

# 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	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
2	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
3	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
4	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
5	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
6	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
7	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
8	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
9	Rare and low-frequency coding variants alter human adult height. <i>Nature</i> , 2017, 542, 186-190.	27.8	544
10	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
11	1000 Genomes-based meta-analysis identifies 10 novel loci for kidney function. <i>Scientific Reports</i> , 2017, 7, 45040.	3.3	98
12	Genetic and Pharmacologic Inactivation of <i>ANGPTL3</i> and Cardiovascular Disease. <i>New England Journal of Medicine</i> , 2017, 377, 211-221.	27.0	633
13	<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
14	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
15	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
16	Genome-wide physical activity interactions in adiposity – A meta-analysis of 200,452 adults. <i>PLoS Genetics</i> , 2017, 13, e1006528.	3.5	158
17	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
18	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

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19	Meta-analysis of 49â€¦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
20	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
21	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
22	Genome-wide association study identifies 74 loci associated with educational attainment. <i>Nature</i> , 2016, 533, 539-542.	27.8	1,204
23	General Framework for Meta-Analysis of Haplotype Association Tests. <i>Genetic Epidemiology</i> , 2016, 40, 244-252.	1.3	0
24	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
25	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
26	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
27	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
28	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
29	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
30	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
31	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
32	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. <i>Nature Communications</i> , 2016, 7, 10495.	12.8	245
33	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. <i>Nature Communications</i> , 2016, 7, 10494.	12.8	153
34	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
35	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
36	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

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37	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
38	Parent-of-Origin Effects of the APOB Gene on Adiposity in Young Adults. <i>PLoS Genetics</i> , 2015, 11, e1005573.	3.5	16
39	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
40	New genetic loci link adipose and insulin biology to body fat distribution. <i>Nature</i> , 2015, 518, 187-196.	27.8	1,328
41	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015, 518, 197-206.	27.8	3,823
42	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
43	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
44	Directional dominance on stature and cognition in diverse human populations. <i>Nature</i> , 2015, 523, 459-462.	27.8	173
45	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
46	Genome of the Netherlands population-specific imputations identify an ABCA6 variant associated with cholesterol levels. <i>Nature Communications</i> , 2015, 6, 6065.	12.8	45
47	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
48	Genome-wide meta-analysis identifies six novel loci associated with habitual coffee consumption. <i>Molecular Psychiatry</i> , 2015, 20, 647-656.	7.9	235
49	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
50	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
51	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
52	Pleiotropic genes for metabolic syndrome and inflammation. <i>Molecular Genetics and Metabolism</i> , 2014, 112, 317-338.	1.1	107
53	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
54	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

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55	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
56	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
57	Discovery and refinement of loci associated with lipid levels. <i>Nature Genetics</i> , 2013, 45, 1274-1283.	21.4	2,641
58	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
59	Genome-wide contribution of genotype by environment interaction to blood lipid variation. <i>FASEB Journal</i> , 2013, 27, 222.4.	0.5	0
60	A CORRELATED META-ANALYSIS STRATEGY FOR DATA MINING "OMIC" SCANS. , 2012, , .		7
61	Hundreds of variants clustered in genomic loci and biological pathways affect human height. <i>Nature</i> , 2010, 467, 832-838.	27.8	1,789
62	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
63	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
64	The SCARB1 gene is associated with lipid response to dietary and pharmacological interventions. <i>Journal of Human Genetics</i> , 2008, 53, 709-717.	2.3	32
65	Linkage and Association: Basic Concepts. <i>Advances in Genetics</i> , 2008, 60, 51-74.	1.8	16
66	Genetic and Genomic Discovery Using Family Studies. <i>Circulation</i> , 2008, 118, 1057-1063.	1.6	38
67	Evolution of the Simulated Data Problem. <i>Genetic Epidemiology</i> , 2001, 21, S325-S331.	1.3	4
68	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
69	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
70	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
71	The impact of marker allele frequency misspecification in variance components quantitative trait locus analysis using sibship data. <i>Genetic Epidemiology</i> , 1999, 17, S73-S77.	1.3	3
72	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

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73	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
74	Interval mapping of quantitative trait loci using a sib-pair linkage method. <i>Genetic Epidemiology</i> , 1995, 12, 723-728.	1.3	0
75	Major Gene Influence on the Propensity to Store Fat in Trunk Versus Extremity Depots: Evidence From the Québec Family Study. <i>Obesity</i> , 1995, 3, 1-8.	4.0	32
76	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
77	Examination of heterogeneity in 200 Danish breast cancer pedigrees. <i>Genetic Epidemiology</i> , 1986, 3, 67-72.	1.3	9
78	A method to assess the environment for genetic studies: The common environment index and the household relationships interview. <i>American Journal of Medical Genetics Part A</i> , 1985, 21, 325-335.	2.4	2