Saonli Basu

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/7755634/publications.pdf

Version: 2024-02-01

		186265	155660
87	3,416	28	55
papers	citations	h-index	g-index

93	93	93	7663
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Estimating SNP heritability in presence of population substructure in biobank-scale datasets. Genetics, 2022, 220, .	2.9	5
2	Elucidating mechanisms of genetic cross-disease associations at the PROCR vascular disease locus. Nature Communications, 2022, 13, 1222.	12.8	5
3	Efficient estimation of SNP heritability using Gaussian predictive process in large scale cohort studies. PLoS Genetics, 2022, 18, e1010151.	3.5	4
4	Comparing heritability estimators under alternative structures of linkage disequilibrium. G3: Genes, Genomes, Genetics, 2022, 12, .	1.8	4
5	Impact of body mass index on pathological complete response following neoadjuvant chemotherapy in operable breast cancer: a meta-analysis. Breast Cancer, 2021, 28, 618-629.	2.9	20
6	A Bayesian hierarchically structured prior for rareâ€variant association testing. Genetic Epidemiology, 2021, 45, 413-424.	1.3	2
7	A Bayesian hierarchically structured prior for geneâ€based association testing with multiple traits in genomeâ€wide association studies. Genetic Epidemiology, 2021, , .	1.3	0
8	Burden of rare exome sequence variants in PROC gene is associated with venous thromboembolism: a populationâ€based study. Journal of Thrombosis and Haemostasis, 2020, 18, 445-453.	3.8	11
9	A Bayesian hierarchical variable selection prior for pathwayâ€based GWAS using summary statistics. Statistics in Medicine, 2020, 39, 724-739.	1.6	3
10	Modeling the Dependence Structure in Genome Wide Association Studies of Binary Phenotypes in Family Data. Behavior Genetics, 2020, 50, 423-439.	2.1	1
11	Longâ€Term Association of Venous Thromboembolism With Frailty, Physical Functioning, and Quality of Life: The Atherosclerosis Risk in Communities Study. Journal of the American Heart Association, 2020, 9, e015656.	3.7	14
12	A robust and unified framework for estimating heritability in twin studies using generalized estimating equations. Statistics in Medicine, 2020, 39, 3897-3913.	1.6	8
13	A largeâ€scale exome array analysis of venous thromboembolism. Genetic Epidemiology, 2019, 43, 449-457.	1.3	22
14	Reasons for Differences in the Incidence of Venous Thromboembolism in Black Versus White Americans. American Journal of Medicine, 2019, 132, 970-976.	1.5	36
15	Plasma Concentrations of High Molecular Weight Kininogen and Prekallikrein and Venous Thromboembolism Incidence in the General Population. Thrombosis and Haemostasis, 2019, 119, 834-843.	3.4	9
16	The Reply. American Journal of Medicine, 2019, 132, e808.	1.5	0
17	Transethnic Evaluation Identifies Low-Frequency Loci Associated With 25-Hydroxyvitamin D Concentrations. Journal of Clinical Endocrinology and Metabolism, 2018, 103, 1380-1392.	3.6	33
18	Adaptive SNP-Set Association Testing in Generalized Linear Mixed Models with Application to Family Studies. Behavior Genetics, 2018, 48, 55-66.	2.1	13

#	Article	IF	Citations
19	Prospective Study of Endogenous Hormones and Incidence of Venous Thromboembolism: The Atherosclerosis Risk in Communities Study. Thrombosis and Haemostasis, 2018, 118, 1940-1950.	3.4	17
20	A linear mixed model framework for geneâ€based geneâ€“environment interaction tests in twin studies. Genetic Epidemiology, 2018, 42, 648-663.	1.3	2
21	Targeted sequencing to identify novel genetic risk factors for deep vein thrombosis: a study of 734 genes. Journal of Thrombosis and Haemostasis, 2018, 16, 2432-2441.	3.8	17
22	A Bayesian Gene-Based Genome-Wide Association Study Analysis of Osteosarcoma Trio Data Using a Hierarchically Structured Prior. Cancer Informatics, 2018, 17, 117693511877510.	1.9	12
23	Longitudinal increases in blood biomarkers of inflammation or cardiovascular disease and the incidence of venous thromboembolism. Journal of Thrombosis and Haemostasis, 2018, 16, 1964-1972.	3.8	9
24	Pleiotropic effects of n-6 and n-3 fatty acid-related genetic variants on circulating hemostatic variables. Thrombosis Research, 2018, 168, 53-59.	1.7	1
25	Letter to the editor comments on Groparu-cojocaru and Doray (2013). Communications in Statistics Part B: Simulation and Computation, 2017, 46, 1-8.	1.2	0
26	Genome-wide association study with additional genetic and post-transcriptional analyses reveals novel regulators of plasma factor XI levels. Human Molecular Genetics, 2017, 26, ddw401.	2.9	35
27	A novel association test for multiple secondary phenotypes from a case-control GWAS. Genetic Epidemiology, 2017, 41, 413-426.	1.3	10
28	A combination test for detection of gene-environment interaction in cohort studies. Genetic Epidemiology, 2017, 41, 396-412.	1.3	7
29	Causal Effect of Plasminogen Activator Inhibitor Type 1 on Coronary Heart Disease. Journal of the American Heart Association, 2017, 6, .	3.7	89
30	Galectinâ€3 and venous thromboembolism incidence: the Atherosclerosis Risk in Communities (ARIC) Study. Research and Practice in Thrombosis and Haemostasis, 2017, 1, 223-230.	2.3	15
31	Resampling-based tests for Lasso in genome-wide association studies. BMC Genetics, 2017, 18, 70.	2.7	12
32	Comparison of HapMap and 1000 Genomes Reference Panels in a Large-Scale Genome-Wide Association Study. PLoS ONE, 2017, 12, e0167742.	2.5	29
33	USAT: A Unified Scoreâ€Based Association Test for Multiple Phenotypeâ€Genotype Analysis. Genetic Epidemiology, 2016, 40, 20-34.	1.3	42
34	Replication of a genetic risk score for venous thromboembolism in whites but not in African Americans. Journal of Thrombosis and Haemostasis, 2016, 14, 83-88.	3.8	18
35	Powerful association test combining rare variant and gene expression using family data from Genetic Analysis Workshop 19. BMC Proceedings, 2016, 10, 251-255.	1.6	3
36	Lifetime Risk of Venous Thromboembolism in Two Cohort Studies. American Journal of Medicine, 2016, 129, 339.e19-339.e26.	1.5	85

#	Article	IF	Citations
37	A meta-analysis of 120 246 individuals identifies 18 new loci for fibrinogen concentration. Human Molecular Genetics, 2016, 25, 358-370.	2.9	73
38	Genome-wide association studies identify genetic loci for low von Willebrand factor levels. European Journal of Human Genetics, 2016, 24, 1035-1040.	2.8	45
39	Weighted Score Tests Implementing Model-Averaging Schemes in Detection of Rare Variants in Case-Control Studies. PLoS ONE, 2015, 10, e0139355.	2.5	5
40	A Bayesian Partitioning Model for the Detection of Multilocus Effects in Case-Control Studies. Human Heredity, 2015, 79, 69-79.	0.8	4
41	A genetic association study of activated partial thromboplastin time in European Americans and African Americans: the ARIC Study. Human Molecular Genetics, 2015, 24, 2401-2408.	2.9	6
42	Meta-analysis of 65,734 Individuals Identifies TSPAN15 and SLC44A2 as Two Susceptibility Loci for Venous Thromboembolism. American Journal of Human Genetics, 2015, 96, 532-542.	6.2	222
43	Geneâ€centric approach identifies new and known loci for <scp>F</scp>VIII activity and <scp>VWF</scp> antigen levels in <scp>E</scp>uropean <scp>A</scp>mericans and <scp>A</scp>frican <scp>A</scp>mericans. American Journal of Hematology, 2015, 90, 534-540.	4.1	20
44	Prospective study of sickle cell trait and venous thromboembolism incidence. Journal of Thrombosis and Haemostasis, 2015, 13, 2-9.	3.8	113
45	No Evidence for Genome-Wide Interactions on Plasma Fibrinogen by Smoking, Alcohol Consumption and Body Mass Index: Results from Meta-Analyses of 80,607 Subjects. PLoS ONE, 2014, 9, e111156.	2.5	8
46	Genetic Markers Associated With Plasma Protein C Level in African Americans: The Atherosclerosis Risk in Communities (ARIC) Study. Genetic Epidemiology, 2014, 38, 709-713.	1.3	9
47	Genome-Wide Association Study for Circulating Tissue Plasminogen Activator Levels and Functional Follow-Up Implicates Endothelial STXBP5 and STX2. Arteriosclerosis, Thrombosis, and Vascular Biology, 2014, 34, 1093-1101.	2.4	43
48	Serum 25â€hydroxyvitaminÂD and risk of venous thromboembolism: the Atherosclerosis Risk in Communities (ARIC) Study. Journal of Thrombosis and Haemostasis, 2014, 12, 1455-1460.	3.8	23
49	Heritability and molecularâ€genetic basis of the <scp>P</scp>3 eventâ€related brain potential: A genomeâ€wide association study. Psychophysiology, 2014, 51, 1246-1258.	2.4	32
50	Elevated hepatic enzymes and incidence of venous thromboembolism: a prospective study. Annals of Epidemiology, 2014, 24, 817-821.e2.	1.9	14
51	Low-frequency copy-number variants and general cognitive ability: No evidence of association. Intelligence, 2014, 42, 98-106.	3.0	10
52	A genetic association study of D-dimer levels with 50K SNPs from a candidate gene chip in four ethnic groups. Thrombosis Research, 2014, 134, 462-467.	1.7	8
53	Results of a â€œGWAS Plus:â€•General Cognitive Ability Is Substantially Heritable and Massively Polygenic. PLoS ONE, 2014, 9, e112390.	2.5	41
54	A Genomeâ€Wide Association Study for Venous Thromboembolism: The Extended Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium. Genetic Epidemiology, 2013, 37, 512-521.	1.3	99

#	Article	IF	Citations
55	A Rapid Gene-Based Genome-Wide Association Test with Multivariate Traits. Human Heredity, 2013, 76, 53-63.	0.8	17
56	A Genome-Wide Association Study of Behavioral Disinhibition. Behavior Genetics, 2013, 43, 363-373.	2.1	119
57	Prevalence of Sinus Augmentation Associated With Maxillary Posterior Implants. Journal of Oral Implantology, 2013, 39, 680-688.	1.0	18
58	Multiethnic Meta-Analysis of Genome-Wide Association Studies in >100 000 Subjects Identifies 23 Fibrinogen-Associated Loci but No Strong Evidence of a Causal Association Between Circulating Fibrinogen and Cardiovascular Disease. Circulation, 2013, 128, 1310-1324.	1.6	128
59	The Minnesota Center for Twin and Family Research Genome-Wide Association Study. Twin Research and Human Genetics, 2012, 15, 767-774.	0.6	70
60	Genome-wide association study for circulating levels of PAI-1 provides novel insights into its regulation. Blood, 2012, 120, 4873-4881.	1.4	90
61	Genetic Associations for Activated Partial Thromboplastin Time and Prothrombin Time, their Gene Expression Profiles, and Risk of Coronary Artery Disease. American Journal of Human Genetics, 2012, 91, 152-162.	6.2	85
62	New gene functions in megakaryopoiesis and platelet formation. Nature, 2011, 480, 201-208.	27.8	401
63	Comparison of statistical tests for disease association with rare variants. Genetic Epidemiology, 2011, 35, 606-619.	1.3	205
64	Multilocus association testing with penalized regression. Genetic Epidemiology, 2011, 35, 755-765.	1.3	14
65	A Rapid Generalized Least Squares Model for a Genome-Wide Quantitative Trait Association Analysis in Families. Human Heredity, 2011, 71, 67-82.	0.8	27
66	A Dimension Reduction Approach for Modeling Multi-Locus Interaction in Case-Control Studies. Human Heredity, 2011, 71, 234-245.	0.8	9
67	Adaptive Tests for Detecting Gene-Gene and Gene-Environment Interactions. Human Heredity, 2011, 72, 98-109.	0.8	11
68	Retrospective cohort study of the predictors of implant failure in the posterior maxilla. International Journal of Oral and Maxillofacial Implants, 2011, 26, 154-62.	1.4	17
69	Genome-wide association study identifies novel loci for plasma levels of protein C: the ARIC study. Blood, 2010, 116, 5032-5036.	1.4	74
70	An Alternative Model for Quantitative Trait Loci (QTL) Analysis in General Pedigrees. Annals of Human Genetics, 2010, 75, no-no.	0.8	1
71	A Likelihoodâ€Based Traitâ€Modelâ€Free Approach for Linkage Detection of Binary Trait. Biometrics, 2010, 66, 205-213.	1.4	11
72	Polymorphisms in the base excision repair pathway and graft-versus-host disease. Leukemia, 2010, 24, 1470-1475.	7.2	21

#	Article	IF	Citations
73	Novel Associations of Multiple Genetic Loci With Plasma Levels of Factor VII, Factor VIII, and von Willebrand Factor. Circulation, 2010, 121, 1382-1392.	1.6	311
74	Pair-Wise Multifactor Dimensionality Reduction Method to Detect Gene-Gene Interactions in A Case-Control Study. Human Heredity, 2010, 69, 60-70.	0.8	13
75	Association between Genetic Variants in the Base Excision Repair Pathway and Outcomes after Hematopoietic Cell Transplantations. Biology of Blood and Marrow Transplantation, 2010, 16, 1084-1089.	2.0	14
76	Association of Novel Genetic Loci With Circulating Fibrinogen Levels. Circulation: Cardiovascular Genetics, 2009, 2, 125-133.	5.1	86
77	Bisphosphonate-Related Osteonecrosis of the Jaw: Clinical Features, Risk Factors, Management, and Treatment Outcomes of 26 Patients. Journal of Oral and Maxillofacial Surgery, 2009, 67, 1904-1913.	1.2	84
78	Power of multifactor dimensionality reduction and penalized logistic regression for detecting gene-gene Interaction in a case-control study. BMC Medical Genetics, 2009, 10, 127.	2.1	28
79	Pharmacogenetic effect of the UGT polymorphisms on mycophenolate is modified by calcineurin inhibitors. European Journal of Clinical Pharmacology, 2008, 64, 1047-1056.	1.9	43
80	Exact Traitâ€Modelâ€Free Tests for Linkage Detection in Pedigrees. Annals of Human Genetics, 2008, 72, 676-682.	0.8	5
81	Accuracy of friction-style and spring-style mechanical torque limiting devices for dental implants. Journal of Prosthetic Dentistry, 2008, 100, 86-92.	2.8	43
82	Allergen-Specific IgG1 Provides Parsimonious Heritability Estimates for Atopy-Associated Immune Responses to Allergens. Human Immunology, 2007, 68, 113-121.	2.4	6
83	Using linkage and association to identify and model genetic effects: summary of GAW15 Group 4. Genetic Epidemiology, 2007, 31, S34-S42.	1.3	3
84	CD14 Promoter Polymorphisms in Atopic Families: Implications for Modulated Allergen-Specific Immunoglobulin E and G1 Responses. International Archives of Allergy and Immunology, 2006, 139, 217-224.	2.1	20
85	Comparison of marker types and map assumptions using Markov chain Monte Carlo-based linkage analysis of COGA data. BMC Genetics, 2005, 6, S11.	2.7	14
86	Genome Sharing in Large Pedigrees: Multiple Imputation of ibd for Linkage Detection. Human Heredity, 2003, 56, 119-125.	0.8	6
87	Prevalence and incidence of hepatitis B virus infection in STD clinic attendees in Pune, India. Sexually Transmitted Infections, 2002, 78, 169-173.	1.9	44