case-control finding: What can be said, what cannot be said and implications in Indian populations. Indian Journal of Human Genetics, 2007, 13, 1.	0.7	2
45	An improved procedure of mapping a quantitative trait locus via the EM algorithm using posterior probabilities. Journal of Genetics, 2000, 79, 47-53.	0.7	1
46	How Do Homozygous Parents Affect TDT as a Test for Association?. Human Heredity, 2002, 53, 181-186.	0.8	1
47	Linkage mapping of total cholesterol level in a young cohort via nonparametric regression. BMC Genetics, 2003, 4, S92.	2.7	1
48	Linkage analyses of rheumatoid arthritis and related quantitative phenotypes: the GAW15 experience. Genetic Epidemiology, 2007, 31, S86-S95.	1.3	1
49	Including non-informative parents in transmission-based association tests. Journal of Human Genetics, 2017, 62, 621-629.	2.3	1
50	Transmission-based association mapping of triglyceride levels in a longitudinal framework using quasi-likelihood. BMC Proceedings, 2018, 12, 39.	1.6	1
51	Association analyses of repeated measures on triglyceride and high-density lipoprotein levels: insights from GAW20. BMC Genetics, 2018, 19, 73.	2.7	1
52	Family-based genome-wide association of inflammation biomarkers and fenofibrate treatment response in the GOLDN study. BMC Proceedings, 2018, 12, 41.	1.6	1
53	Genetic insight into Birtâ€“Hoggâ€“DubÃ© syndrome in Indian patients reveals novel mutations at FLCN. Orphanet Journal of Rare Diseases, 2022, 17, 176.	2.7	1
54	Dissecting the correlation structure of a bivariate phenotype: Common genes or shared environment?. Journal of Genetics, 2005, 84, 143-146.	0.7	0

#	Article	IF	Citations
55	Genetic Mapping of Quantitative Traits: Model-Free Sib-Pair Linkage Approaches. , 0, , 487-498.		0
56	Competing analytical strategies of combining associated SNPs for estimating genetic risks. Journal of Genetics, 2022, 101, 1.	0.7	0
57	Competing analytical strategies of combining associated SNPs for estimating genetic risks.. Journal of Genetics, 2022, 101, .	0.7	0