

# Claudia Schurmann

## List of Publications by Year in descending order

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Version: 2024-02-01

74  
papers

12,659  
citations

66343

42  
h-index

66911

78  
g-index

89  
all docs

89  
docs citations

89  
times ranked

25764  
citing authors

#	ARTICLE	IF	CITATIONS
1	Rare coding variants in 35 genes associate with circulating lipid levelsâ€”A multi-ancestry analysis of 170,000 exomes. <i>American Journal of Human Genetics</i> , 2022, 109, 81-96.	6.2	24
2	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. <i>Nature Genetics</i> , 2022, 54, 560-572.	21.4	250
3	transferGWAS: GWAS of images using deep transfer learning. <i>Bioinformatics</i> , 2022, 38, 3621-3628.	4.1	15
4	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
5	Genetic discovery and risk characterization in type 2 diabetes across diverse populations. <i>Human Genetics and Genomics Advances</i> , 2021, 2, 100029.	1.7	23
6	The trans-ancestral genomic architecture of glyceemic traits. <i>Nature Genetics</i> , 2021, 53, 840-860.	21.4	341
7	Determinants of penetrance and variable expressivity in monogenic metabolic conditions across 77,184 exomes. <i>Nature Communications</i> , 2021, 12, 3505.	12.8	49
8	Exome sequencing and characterization of 49,960 individuals in the UK Biobank. <i>Nature</i> , 2020, 586, 749-756.	27.8	369
9	Genetic Studies of Leptin Concentrations Implicate Leptin in the Regulation of Early Adiposity. <i>Diabetes</i> , 2020, 69, 2806-2818.	0.6	26
10	A Genome-Wide Association Study Identifies Blood Disorderâ€”Related Variants Influencing Hemoglobin A1c With Implications for Glycemic Status in U.S. Hispanics/Latinos. <i>Diabetes Care</i> , 2019, 42, 1784-1791.	8.6	9
11	Associations of autozygosity with a broad range of human phenotypes. <i>Nature Communications</i> , 2019, 10, 4957.	12.8	84
12	Genetic analyses of diverse populations improves discovery for complex traits. <i>Nature</i> , 2019, 570, 514-518.	27.8	679
13	Exome-Derived Adiponectin-Associated Variants Implicate Obesity and Lipid Biology. <i>American Journal of Human Genetics</i> , 2019, 105, 15-28.	6.2	21
14	Exome sequencing of 20,791 cases of type 2 diabetes and 24,440 controls. <i>Nature</i> , 2019, 570, 71-76.	27.8	248
15	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
16	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
17	Genome-Wide Association Study of Heavy Smoking and Daily/Nondaily Smoking in the Hispanic Community Health Study/Study of Latinos (HCHS/SOL). <i>Nicotine and Tobacco Research</i> , 2018, 20, 448-457.	2.6	21
18	Fine-mapping type 2 diabetes loci to single-variant resolution using high-density imputation and islet-specific epigenome maps. <i>Nature Genetics</i> , 2018, 50, 1505-1513.	21.4	1,331

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19	Genome-wide association study of primary open-angle glaucoma in continental and admixed African populations. <i>Human Genetics</i> , 2018, 137, 847-862.	3.8	40
20	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
21	Generalization and fine mapping of red blood cell trait genetic associations to multi-ethnic populations: The PAGE study. <i>American Journal of Hematology</i> , 2018, 93, 1061-1073.	4.1	5
22	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
23	Rare and low-frequency coding variants alter human adult height. <i>Nature</i> , 2017, 542, 186-190.	27.8	544
24	Genome-wide association analyses for lung function and chronic obstructive pulmonary disease identify new loci and potential druggable targets. <i>Nature Genetics</i> , 2017, 49, 416-425.	21.4	257
25	Large-scale analyses of common and rare variants identify 12 new loci associated with atrial fibrillation. <i>Nature Genetics</i> , 2017, 49, 946-952.	21.4	279
26	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
27	Genome-wide association of white blood cell counts in Hispanic/Latino Americans: the Hispanic Community Health Study/Study of Latinos. <i>Human Molecular Genetics</i> , 2017, 26, 1193-1204.	2.9	38
28	Genetic and Pharmacologic Inactivation of ANGPTL3 and Cardiovascular Disease. <i>New England Journal of Medicine</i> , 2017, 377, 211-221.	27.0	633
29	Protein-altering and regulatory genetic variants near GATA4 implicated in bicuspid aortic valve. <i>Nature Communications</i> , 2017, 8, 15481.	12.8	90
30	Apolipoprotein L1 Variants and Blood Pressure Traits in African Americans. <i>Journal of the American College of Cardiology</i> , 2017, 69, 1564-1574.	2.8	46
31	<i>Helicobacter pylori</i> colonization and obesity – a Mendelian randomization study. <i>Scientific Reports</i> , 2017, 7, 14467.	3.3	21
32	Transcriptome-Wide Analysis Identifies Novel Associations With Blood Pressure. <i>Hypertension</i> , 2017, 70, 743-750.	2.7	34
33	Genome-wide association and targeted analysis of copy number variants with psoriatic arthritis in German patients. <i>BMC Medical Genetics</i> , 2017, 18, 92.	2.1	8
34	Genetic identification of a common collagen disease in Puerto Ricans via identity-by-descent mapping in a health system. <i>ELife</i> , 2017, 6, .	6.0	65
35	Genome-wide association study of red blood cell traits in Hispanics/Latinos: The Hispanic Community Health Study/Study of Latinos. <i>PLoS Genetics</i> , 2017, 13, e1006760.	3.5	53
36	Exome Genotyping Identifies Pleiotropic Variants Associated with Red Blood Cell Traits. <i>American Journal of Human Genetics</i> , 2016, 99, 8-21.	6.2	60

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37	Genomewide meta-analysis identifies loci associated with IGF and IGFBP levels with impact on age-related traits. <i>Aging Cell</i> , 2016, 15, 811-824.	6.7	83
38	A Whole-Blood Transcriptome Meta-Analysis Identifies Gene Expression Signatures of Cigarette Smoking. <i>Human Molecular Genetics</i> , 2016, 25, ddw288.	2.9	76
39	Genome-wide association study of copy number variation with lung function identifies a novel signal of association near BANP for forced vital capacity. <i>BMC Genetics</i> , 2016, 17, 116.	2.7	0
40	Platelet-Related Variants Identified by Exomechip Meta-analysis in 157,293 Individuals. <i>American Journal of Human Genetics</i> , 2016, 99, 40-55.	6.2	82
41	Large-Scale Exome-wide Association Analysis Identifies Loci for White Blood Cell Traits and Pleiotropy with Immune-Mediated Diseases. <i>American Journal of Human Genetics</i> , 2016, 99, 22-39.	6.2	50
42	Testing the role of predicted gene knockouts in human anthropometric trait variation. <i>Human Molecular Genetics</i> , 2016, 25, 2082-2092.	2.9	10
43	Genome-wide Association Study of Platelet Count Identifies Ancestry-Specific Loci in Hispanic/Latino Americans. <i>American Journal of Human Genetics</i> , 2016, 98, 229-242.	6.2	71
44	Analyzing Illumina Gene Expression Microarray Data Obtained From Human Whole Blood Cell and Blood Monocyte Samples. <i>Methods in Molecular Biology</i> , 2016, 1368, 85-97.	0.9	2
45	ABO blood type B and fucosyltransferase 2 non-secretor status as genetic risk factors for chronic pancreatitis. <i>Gut</i> , 2016, 65, 353-354.	12.1	13
46	Blood RNA expression profiles undergo major changes during the seventh decade. <i>Oncotarget</i> , 2016, 7, 71353-71361.	1.8	1
47	Extensive alterations of the whole-blood transcriptome are associated with body mass index: results of an mRNA profiling study involving two large population-based cohorts. <i>BMC Medical Genomics</i> , 2015, 8, 65.	1.5	40
48	Complement Component 5 Mediates Development of Fibrosis, via Activation of Stellate Cells, in 2 Mouse Models of Chronic Pancreatitis. <i>Gastroenterology</i> , 2015, 149, 765-776.e10.	1.3	68
49	A functional brain-derived neurotrophic factor (BDNF) gene variant increases the risk of moderate-to-severe allergic rhinitis. <i>Journal of Allergy and Clinical Immunology</i> , 2015, 135, 1486-1493.e8.	2.9	24
50	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
51	Translating Pharmacological Findings from Hypothyroid Rodents to Euthyroid Humans: Is There a Functional Role of Endogenous 3,5-T <sub>2</sub> ? <i>Thyroid</i> , 2015, 25, 188-197.	4.5	35
52	Fucosyltransferase 2 (FUT2) non-secretor status and blood group B are associated with elevated serum lipase activity in asymptomatic subjects, and an increased risk for chronic pancreatitis: a genetic association study. <i>Gut</i> , 2015, 64, 646-656.	12.1	82
53	Cell Specific eQTL Analysis without Sorting Cells. <i>PLoS Genetics</i> , 2015, 11, e1005223.	3.5	115
54	Directional dominance on stature and cognition in diverse human populations. <i>Nature</i> , 2015, 523, 459-462.	27.8	173

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55	A Meta-analysis of Gene Expression Signatures of Blood Pressure and Hypertension. <i>PLoS Genetics</i> , 2015, 11, e1005035.	3.5	107
56	Burden Analysis of Rare Microdeletions Suggests a Strong Impact of Neurodevelopmental Genes in Genetic Generalised Epilepsies. <i>PLoS Genetics</i> , 2015, 11, e1005226.	3.5	91
57	The transcriptional landscape of age in human peripheral blood. <i>Nature Communications</i> , 2015, 6, 8570.	12.8	533
58	Modulation of Genetic Associations with Serum Urate Levels by Body-Mass-Index in Humans. <i>PLoS ONE</i> , 2015, 10, e0119752.	2.5	64
59	Associations between Serum Sex Hormone Concentrations and Whole Blood Gene Expression Profiles in the General Population. <i>PLoS ONE</i> , 2015, 10, e0127466.	2.5	4
60	Mapping the Genetic Architecture of Gene Regulation in Whole Blood. <i>PLoS ONE</i> , 2014, 9, e93844.	2.5	31
61	A Genetic Variant in the Seed Region of miR-4513 Shows Pleiotropic Effects on Lipid and Glucose Homeostasis, Blood Pressure, and Coronary Artery Disease. <i>Human Mutation</i> , 2014, 35, 1524-1531.	2.5	45
62	Blood cis-eQTL Analysis Fails to Identify Novel Association Signals among Sub-Threshold Candidates from Genome-Wide Association Studies in Restless Legs Syndrome. <i>PLoS ONE</i> , 2014, 9, e98092.	2.5	2
63	Impact of common regulatory single-nucleotide variants on gene expression profiles in whole blood. <i>European Journal of Human Genetics</i> , 2013, 21, 48-54.	2.8	43
64	A proteomics workflow for quantitative and time-resolved analysis of adaptation reactions of internalized bacteria. <i>Methods</i> , 2013, 61, 244-250.	3.8	25
65	Systematic identification of trans eQTLs as putative drivers of known disease associations. <i>Nature Genetics</i> , 2013, 45, 1238-1243.	21.4	1,544
66	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. <i>Nature Genetics</i> , 2013, 45, 145-154.	21.4	675
67	Meta-Analysis of Genome-Wide Association Studies Identifies Six New Loci for Serum Calcium Concentrations. <i>PLoS Genetics</i> , 2013, 9, e1003796.	3.5	142
68	Identification of Genetic Loci Associated With <i>Helicobacter pylori</i> Serologic Status. <i>JAMA - Journal of the American Medical Association</i> , 2013, 309, 1912.	7.4	142
69	Exon-disrupting deletions of <i>NRXN1</i> in idiopathic generalized epilepsy. <i>Epilepsia</i> , 2013, 54, 256-264.	5.1	59
70	Rare Genomic Structural Variants in Complex Disease: Lessons from the Replication of Associations with Obesity. <i>PLoS ONE</i> , 2013, 8, e58048.	2.5	33
71	Life and Death of Proteins: A Case Study of Glucose-starved <i>Staphylococcus aureus</i> . <i>Molecular and Cellular Proteomics</i> , 2012, 11, 558-570.	3.8	42
72	A Genome-Wide Association Study Identifies Five Loci Influencing Facial Morphology in Europeans. <i>PLoS Genetics</i> , 2012, 8, e1002932.	3.5	274

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73	Analyzing Illumina Gene Expression Microarray Data from Different Tissues: Methodological Aspects of Data Analysis in the MetaXpress Consortium. PLoS ONE, 2012, 7, e50938.	2.5	71
74	Mirror extreme BMI phenotypes associated with gene dosage at the chromosome 16p11.2 locus. Nature, 2011, 478, 97-102.	27.8	394