Claudia Schurmann

List of Publications by Year
in descending order

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	Systematic identification of trans eQTLs as putative drivers of known disease associations. Nature Genetics, 2013, 45, 1238-1243.	21.4	1,544
2	Fine-mapping type 2 diabetes loci to single-variant resolution using high-density imputation and islet-specific epigenome maps. Nature Genetics, 2018, 50, 1505-1513.	21.4	1,331
3	Genetic analyses of diverse populations improves discovery for complex traits. Nature, 2019, 570, 514-518.	27.8	679
4	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. Nature Genetics, 2013, 45, 145-154.	21.4	675
5	Genetic and Pharmacologic Inactivation of ANGPTL3 and Cardiovascular Disease. New England Journal of Medicine, 2017, 377, 211-221.	27.0	633
6	A Protein-TruncatingHSD17B13Variant and Protection from Chronic Liver Disease. New England Journal of Medicine, 2018, 378, 1096-1106.	27.0	556
7	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	27.8	544
8	The transcriptional landscape of age in human peripheral blood. Nature Communications, 2015, 6, 8570.	12.8	533
9	Mirror extreme BMI phenotypes associated with gene dosage at the chromosome 16p11.2 locus. Nature, 2011, 478, 97-102.	27.8	394
10	Exome sequencing and characterization of 49,960 individuals in the UK Biobank. Nature, 2020, 586, 749-756.	27.8	369
11	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	21.4	341
12	Genome Analyses of >200,000 Individuals Identify 58 Loci for Chronic Inflammation and Highlight Pathways that Link Inflammation and Complex Disorders. American Journal of Human Genetics, 2018, 103, 691-706.	6.2	326
13	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. Nature Genetics, 2018, 50, 26-41.	21.4	286
14	Large-scale analyses of common and rare variants identify 12 new loci associated with atrial fibrillation. Nature Genetics, 2017, 49, 946-952.	21.4	279
15	A Genome-Wide Association Study Identifies Five Loci Influencing Facial Morphology in Europeans. PLoS Genetics, 2012, 8, e1002932.	3.5	274
16	Genome-wide association analyses for lung function and chronic obstructive pulmonary disease identify new loci and potential druggable targets. Nature Genetics, 2017, 49, 416-425.	21.4	257
17	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. Nature Genetics, 2022, 54, 560-572.	21.4	250
18	Exome sequencing of 20,791Âcases of type 2 diabetes and 24,440Âcontrols. Nature, 2019, 570, 71-76.	27.8	248

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19	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. Nature Communications, 2015, 6, 5897.	12.8	173
20	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	27.8	173
21	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. Nature Communications, 2017, 8, 14977.	12.8	169
22	Meta-Analysis of Genome-Wide Association Studies Identifies Six New Loci for Serum Calcium Concentrations. PLoS Genetics, 2013, 9, e1003796.	3.5	142
23	Identification of Genetic Loci Associated With Helicobacter pylori Serologic Status. JAMA - Journal of the American Medical Association, 2013, 309, 1912.	7.4	142
24	Cell Specific eQTL Analysis without Sorting Cells. PLoS Genetics, 2015, 11, e1005223.	3.5	115
25	A Meta-analysis of Gene Expression Signatures of Blood Pressure and Hypertension. PLoS Genetics, 2015, 11, e1005035.	3.5	107
26	Burden Analysis of Rare Microdeletions Suggests a Strong Impact of Neurodevelopmental Genes in Genetic Generalised Epilepsies. PLoS Genetics, 2015, 11, e1005226.	3.5	91
27	Protein-altering and regulatory genetic variants near GATA4 implicated in bicuspid aortic valve. Nature Communications, 2017, 8, 15481.	12.8	90
28	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	21.4	89
29	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	12.8	84
30	Genomewide metaâ€analysis identifies loci associated with <scp>IGF</scp> â€I and <scp>IGFBP</scp> â€3 levels with impact on ageâ€related traits. Aging Cell, 2016, 15, 811-824.	6.7	83
31	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. Gut, 2015, 64, 646-656.	12.1	82
32	Platelet-Related Variants Identified by Exomechip Meta-analysis in 157,293 Individuals. American Journal of Human Genetics, 2016, 99, 40-55.	6.2	82
33	A Whole-Blood Transcriptome Meta-Analysis Identifies Gene Expression Signatures of Cigarette Smoking. Human Molecular Genetics, 2016, 25, ddw288.	2.9	76
34	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
35	Genome-wide Association Study of Platelet Count Identifies Ancestry-Specific Loci in Hispanic/Latino Americans. American Journal of Human Genetics, 2016, 98, 229-242.	6.2	71
36	Complement Component 5 Mediates Development of Fibrosis, via Activation of Stellate Cells, in 2 Mouse Models of Chronic Pancreatitis. Gastroenterology, 2015, 149, 765-776.e10.	1.3	68

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37	Genetic identification of a common collagen disease in Puerto Ricans via identity-by-descent mapping in a health system. ELife, 2017, 6, .	6.0	65
38	Modulation of Genetic Associations with Serum Urate Levels by Body-Mass-Index in Humans. PLoS ONE, 2015, 10, e0119752.	2.5	64
39	Exome Genotyping Identifies Pleiotropic Variants Associated with Red Blood Cell Traits. American Journal of Human Genetics, 2016, 99, 8-21.	6.2	60
40	Exonâ€disrupting deletions of <scp>NRXN1</scp> in idiopathic generalized epilepsy. Epilepsia, 2013, 54, 256-264.	5.1	59
41	Genome-wide association study of red blood cell traits in Hispanics/Latinos: The Hispanic Community Health Study/Study of Latinos. PLoS Genetics, 2017, 13, e1006760.	3.5	53
42	Large-Scale Exome-wide Association Analysis Identifies Loci for White Blood Cell Traits and Pleiotropy with Immune-Mediated Diseases. American Journal of Human Genetics, 2016, 99, 22-39.	6.2	50
43	Determinants of penetrance and variable expressivity in monogenic metabolic conditions across 77,184 exomes. Nature Communications, 2021, 12, 3505.	12.8	49
44	Apolipoprotein L1 VariantsÂand Blood Pressure Traits inÂAfrican Americans. Journal of the American College of Cardiology, 2017, 69, 1564-1574.	2.8	46
45	A Genetic Variant in the Seed Region of miR-4513 Shows Pleiotropic Effects on Lipid and Glucose Homeostasis, Blood Pressure, and Coronary Artery Disease. Human Mutation, 2014, 35, 1524-1531.	2.5	45
46	Impact of common regulatory single-nucleotide variants on gene expression profiles in whole blood. European Journal of Human Genetics, 2013, 21, 48-54.	2.8	43
47	Life and Death of Proteins: A Case Study of Glucose-starved Staphylococcus aureus. Molecular and Cellular Proteomics, 2012, 11, 558-570.	3.8	42
48	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. BMC Medical Genomics, 2015, 8, 65.	1.5	40
49	Genome-wide association study of primary open-angle glaucoma in continental and admixed African populations. Human Genetics, 2018, 137, 847-862.	3.8	40
50	Genome-wide association of white blood cell counts in Hispanic/Latino Americans: the Hispanic Community Health Study/Study of Latinos. Human Molecular Genetics, 2017, 26, 1193-1204.	2.9	38
51	Translating Pharmacological Findings from Hypothyroid Rodents to Euthyroid Humans: Is There a Functional Role of Endogenous 3,5-T2?. Thyroid, 2015, 25, 188-197.	4.5	35
52	Transcriptome-Wide Analysis Identifies Novel Associations With Blood Pressure. Hypertension, 2017, 70, 743-750.	2.7	34
53	Rare Genomic Structural Variants in Complex Disease: Lessons from the Replication of Associations with Obesity. PLoS ONE, 2013, 8, e58048.	2.5	33
54	Mapping the Genetic Architecture of Gene Regulation in Whole Blood. PLoS ONE, 2014, 9, e93844.	2.5	31

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55	Genetic Studies of Leptin Concentrations Implicate Leptin in the Regulation of Early Adiposity. Diabetes, 2020, 69, 2806-2818.	0.6	26
56	A proteomics workflow for quantitative and time-resolved analysis of adaptation reactions of internalized bacteria. Methods, 2013, 61, 244-250.	3.8	25
57	A functional brain-derived neurotrophic factor (BDNF) gene variant increases the risk of moderate-to-severe allergic rhinitis. Journal of Allergy and Clinical Immunology, 2015, 135, 1486-1493.e8.	2.9	24
58	Rare coding variants in 35 genes associate with circulating lipid levelsâ€"A multi-ancestry analysis of 170,000 exomes. American Journal of Human Genetics, 2022, 109, 81-96.	6.2	24
59	Genetic discovery and risk characterization in type 2 diabetes across diverse populations. Human Genetics and Genomics Advances, 2021, 2, 100029.	1.7	23
60	Helicobacter pylori colonization and obesity â€“ a Mendelian randomization study. Scientific Reports, 2017, 7, 14467.	3.3	21
61	Genome-Wide Association Study of Heavy Smoking and Daily/Nondaily Smoking in the Hispanic Community Health Study/Study of Latinos (HCHS/SOL). Nicotine and Tobacco Research, 2018, 20, 448-457.	2.6	21
62	Exome-Derived Adiponectin-Associated Variants Implicate Obesity and Lipid Biology. American Journal of Human Genetics, 2019, 105, 15-28.	6.2	21
63	Discovery and fine-mapping of height loci via high-density imputation of GWASs in individuals of African ancestry. American Journal of Human Genetics, 2021, 108, 564-582.	6.2	18
64	transferGWAS: GWAS of images using deep transfer learning. Bioinformatics, 2022, 38, 3621-3628.	4.1	15
65	ABO blood type B and fucosyltransferase 2 non-secretor status as genetic risk factors for chronic pancreatitis. Gut, 2016, 65, 353-354.	12.1	13
66	Testing the role of predicted gene knockouts in human anthropometric trait variation. Human Molecular Genetics, 2016, 25, 2082-2092.	2.9	10
67	A Genome-Wide Association Study Identifies Blood Disorderâ€"Related Variants Influencing Hemoglobin A1c With Implications for Glycemic Status in U.S. Hispanics/Latinos. Diabetes Care, 2019, 42, 1784-1791.	8.6	9
68	Genome-wide association and targeted analysis of copy number variants with psoriatic arthritis in German patients. BMC Medical Genetics, 2017, 18, 92.	2.1	8
69	Generalization and fine mapping of red blood cell trait genetic associations to multiâ€ethnic populations: The PAGE study. American Journal of Hematology, 2018, 93, 1061-1073.	4.1	5
70	Associations between Serum Sex Hormone Concentrations and Whole Blood Gene Expression Profiles in the General Population. PLoS ONE, 2015, 10, e0127466.	2.5	4
71	Analyzing Illumina Gene Expression Microarray Data Obtained From Human Whole Blood Cell and Blood Monocyte Samples. Methods in Molecular Biology, 2016, 1368, 85-97.	0.9	2
72	Blood cis-eQTL Analysis Fails to Identify Novel Association Signals among Sub-Threshold Candidates from Genome-Wide Association Studies in Restless Legs Syndrome. PLoS ONE, 2014, 9, e98092.	2.5	2

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73	Blood RNA expression profiles undergo major changes during the seventh decade. Oncotarget, 2016, 7, 71353-71361.	1.8	1
74	Genome-wide association study of copy number variation with lung function identifies a novel signal of association near BANP for forced vital capacity. BMC Genetics, 2016, 17, 116.	2.7	0