

# Saonli Basu

## List of Publications by Year in descending order

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Version: 2024-02-01

87  
papers

3,416  
citations

186265

28  
h-index

155660

55  
g-index

93  
all docs

93  
docs citations

93  
times ranked

7663  
citing authors

| #  | ARTICLE   | IF   | CITATIONS |
|----|---|------|-----------|
| 1  | New gene functions in megakaryopoiesis and platelet formation. <i>Nature</i> , 2011, 480, 201-208.  | 27.8 | 401       |
| 2  | Novel Associations of Multiple Genetic Loci With Plasma Levels of Factor VII, Factor VIII, and von Willebrand Factor. <i>Circulation</i> , 2010, 121, 1382-1392.  | 1.6  | 311       |
| 3  | Meta-analysis of 65,734 Individuals Identifies TSPAN15 and SLC44A2 as Two Susceptibility Loci for Venous Thromboembolism. <i>American Journal of Human Genetics</i> , 2015, 96, 532-542.  | 6.2  | 222       |
| 4  | Comparison of statistical tests for disease association with rare variants. <i>Genetic Epidemiology</i> , 2011, 35, 606-619.  | 1.3  | 205       |
| 5  | 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. <i>Circulation</i> , 2013, 128, 1310-1324. | 1.6  | 128       |
| 6  | A Genome-Wide Association Study of Behavioral Disinhibition. <i>Behavior Genetics</i> , 2013, 43, 363-373.  | 2.1  | 119       |
| 7  | Prospective study of sickle cell trait and venous thromboembolism incidence. <i>Journal of Thrombosis and Haemostasis</i> , 2015, 13, 2-9.  | 3.8  | 113       |
| 8  | A Genome-Wide Association Study for Venous Thromboembolism: The Extended Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium. <i>Genetic Epidemiology</i> , 2013, 37, 512-521.   | 1.3  | 99        |
| 9  | Genome-wide association study for circulating levels of PAI-1 provides novel insights into its regulation. <i>Blood</i> , 2012, 120, 4873-4881.   | 1.4  | 90        |
| 10 | Causal Effect of Plasminogen Activator Inhibitor Type 1 on Coronary Heart Disease. <i>Journal of the American Heart Association</i> , 2017, 6, .  | 3.7  | 89        |
| 11 | Association of Novel Genetic Loci With Circulating Fibrinogen Levels. <i>Circulation: Cardiovascular Genetics</i> , 2009, 2, 125-133.   | 5.1  | 86        |
| 12 | Genetic Associations for Activated Partial Thromboplastin Time and Prothrombin Time, their Gene Expression Profiles, and Risk of Coronary Artery Disease. <i>American Journal of Human Genetics</i> , 2012, 91, 152-162.  | 6.2  | 85        |
| 13 | Lifetime Risk of Venous Thromboembolism in Two Cohort Studies. <i>American Journal of Medicine</i> , 2016, 129, 339.e19-339.e26.  | 1.5  | 85        |
| 14 | Bisphosphonate-Related Osteonecrosis of the Jaw: Clinical Features, Risk Factors, Management, and Treatment Outcomes of 26 Patients. <i>Journal of Oral and Maxillofacial Surgery</i> , 2009, 67, 1904-1913.  | 1.2  | 84        |
| 15 | Genome-wide association study identifies novel loci for plasma levels of protein C: the ARIC study. <i>Blood</i> , 2010, 116, 5032-5036.  | 1.4  | 74        |
| 16 | A meta-analysis of 120 246 individuals identifies 18 new loci for fibrinogen concentration. <i>Human Molecular Genetics</i> , 2016, 25, 358-370.  | 2.9  | 73        |
| 17 | The Minnesota Center for Twin and Family Research Genome-Wide Association Study. <i>Twin Research and Human Genetics</i> , 2012, 15, 767-774.   | 0.6  | 70        |
| 18 | Genome-wide association studies identify genetic loci for low von Willebrand factor levels. <i>European Journal of Human Genetics</i> , 2016, 24, 1035-1040.  | 2.8  | 45        |

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|----|--|-----|-----------|
| 19 | 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        |
| 20 | 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        |
| 21 | 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        |
| 22 | Genome-Wide Association Study for Circulating Tissue Plasminogen Activator Levels and Functional Follow-Up Implicates Endothelial <i>STXBP5</i> and <i>STX2</i> . Arteriosclerosis, Thrombosis, and Vascular Biology, 2014, 34, 1093-1101. | 2.4 | 43        |
| 23 | USAT: A Unified Score-Based Association Test for Multiple Phenotype-Genotype Analysis. Genetic Epidemiology, 2016, 40, 20-34.  | 1.3 | 42        |
| 24 | Results of a GWAS Plus: General Cognitive Ability Is Substantially Heritable and Massively Polygenic. PLoS ONE, 2014, 9, e112390.  | 2.5 | 41        |
| 25 | 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        |
| 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 | 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        |
| 28 | Heritability and molecular genetic basis of the P3 event-related brain potential: A genome-wide association study. Psychophysiology, 2014, 51, 1246-1258.  | 2.4 | 32        |
| 29 | Comparison of HapMap and 1000 Genomes Reference Panels in a Large-Scale Genome-Wide Association Study. PLoS ONE, 2017, 12, e0167742.   | 2.5 | 29        |
| 30 | 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        |
| 31 | 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        |
| 32 | Serum 25-Hydroxyvitamin D and risk of venous thromboembolism: the Atherosclerosis Risk in Communities (ARIC) Study. Journal of Thrombosis and Haemostasis, 2014, 12, 1455-1460.  | 3.8 | 23        |
| 33 | A large-scale exome array analysis of venous thromboembolism. Genetic Epidemiology, 2019, 43, 449-457.   | 1.3 | 22        |
| 34 | Polymorphisms in the base excision repair pathway and graft-versus-host disease. Leukemia, 2010, 24, 1470-1475.  | 7.2 | 21        |
| 35 | 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        |
| 36 | Gene-centric approach identifies new and known loci for FVIII activity and VWF antigen levels in European Americans and African Americans. American Journal of Hematology, 2015, 90, 534-540.  | 4.1 | 20        |

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|----|--|-----|-----------|
| 37 | Impact of body mass index on pathological complete response following neoadjuvant chemotherapy in operable breast cancer: a meta-analysis. <i>Breast Cancer</i> , 2021, 28, 618-629.   | 2.9 | 20        |
| 38 | Prevalence of Sinus Augmentation Associated With Maxillary Posterior Implants. <i>Journal of Oral Implantology</i> , 2013, 39, 680-688.  | 1.0 | 18        |
| 39 | Replication of a genetic risk score for venous thromboembolism in whites but not in African Americans. <i>Journal of Thrombosis and Haemostasis</i> , 2016, 14, 83-88.   | 3.8 | 18        |
| 40 | A Rapid Gene-Based Genome-Wide Association Test with Multivariate Traits. <i>Human Heredity</i> , 2013, 76, 53-63.   | 0.8 | 17        |
| 41 | Prospective Study of Endogenous Hormones and Incidence of Venous Thromboembolism: The Atherosclerosis Risk in Communities Study. <i>Thrombosis and Haemostasis</i> , 2018, 118, 1940-1950.                                   | 3.4 | 17        |
| 42 | Targeted sequencing to identify novel genetic risk factors for deep vein thrombosis: a study of 734 genes. <i>Journal of Thrombosis and Haemostasis</i> , 2018, 16, 2432-2441.   | 3.8 | 17        |
| 43 | Retrospective cohort study of the predictors of implant failure in the posterior maxilla. <i>International Journal of Oral and Maxillofacial Implants</i> , 2011, 26, 154-62.  | 1.4 | 17        |
| 44 | Galectin-3 and venous thromboembolism incidence: the Atherosclerosis Risk in Communities (ARIC) Study. <i>Research and Practice in Thrombosis and Haemostasis</i> , 2017, 1, 223-230.  | 2.3 | 15        |
| 45 | Comparison of marker types and map assumptions using Markov chain Monte Carlo-based linkage analysis of COGA data. <i>BMC Genetics</i> , 2005, 6, S11.   | 2.7 | 14        |
| 46 | Association between Genetic Variants in the Base Excision Repair Pathway and Outcomes after Hematopoietic Cell Transplantations. <i>Biology of Blood and Marrow Transplantation</i> , 2010, 16, 1084-1089.                   | 2.0 | 14        |
| 47 | Multilocus association testing with penalized regression. <i>Genetic Epidemiology</i> , 2011, 35, 755-765.   | 1.3 | 14        |
| 48 | Elevated hepatic enzymes and incidence of venous thromboembolism: a prospective study. <i>Annals of Epidemiology</i> , 2014, 24, 817-821.e2.   | 1.9 | 14        |
| 49 | Long-Term Association of Venous Thromboembolism With Frailty, Physical Functioning, and Quality of Life: The Atherosclerosis Risk in Communities Study. <i>Journal of the American Heart Association</i> , 2020, 9, e015656. | 3.7 | 14        |
| 50 | Pair-Wise Multifactor Dimensionality Reduction Method to Detect Gene-Gene Interactions in A Case-Control Study. <i>Human Heredity</i> , 2010, 69, 60-70.   | 0.8 | 13        |
| 51 | Adaptive SNP-Set Association Testing in Generalized Linear Mixed Models with Application to Family Studies. <i>Behavior Genetics</i> , 2018, 48, 55-66.  | 2.1 | 13        |
| 52 | Resampling-based tests for Lasso in genome-wide association studies. <i>BMC Genetics</i> , 2017, 18, 70.   | 2.7 | 12        |
| 53 | A Bayesian Gene-Based Genome-Wide Association Study Analysis of Osteosarcoma Trio Data Using a Hierarchically Structured Prior. <i>Cancer Informatics</i> , 2018, 17, 117693511877510.                                       | 1.9 | 12        |
| 54 | A Likelihood-Based Trait-Model-Free Approach for Linkage Detection of Binary Trait. <i>Biometrics</i> , 2010, 66, 205-213.   | 1.4 | 11        |

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|----|---|-----|-----------|
| 55 | Adaptive Tests for Detecting Gene-Gene and Gene-Environment Interactions. <i>Human Heredity</i> , 2011, 72, 98-109.   | 0.8 | 11        |
| 56 | Burden of rare exome sequence variants in PROC gene is associated with venous thromboembolism: a population-based study. <i>Journal of Thrombosis and Haemostasis</i> , 2020, 18, 445-453.            | 3.8 | 11        |
| 57 | Low-frequency copy-number variants and general cognitive ability: No evidence of association. <i>Intelligence</i> , 2014, 42, 98-106.   | 3.0 | 10        |
| 58 | A novel association test for multiple secondary phenotypes from a case-control GWAS. <i>Genetic Epidemiology</i> , 2017, 41, 413-426.   | 1.3 | 10        |
| 59 | A Dimension Reduction Approach for Modeling Multi-Locus Interaction in Case-Control Studies. <i>Human Heredity</i> , 2011, 71, 234-245.   | 0.8 | 9         |
| 60 | Genetic Markers Associated With Plasma Protein C Level in African Americans: The Atherosclerosis Risk in Communities (ARIC) Study. <i>Genetic Epidemiology</i> , 2014, 38, 709-713.                   | 1.3 | 9         |
| 61 | Longitudinal increases in blood biomarkers of inflammation or cardiovascular disease and the incidence of venous thromboembolism. <i>Journal of Thrombosis and Haemostasis</i> , 2018, 16, 1964-1972. | 3.8 | 9         |
| 62 | Plasma Concentrations of High Molecular Weight Kininogen and Prekallikrein and Venous Thromboembolism Incidence in the General Population. <i>Thrombosis and Haemostasis</i> , 2019, 119, 834-843.    | 3.4 | 9         |
| 63 | 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. <i>PLoS ONE</i> , 2014, 9, e111156. | 2.5 | 8         |
| 64 | A genetic association study of D-dimer levels with 50K SNPs from a candidate gene chip in four ethnic groups. <i>Thrombosis Research</i> , 2014, 134, 462-467.  | 1.7 | 8         |
| 65 | A robust and unified framework for estimating heritability in twin studies using generalized estimating equations. <i>Statistics in Medicine</i> , 2020, 39, 3897-3913.                               | 1.6 | 8         |
| 66 | A combination test for detection of gene-environment interaction in cohort studies. <i>Genetic Epidemiology</i> , 2017, 41, 396-412.  | 1.3 | 7         |
| 67 | Genome Sharing in Large Pedigrees: Multiple Imputation of <i>i</i> for Linkage Detection. <i>Human Heredity</i> , 2003, 56, 119-125.  | 0.8 | 6         |
| 68 | Allergen-Specific IgG1 Provides Parsimonious Heritability Estimates for Atopy-Associated Immune Responses to Allergens. <i>Human Immunology</i> , 2007, 68, 113-121.                                  | 2.4 | 6         |
| 69 | A genetic association study of activated partial thromboplastin time in European Americans and African Americans: the ARIC Study. <i>Human Molecular Genetics</i> , 2015, 24, 2401-2408.              | 2.9 | 6         |
| 70 | Exact Trait-Free Tests for Linkage Detection in Pedigrees. <i>Annals of Human Genetics</i> , 2008, 72, 676-682.   | 0.8 | 5         |
| 71 | Weighted Score Tests Implementing Model-Averaging Schemes in Detection of Rare Variants in Case-Control Studies. <i>PLoS ONE</i> , 2015, 10, e0139355.  | 2.5 | 5         |
| 72 | Estimating SNP heritability in presence of population substructure in biobank-scale datasets. <i>Genetics</i> , 2022, 220, .  | 2.9 | 5         |

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|----|--|------|-----------|
| 73 | Elucidating mechanisms of genetic cross-disease associations at the PROCRA vascular disease locus. <i>Nature Communications</i> , 2022, 13, 1222.                              | 12.8 | 5         |
| 74 | A Bayesian Partitioning Model for the Detection of Multilocus Effects in Case-Control Studies. <i>Human Heredity</i> , 2015, 79, 69-79.  | 0.8  | 4         |
| 75 | Efficient estimation of SNP heritability using Gaussian predictive process in large scale cohort studies. <i>PLoS Genetics</i> , 2022, 18, e1010151.                           | 3.5  | 4         |
| 76 | Comparing heritability estimators under alternative structures of linkage disequilibrium. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .                                    | 1.8  | 4         |
| 77 | Using linkage and association to identify and model genetic effects: summary of GAW15 Group 4. <i>Genetic Epidemiology</i> , 2007, 31, S34-S42.                                | 1.3  | 3         |
| 78 | Powerful association test combining rare variant and gene expression using family data from Genetic Analysis Workshop 19. <i>BMC Proceedings</i> , 2016, 10, 251-255.          | 1.6  | 3         |
| 79 | A Bayesian hierarchical variable selection prior for pathway-based GWAS using summary statistics. <i>Statistics in Medicine</i> , 2020, 39, 724-739.                           | 1.6  | 3         |
| 80 | A linear mixed model framework for gene-based gene-environment interaction tests in twin studies. <i>Genetic Epidemiology</i> , 2018, 42, 648-663.                             | 1.3  | 2         |
| 81 | A Bayesian hierarchically structured prior for rare-variant association testing. <i>Genetic Epidemiology</i> , 2021, 45, 413-424.  | 1.3  | 2         |
| 82 | An Alternative Model for Quantitative Trait Loci (QTL) Analysis in General Pedigrees. <i>Annals of Human Genetics</i> , 2010, 75, no-no.                                       | 0.8  | 1         |
| 83 | Pleiotropic effects of n-6 and n-3 fatty acid-related genetic variants on circulating hemostatic variables. <i>Thrombosis Research</i> , 2018, 168, 53-59.                     | 1.7  | 1         |
| 84 | Modeling the Dependence Structure in Genome Wide Association Studies of Binary Phenotypes in Family Data. <i>Behavior Genetics</i> , 2020, 50, 423-439.                        | 2.1  | 1         |
| 85 | Letter to the editor comments on Groparu-cojocar and Doray (2013). <i>Communications in Statistics Part B: Simulation and Computation</i> , 2017, 46, 1-8.                     | 1.2  | 0         |
| 86 | The Reply. <i>American Journal of Medicine</i> , 2019, 132, e808.  | 1.5  | 0         |
| 87 | A Bayesian hierarchically structured prior for gene-based association testing with multiple traits in genome-wide association studies. <i>Genetic Epidemiology</i> , 2021, , . | 1.3  | 0         |