

Ingrid B Borecki

List of Publications by Year in descending order

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Version: 2024-02-01

78
papers

27,171
citations

53794

45
h-index

66911

78
g-index

83
all docs

83
docs citations

83
times ranked

33412
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015, 518, 197-206. | 27.8 | 3,823 |
| 2 | Discovery and refinement of loci associated with lipid levels. <i>Nature Genetics</i> , 2013, 45, 1274-1283. | 21.4 | 2,641 |
| 3 | Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. <i>Nature Genetics</i> , 2010, 42, 937-948. | 21.4 | 2,634 |
| 4 | A comprehensive 1000 Genomes-based genome-wide association meta-analysis of coronary artery disease. <i>Nature Genetics</i> , 2015, 47, 1121-1130. | 21.4 | 2,054 |
| 5 | Defining the role of common variation in the genomic and biological architecture of adult human height. <i>Nature Genetics</i> , 2014, 46, 1173-1186. | 21.4 | 1,818 |
| 6 | Hundreds of variants clustered in genomic loci and biological pathways affect human height. <i>Nature</i> , 2010, 467, 832-838. | 27.8 | 1,789 |
| 7 | New genetic loci link adipose and insulin biology to body fat distribution. <i>Nature</i> , 2015, 518, 187-196. | 27.8 | 1,328 |
| 8 | Genome-wide association study identifies 74 loci associated with educational attainment. <i>Nature</i> , 2016, 533, 539-542. | 27.8 | 1,204 |
| 9 | Meta-analysis identifies 13 new loci associated with waist-hip ratio and reveals sexual dimorphism in the genetic basis of fat distribution. <i>Nature Genetics</i> , 2010, 42, 949-960. | 21.4 | 836 |
| 10 | Genetic and Pharmacologic Inactivation of ANGPTL3 and Cardiovascular Disease. <i>New England Journal of Medicine</i> , 2017, 377, 211-221. | 27.0 | 633 |
| 11 | Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. <i>Nature Genetics</i> , 2013, 45, 501-512. | 21.4 | 578 |
| 12 | A Protein-Truncating <i>HSD17B13</i> Variant and Protection from Chronic Liver Disease. <i>New England Journal of Medicine</i> , 2018, 378, 1096-1106. | 27.0 | 556 |
| 13 | Rare and low-frequency coding variants alter human adult height. <i>Nature</i> , 2017, 542, 186-190. | 27.8 | 544 |
| 14 | Distribution and clinical impact of functional variants in 50,726 whole-exome sequences from the DiscovEHR study. <i>Science</i> , 2016, 354, . | 12.6 | 464 |
| 15 | Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. <i>Nature Communications</i> , 2016, 7, 10023. | 12.8 | 412 |
| 16 | Inactivating Variants in <i>ANGPTL4</i> and Risk of Coronary Artery Disease. <i>New England Journal of Medicine</i> , 2016, 374, 1123-1133. | 27.0 | 411 |
| 17 | The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. <i>PLoS Genetics</i> , 2015, 11, e1005378. | 3.5 | 331 |
| 18 | Genome Analyses of >200,000 Individuals Identify 58 Loci for Chronic Inflammation and Highlight Pathways that Link Inflammation and Complex Disorders. <i>American Journal of Human Genetics</i> , 2018, 103, 691-706. | 6.2 | 326 |

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|----|---|------|-----------|
| 19 | Association of Low-Frequency and Rare Coding-Sequence Variants with Blood Lipids and Coronary Heart Disease in 56,000 Whites and Blacks. <i>American Journal of Human Genetics</i> , 2014, 94, 223-232. | 6.2 | 287 |
| 20 | Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. <i>Nature Genetics</i> , 2018, 50, 26-41. | 21.4 | 286 |
| 21 | New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. <i>Nature Communications</i> , 2016, 7, 10495. | 12.8 | 245 |
| 22 | Genome-wide meta-analysis identifies six novel loci associated with habitual coffee consumption. <i>Molecular Psychiatry</i> , 2015, 20, 647-656. | 7.9 | 235 |
| 23 | Meta-analysis identifies common and rare variants influencing blood pressure and overlapping with metabolic trait loci. <i>Nature Genetics</i> , 2016, 48, 1162-1170. | 21.4 | 223 |
| 24 | Whole-Exome Sequencing Identifies Rare and Low-Frequency Coding Variants Associated with LDL Cholesterol. <i>American Journal of Human Genetics</i> , 2014, 94, 233-245. | 6.2 | 193 |
| 25 | Meta-Analysis of Genome-Wide Association Studies in African Americans Provides Insights into the Genetic Architecture of Type 2 Diabetes. <i>PLoS Genetics</i> , 2014, 10, e1004517. | 3.5 | 191 |
| 26 | Genetic Evidence for a Normal-Weight "Metabolically Obese" Phenotype Linking Insulin Resistance, Hypertension, Coronary Artery Disease, and Type 2 Diabetes. <i>Diabetes</i> , 2014, 63, 4369-4377. | 0.6 | 185 |
| 27 | Microbiome Signatures Associated With Steatohepatitis and Moderate to Severe Fibrosis in Children With Nonalcoholic Fatty Liver Disease. <i>Gastroenterology</i> , 2019, 157, 1109-1122. | 1.3 | 184 |
| 28 | Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. <i>Nature Communications</i> , 2015, 6, 5897. | 12.8 | 173 |
| 29 | Directional dominance on stature and cognition in diverse human populations. <i>Nature</i> , 2015, 523, 459-462. | 27.8 | 173 |
| 30 | Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. <i>Nature Communications</i> , 2017, 8, 14977. | 12.8 | 169 |
| 31 | Genome-wide physical activity interactions in adiposity "A meta-analysis of 200,452 adults. <i>PLoS Genetics</i> , 2017, 13, e1006528. | 3.5 | 158 |
| 32 | Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. <i>Nature Communications</i> , 2016, 7, 10494. | 12.8 | 153 |
| 33 | Large meta-analysis of genome-wide association studies identifies five loci for lean body mass. <i>Nature Communications</i> , 2017, 8, 80. | 12.8 | 147 |
| 34 | FTO genetic variants, dietary intake and body mass index: insights from 177 330 individuals. <i>Human Molecular Genetics</i> , 2014, 23, 6961-6972. | 2.9 | 143 |
| 35 | Genetic variants linked to education predict longevity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 13366-13371. | 7.1 | 110 |
| 36 | Pleiotropic genes for metabolic syndrome and inflammation. <i>Molecular Genetics and Metabolism</i> , 2014, 112, 317-338. | 1.1 | 107 |

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|----|--|------|-----------|
| 37 | A genomic approach to therapeutic target validation identifies a glucose-lowering <i>GLP1R</i> variant protective for coronary heart disease. <i>Science Translational Medicine</i> , 2016, 8, 341ra76. | 12.4 | 100 |
| 38 | Genetic inactivation of <i>ANGPTL4</i> improves glucose homeostasis and is associated with reduced risk of diabetes. <i>Nature Communications</i> , 2018, 9, 2252. | 12.8 | 99 |
| 39 | 1000 Genomes-based meta-analysis identifies 10 novel loci for kidney function. <i>Scientific Reports</i> , 2017, 7, 45040. | 3.3 | 98 |
| 40 | Discovery and fine-mapping of adiposity loci using high density imputation of genome-wide association studies in individuals of African ancestry: African Ancestry Anthropometry Genetics Consortium. <i>PLoS Genetics</i> , 2017, 13, e1006719. | 3.5 | 98 |
| 41 | Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. <i>PLoS ONE</i> , 2018, 13, e0198166. | 2.5 | 94 |
| 42 | Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. <i>Nature Genetics</i> , 2019, 51, 452-469. | 21.4 | 89 |
| 43 | Gene × dietary pattern interactions in obesity: analysis of up to 68 317 adults of European ancestry. <i>Human Molecular Genetics</i> , 2015, 24, 4728-4738. | 2.9 | 84 |
| 44 | A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. <i>Nature Communications</i> , 2016, 7, 13357. | 12.8 | 74 |
| 45 | Familial aggregation of resting blood pressure and heart rate in a sedentary population The heritage family study. <i>American Journal of Hypertension</i> , 1999, 12, 264-270. | 2.0 | 49 |
| 46 | Genome of the Netherlands population-specific imputations identify an <i>ABCA6</i> variant associated with cholesterol levels. <i>Nature Communications</i> , 2015, 6, 6065. | 12.8 | 45 |
| 47 | The effects of omega-3 polyunsaturated fatty acids and genetic variants on methylation levels of the interleukin-6 gene promoter. <i>Molecular Nutrition and Food Research</i> , 2016, 60, 410-419. | 3.3 | 41 |
| 48 | <i>SOS2</i> and <i>ACP1</i> Loci Identified through Large-Scale Exome Chip Analysis Regulate Kidney Development and Function. <i>Journal of the American Society of Nephrology: JASN</i> , 2017, 28, 981-994. | 6.1 | 39 |
| 49 | Genetic and Genomic Discovery Using Family Studies. <i>Circulation</i> , 2008, 118, 1057-1063. | 1.6 | 38 |
| 50 | Meta-analysis of 49,549 individuals imputed with the 1000 Genomes Project reveals an exonic damaging variant in <i>ANGPTL4</i> determining fasting TG levels. <i>Journal of Medical Genetics</i> , 2016, 53, 441-449. | 3.2 | 34 |
| 51 | Genome-wide association study of triglyceride response to a high-fat meal among participants of the NHLBI Genetics of Lipid Lowering Drugs and Diet Network (GOLDN). <i>Metabolism: Clinical and Experimental</i> , 2015, 64, 1359-1371. | 3.4 | 33 |
| 52 | Major Gene Influence on the Propensity to Store Fat in Trunk Versus Extremity Depots: Evidence From the Quebec Family Study. <i>Obesity</i> , 1995, 3, 1-8. | 4.0 | 32 |
| 53 | The <i>SCARB1</i> gene is associated with lipid response to dietary and pharmacological interventions. <i>Journal of Human Genetics</i> , 2008, 53, 709-717. | 2.3 | 32 |
| 54 | Complex Segregation Analysis of Blood Pressure and Heart Rate Measured before and after a 20-Week Endurance Exercise Training Program: the Heritage Family Study. <i>American Journal of Hypertension</i> , 2000, 13, 488-497. | 2.0 | 30 |

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|----|---|-----|-----------|
| 55 | Higher chylomicron remnants and LDL particle numbers associate with CD36 SNPs and DNA methylation sites that reduce CD36. <i>Journal of Lipid Research</i> , 2016, 57, 2176-2184. | 4.2 | 26 |
| 56 | Interaction of methylation-related genetic variants with circulating fatty acids on plasma lipids: a meta-analysis of 7 studies and methylation analysis of 3 studies in the Cohorts for Heart and Aging Research in Genomic Epidemiology consortium. <i>American Journal of Clinical Nutrition</i> , 2016, 103, 567-578. | 4.7 | 24 |
| 57 | Genetic association of long-chain acyl-CoA synthetase 1 variants with fasting glucose, diabetes, and subclinical atherosclerosis. <i>Journal of Lipid Research</i> , 2016, 57, 433-442. | 4.2 | 24 |
| 58 | Genome-wide association study identifies common loci influencing circulating glycosylated hemoglobin (HbA1c) levels in non-diabetic subjects: The Long Life Family Study (LLFS). <i>Metabolism: Clinical and Experimental</i> , 2014, 63, 461-468. | 3.4 | 22 |
| 59 | Rare Variation in <i>TET2</i> Is Associated with Clinically Relevant Prostate Carcinoma in African Americans. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2016, 25, 1456-1463. | 2.5 | 22 |
| 60 | An Empirical Comparison of Joint and Stratified Frameworks for Studying G × E Interactions: Systolic Blood Pressure and Smoking in the CHARGE Gene-Lifestyle Interactions Working Group. <i>Genetic Epidemiology</i> , 2016, 40, 404-415. | 1.3 | 18 |
| 61 | Genome-wide association meta-analysis of fish and EPA+DHA consumption in 17 US and European cohorts. <i>PLoS ONE</i> , 2017, 12, e0186456. | 2.5 | 18 |
| 62 | Discovery and fine-mapping of height loci via high-density imputation of GWASs in individuals of African ancestry. <i>American Journal of Human Genetics</i> , 2021, 108, 564-582. | 6.2 | 18 |
| 63 | Linkage and Association: Basic Concepts. <i>Advances in Genetics</i> , 2008, 60, 51-74. | 1.8 | 16 |
| 64 | Parent-of-Origin Effects of the APOB Gene on Adiposity in Young Adults. <i>PLoS Genetics</i> , 2015, 11, e1005573. | 3.5 | 16 |
| 65 | Inheritance of the Waist-to-Hip Ratio in the National Heart, Lung, and Blood Institute Family Heart Study. <i>Obesity</i> , 2000, 8, 294-301. | 4.0 | 15 |
| 66 | Cincinnati myocardial infarction and hormone family study: Family resemblance for testosterone in random and MI families. <i>American Journal of Medical Genetics Part A</i> , 1993, 47, 542-549. | 2.4 | 14 |
| 67 | Selection of models for the analysis of risk-factor trees: leveraging biological knowledge to mine large sets of risk factors with application to microbiome data. <i>Bioinformatics</i> , 2015, 31, 1607-1613. | 4.1 | 12 |
| 68 | Exploring genetic analysis of complex traits through the paradigm of alcohol dependence: Summary of GAW11 contributions. <i>Genetic Epidemiology</i> , 1999, 17, S1-24. | 1.3 | 10 |
| 69 | Examination of heterogeneity in 200 Danish breast cancer pedigrees. <i>Genetic Epidemiology</i> , 1986, 3, 67-72. | 1.3 | 9 |
| 70 | Fine mapping the CETP region reveals a common intronic insertion associated to HDL-C. <i>Npj Aging and Mechanisms of Disease</i> , 2015, 1, 15011. | 4.5 | 8 |
| 71 | Population differences in the pattern of familial aggregation for sex hormone-binding globulin and its response to exercise training: The HERITAGE family study. <i>American Journal of Human Biology</i> , 2001, 13, 832-837. | 1.6 | 7 |
| 72 | A CORRELATED META-ANALYSIS STRATEGY FOR DATA MINING ÆOMICÆ-SCANS. , 2012, , . | | 7 |

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|----|---|-----|-----------|
| 73 | Evolution of the Simulated Data Problem. Genetic Epidemiology, 2001, 21, S325-S331. | 1.3 | 4 |
| 74 | The impact of marker allele frequency misspecification in variance components quantitative trait locus analysis using sibship data. Genetic Epidemiology, 1999, 17, S73-S77. | 1.3 | 3 |
| 75 | A method to assess the environment for genetic studies: The common environment index and the household relationships interview. American Journal of Medical Genetics Part A, 1985, 21, 325-335. | 2.4 | 2 |
| 76 | Interval mapping of quantitative trait loci using a sib-pair linkage method. Genetic Epidemiology, 1995, 12, 723-728. | 1.3 | 0 |
| 77 | General Framework for Meta-Analysis of Haplotype Association Tests. Genetic Epidemiology, 2016, 40, 244-252. | 1.3 | 0 |
| 78 | Genome-wide contribution of genotype by environment interaction to blood lipid variation. FASEB Journal, 2013, 27, 222.4. | 0.5 | 0 |