Christian Fuchsberger

List of Publications by Year
in descending order

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126 papers	45,276 citations	25034 57 h-index	18130 120 g-index
148 all docs	148 docs citations	148 times ranked	62129 citing authors

#	Article	IF	Citations
1	Prospective epidemiological, molecular, and genetic characterization of a novel coronavirus disease in the Val Venosta/Vinschgau: the CHRIS COVID-19 study protocol. Pathogens and Global Health, 2022, 116, 128-136.	2.3	4
2	Genome-wide association studies of metabolites in Finnish men identify disease-relevant loci. Nature Communications, 2022, 13, 1644.	12.8	63
3	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
4	Meta-imputation: An efficient method to combine genotype data after imputation with multiple reference panels. American Journal of Human Genetics, 2022, 109, 1007-1015.	6.2	15
5	Genetic loci and prioritization of genes for kidney function decline derived from a meta-analysis of 62 longitudinal genome-wide association studies. Kidney International, 2022, 102, 624-639.	5.2	18
6	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. Communications Biology, 2022, 5, .	4.4	17
7	Whole Exome Sequencing Enhanced Imputation Identifies 85 Metabolite Associations in the Alpine CHRIS Cohort. Metabolites, 2022, 12, 604.	2.9	6
8	Association of mitochondrial DNA copy number with metabolic syndrome and type 2 diabetes in 14Â176 individuals. Journal of Internal Medicine, 2021, 290, 190-202.	6.0	61
9	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299.	27.8	1,069
10	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	21.4	341
11	Frequency of Heterozygous Parkin (PRKN) Variants and Penetrance of Parkinson's Disease Risk Markers in the Population-Based CHRIS Cohort. Frontiers in Neurology, 2021, 12, 706145.	2.4	14
12	A high-resolution HLA reference panel capturing global population diversity enables multi-ancestry fine-mapping in HIV host response. Nature Genetics, 2021, 53, 1504-1516.	21.4	69
13	Genetic and Metabolic Determinants of Atrial Fibrillation in a General Population Sample: The CHRIS Study. Biomolecules, 2021, 11, 1663.	4.0	5
14	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	27.8	353
15	Combining sequence data from multiple studies: Impact of analysis strategies on rare variant calling and association results. Genetic Epidemiology, 2020, 44, 41-51.	1.3	2
16	Adiponectin GWAS loci harboring extensive allelic heterogeneity exhibit distinct molecular consequences. PLoS Genetics, 2020, 16, e1009019.	3.5	11
17	Loss-of-function genomic variants highlight potential therapeutic targets for cardiovascular disease. Nature Communications, 2020, 11, 6417.	12.8	39
18	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. Nature Communications, 2020, 11, 2542.	12.8	59

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19	Sequencing and imputation in GWAS: Costâ€effective strategies to increase power and genomic coverage across diverse populations. Genetic Epidemiology, 2020, 44, 537-549.	1.3	30
20	emeraLD: rapid linkage disequilibrium estimation with massive datasets. Bioinformatics, 2019, 35, 164-166.	4.1	15
21	Evaluation of the role of STAP1 in Familial Hypercholesterolemia. Scientific Reports, 2019, 9, 11995.	3.3	17
22	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	12.8	84
23	Colocalization of GWAS and eQTL signals at loci with multiple signals identifies additional candidate genes for body fat distribution. Human Molecular Genetics, 2019, 28, 4161-4172.	2.9	41
24	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. Nature Communications, 2019, 10, 4130.	12.8	133
25	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. Nature Genetics, 2019, 51, 1459-1474.	21.4	251
26	Adipose Tissue Gene Expression Associations Reveal Hundreds of Candidate Genes for Cardiometabolic Traits. American Journal of Human Genetics, 2019, 105, 773-787.	6.2	45
27	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	21.4	549
28	Exome sequencing of 20,791Âcases of type 2 diabetes and 24,440Âcontrols. Nature, 2019, 570, 71-76.	27.8	248
29	The GenomeAsia 100K Project enables genetic discoveries across Asia. Nature, 2019, 576, 106-111.	27.8	265
30	Microbiota, type 2 diabetes and non-alcoholic fatty liver disease: protocol of an observational study. Journal of Translational Medicine, 2019, 17, 408.	4.4	7
31	Identification of African-Specific Admixture between Modern and Archaic Humans. American Journal of Human Genetics, 2019, 105, 1254-1261.	6.2	16
32	KCND3 potassium channel gene variant confers susceptibility to electrocardiographic early repolarization pattern. JCI Insight, 2019, 4, .	5.0	15
33	Are Requirements to Deposit Data in Research Repositories Compatible With the European Union's General Data Protection Regulation?. Annals of Internal Medicine, 2019, 170, 332.	3.9	27
34	Identification of seven novel loci associated with amino acid levels using single-variant and gene-based tests in 8545 Finnish men from the METSIM study. Human Molecular Genetics, 2018, 27, 1664-1674.	2.9	30
35	A Common Type 2 Diabetes Risk Variant Potentiates Activity of an Evolutionarily Conserved Islet Stretch Enhancer and Increases C2CD4A and C2CD4B Expression. American Journal of Human Genetics, 2018, 102, 620-635.	6.2	47
36	Evaluating the contribution of rare variants to type 2 diabetes and related traits using pedigrees. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 379-384.	7.1	28

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37	Imputation-Aware Tag SNP Selection To Improve Power for Large-Scale, Multi-ethnic Association Studies. G3: Genes, Genomes, Genetics, 2018, 8, 3255-3267.	1.8	36
38	Genome-wide analyses identify a role for SLC17A4 and AADAT in thyroid hormone regulation. Nature Communications, 2018, 9, 4455.	12.8	181
39	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
40	Reversal of Agingâ€Induced Increases in Aortic Stiffness by Targeting Cytoskeletal Proteinâ€Protein Interfaces. Journal of the American Heart Association, 2018, 7, .	3.7	17
41	Genetic Regulation of Adipose Gene Expression and Cardio-Metabolic Traits. American Journal of Human Genetics, 2017, 100, 428-443.	6.2	141
42	1000 Genomes-based meta-analysis identifies 10 novel loci for kidney function. Scientific Reports, 2017, 7, 45040.	3.3	98
43	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. Diabetes, 2017, 66, 2888-2902.	0.6	615
44	A Low-Frequency Inactivating AKT2 Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. Diabetes, 2017, 66, 2019-2032.	0.6	47
45	SOS2 and ACP1 Loci Identified through Large-Scale Exome Chip Analysis Regulate Kidney Development and Function. Journal of the American Society of Nephrology: JASN, 2017, 28, 981-994.	6.1	39
46	Genome-wide meta-analysis associates HLA-DQA1/DRB1 and LPA and lifestyle factors with human longevity. Nature Communications, 2017, 8, 910.	12.8	118
47	Improving power for rareâ€variant tests by integrating external controls. Genetic Epidemiology, 2017, 41, 610-619.	1.3	18
48	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Scientific Data, 2017, 4, 170179.	5.3	31
49	Enrichment of colorectal cancer associations in functional regions: Insight for using epigenomics data in the analysis of whole genome sequence-imputed GWAS data. PLoS ONE, 2017, 12, e0186518.	2.5	8
50	Common, low-frequency, and rare genetic variants associated with lipoprotein subclasses and triglyceride measures in Finnish men from the METSIM study. PLoS Genetics, 2017, 13, e1007079.	3.5	49
51	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	27.8	952
52	Putative Prostate Cancer Risk SNP in an Androgen Receptorâ€Binding Site of the Melanophilin Gene Illustrates Enrichment of Risk SNPs in Androgen Receptor Target Sites. Human Mutation, 2016, 37, 52-64.	2.5	35
53	mtDNA-Server: next-generation sequencing data analysis of human mitochondrial DNA in the cloud. Nucleic Acids Research, 2016, 44, W64-W69.	14.5	144
54	Reference-based phasing using the Haplotype Reference Consortium panel. Nature Genetics, 2016, 48, 1443-1448.	21.4	1,357

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55	Next-generation genotype imputation service and methods. Nature Genetics, 2016, 48, 1284-1287.	21.4	2,828
56	A reference panel of 64,976 haplotypes for genotype imputation. Nature Genetics, 2016, 48, 1279-1283.	21.4	2,421
57	Prosaposin is a regulator of progranulin levels and oligomerization. Nature Communications, 2016, 7, 11992.	12.8	68
58	Meta-analysis identifies common and rare variants influencing blood pressure and overlapping with metabolic trait loci. Nature Genetics, 2016, 48, 1162-1170.	21.4	223
59	Omics-squared: human genomic, transcriptomic and phenotypic data for genetic analysis workshop 19. BMC Proceedings, 2016, 10, 71-77.	1.6	17
60	Independent test assessment using the extreme value distribution theory. BMC Proceedings, 2016, 10, 245-249.	1.6	1
61	Genome-wide Association Studies Identify Genetic Loci Associated With Albuminuria in Diabetes. Diabetes, 2016, 65, 803-817.	0.6	131
62	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. Nature Communications, 2016, 7, 10023.	12.8	412
63	An efficient resampling method for calibrating single and gene-based rare variant association analysis in caseâ€“control studies. Biostatistics, 2016, 17, 1-15.	1.5	46
64	Abstract 4489: Using functional data from Roadmap Epigenomics to inform analysis of rare variants linked to gene expression in a large colorectal cancer study. , 2016, , .		0
65	The Cooperative Health Research in South Tyrol (CHRIS) study: rationale, objectives, and preliminary results. Journal of Translational Medicine, 2015, 13, 348.	4.4	63
66	Multiple Hepatic Regulatory Variants at the GALNT2 GWAS Locus Associated with High-Density Lipoprotein Cholesterol. American Journal of Human Genetics, 2015, 97, 801-815.	6.2	49
67	miR-22 and miR-29a Are Members of the Androgen Receptor Cistrome Modulating LAMC1 and Mcl-1 in Prostate Cancer. Molecular Endocrinology, 2015, 29, 1037-1054.	3.7	69
68	Structural forms of the human amylase locus and their relationships to SNPs, haplotypes and obesity. Nature Genetics, 2015, 47, 921-925.	21.4	120
69	The Power of Gene-Based Rare Variant Methods to Detect Disease-Associated Variation and Test Hypotheses About Complex Disease. PLoS Genetics, 2015, 11, e1005165.	3.5	124
70	Identification and Functional Characterization of G6PC2 Coding Variants Influencing Glycemic Traits Define an Effector Transcript at the G6PC2-ABCB11 Locus. PLoS Genetics, 2015, 11, e1004876.	3.5	95
71	minimac2: faster genotype imputation. Bioinformatics, 2015, 31, 782-784.	4.1	444
72	A global reference for human genetic variation. Nature, 2015, 526, 68-74.	27.8	13,998

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73	Genome sequencing elucidates Sardinian genetic architecture and augments association analyses for lipid and blood inflammatory markers. Nature Genetics, 2015, 47, 1272-1281.	21.4	193
74	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. Nature Genetics, 2015, 47, 1415-1425.	21.4	365
75	Rare variants in PPARG with decreased activity in adipocyte differentiation are associated with increased risk of type 2 diabetes. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 13127-13132.	7.1	152
76	Whole Genome and Exome Sequencing of Type 2 Diabetes. Frontiers in Diabetes, 2014, , 29-41.	0.4	0
77	Re-sequencing Expands Our Understanding of the Phenotypic Impact of Variants at GWAS Loci. PLoS Genetics, 2014, 10, e1004147.	3.5	50
78	Whole-Exome Sequencing Identifies Rare and Low-Frequency Coding Variants Associated with LDL Cholesterol. American Journal of Human Genetics, 2014, 94, 233-245.	6.2	193
79	Data for Genetic Analysis Workshop 18: human whole genome sequence, blood pressure, and simulated phenotypes in extended pedigrees. BMC Proceedings, 2014, 8, S2.	1.6	65
80	A Common Functional Regulatory Variant at a Type 2 Diabetes Locus Upregulates ARAP1 Expression in the Pancreatic Beta Cell. American Journal of Human Genetics, 2014, 94, 186-197.	6.2	67
81	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. Nature Genetics, 2014, 46, 826-836.	21.4	281
82	Loss-of-function mutations in SLC30A8 protect against type 2 diabetes. Nature Genetics, 2014, 46, 357-363.	21.4	428
83	Simulation of Finnish Population History, Guided by Empirical Genetic Data, to Assess Power of Rare-Variant Tests in Finland. American Journal of Human Genetics, 2014, 94, 710-720.	6.2	24
84	Abstract 3549: miRNAs and androgen receptor interplay in prostate cancer. , 2014, , .		0
85	Genotype Imputation in Genomeâ€Wide Association Studies. Current Protocols in Human Genetics, 2013, 78, Unit 1.25.	3.5	34
86	Fine-Mapping of Restless Legs Locus 4 (RLS4) Identifies a Haplotype over the SPATS2L and KCTD18 Genes. Journal of Molecular Neuroscience, 2013, 49, 600-605.	2.3	12
87	Integrative Annotation of Variants from 1092 Humans: Application to Cancer Genomics. Science, 2013, 342, 1235587.	12.6	341
88	Exome array analysis identifies new loci and low-frequency variants influencing insulin processing and secretion. Nature Genetics, 2013, 45, 197-201.	21.4	247
89	Common Variants in Mendelian Kidney Disease Genes and Their Association with Renal Function. Journal of the American Society of Nephrology: JASN, 2013, 24, 2105-2117.	6.1	33
90	Identification of heart rateâ€“associated loci and their effects on cardiac conduction and rhythm disorders. Nature Genetics, 2013, 45, 621-631.	21.4	282

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91	Anterior gradientÂ2 and 3 â€“ two prototype androgenâ€responsive genes transcriptionally upregulated by androgens and by oestrogens in prostate cancer cells. FEBS Journal, 2013, 280, 1249-1266.	4.7	40
92	Genome-Wide Association and Functional Follow-Up Reveals New Loci for Kidney Function. PLoS Genetics, 2012, 8, e1002584.	3.5	166
93	The Metabochip, a Custom Genotyping Array for Genetic Studies of Metabolic, Cardiovascular, and Anthropometric Traits. PLoS Genetics, 2012, 8, e1002793.	3.5	448
94	Novel Loci for Adiponectin Levels and Their Influence on Type 2 Diabetes and Metabolic Traits: A Multi-Ethnic Meta-Analysis of 45,891 Individuals. PLoS Genetics, 2012, 8, e1002607.	3.5	419
95	Integration of genome-wide association studies with biological knowledge identifies six novel genes related to kidney function. Human Molecular Genetics, 2012, 21, 5329-5343.	2.9	64
96	Common Genetic Variation in the 3â€²- BCL11B Gene Desert Is Associated With Carotid-Femoral Pulse Wave Velocity and Excess Cardiovascular Disease Risk. Circulation: Cardiovascular Genetics, 2012, 5, 81-90.	5.1	90
97	GWAtoolbox: an R package for fast quality control and handling of genome-wide association studies meta-analysis data. Bioinformatics, 2012, 28, 444-445.	4.1	46
98	Fast and accurate genotype imputation in genome-wide association studies through pre-phasing. Nature Genetics, 2012, 44, 955-959.	21.4	1,592
99	An integrated map of genetic variation from 1,092 human genomes. Nature, 2012, 491, 56-65.	27.8	7,199
100	Meta-Analysis of Genome-Wide Association Studies in >80 000 Subjects Identifies Multiple Loci for C-Reactive Protein Levels. Circulation, 2011, 123, 731-738.	1.6	461
101	Proteomics Profiling of Microdissected Low- and High-Grade Prostate Tumors Identifies Lamin A as a Discriminatory Biomarker. Journal of Proteome Research, 2011, 10, 259-268.	3.7	83
102	617 STEROID HORMONES REGULATION OF METASTASIS-ASSOCIATED CHAPERONE PROTEINS AGR2 AND AGR3 IN PROSTATE CANCER CELLS. Journal of Urology, 2011, 185, .	0.4	0
103	CUBN Is a Gene Locus for Albuminuria. Journal of the American Society of Nephrology: JASN, 2011, 22, 555-570.	6.1	208
104	Linkage and association analysis of hyperthyrotropinaemia in an Alpine population reveal two novel loci on chromosomes 3q28-29 and 6q26-27. Journal of Medical Genetics, 2011, 48, 549-556.	3.2	6
105	Heritability Analysis of Life Span in a Semi-isolated Population Followed Across Four Centuries Reveals the Presence of Pleiotropy Between Life Span and Reproduction. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2011, 66A, 26-37.	3.6	44
106	Genome-wide association analysis and fine mapping of NT-proBNP level provide novel insight into the role of the MTHFR-CLCN6-NPPA-NPPB gene cluster. Human Molecular Genetics, 2011, 20, 1660-1671.	2.9	47
107	Copy number variation and association over T-cell receptor genesâ€”influence of DNA source. Immunogenetics, 2010, 62, 561-567.	2.4	14
108	Drawing the history of the Hutterite population on a genetic landscape: inference from Y-chromosome and mtDNA genotypes. European Journal of Human Genetics, 2010, 18, 463-470.	2.8	26

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109	Genes predict village of origin in rural Europe. European Journal of Human Genetics, 2010, 18, 1269-1270.	2.8	22
110	New loci associated with kidney function and chronic kidney disease. Nature Genetics, 2010, 42, 376-384.	21.4	710
111	Common variants in 22 loci are associated with QRS duration and cardiac ventricular conduction. Nature Genetics, 2010, 42, 1068-1076.	21.4	308
112	Genome-wide association analysis identifies multiple loci related to resting heart rate. Human Molecular Genetics, 2010, 19, 3885-3894.	2.9	133
113	Clear detection of ADIPOQ locus as the major gene for plasma adiponectin: Results of genome-wide association analyses including 4659 European individuals. Atherosclerosis, 2010, 208, 412-420.	0.8	146
114	410 LAMIN A/C IS A POTENTIAL DISCRIMINATORY BIOMARKER OF LOW AND HIGH GRADE PROSTATE CANCER. Journal of Urology, 2010, 183, .	0.4	0
115	FERTILITY PATTERN AND FAMILY STRUCTURE IN THREE ALPINE SETTLEMENTS IN SOUTH TYROL (ITALY): MARRIAGE COHORTS FROM 1750 TO 1949. Journal of Biosocial Science, 2009, 41, 697-701.	1.2	4
116	Common variants at ten loci modulate the QT interval duration in the QTSCD Study. Nature Genetics, 2009, 41, 407-414.	21.4	356
117	IMAGING OF PROSTATE TISSUE SECTIONS BY MALDI PROTEIN MASS SPECTROMETRY â€“ TISVIS, A TOOL FOR THE VISUAL DATA PROCESSING. Journal of Urology, 2008, 179, 389-390.	0.4	2
118	Analysis and Visualization of Spatial Proteomic Data for Tissue Characterization. , 2008, , .		0
119	Visual Analytical Methods to Identify Family Clustered Diseases. , 2008, , .		1
120	Jenti: an efficient tool for mining complex inbred genealogies. Bioinformatics, 2008, 24, 724-726.	4.1	15
121	PedVizApi: a Java API for the interactive, visual analysis of extended pedigrees. Bioinformatics, 2008, 24, 279-281.	4.1	8
122	The genetic study of three population microisolates in South Tyrol (MICROS): study design and epidemiological perspectives. BMC Medical Genetics, 2007, 8, 29.	2.1	56
123	Influence of blood sampling on protein profiling and pattern analysis using matrix-assisted laser desorption/ionisation mass spectrometry. BJU International, 2007, 99, 658-662.	2.5	6
124	154: Integration of TPSA and High-Throughput Mass Spectrometry Data Improves Prostate Cancer Prediction. Journal of Urology, 2007, 177, 52-53.	0.4	0
125	Testing Asbru Guidelines and Protocols for Neonatal Intensive Care. Lecture Notes in Computer Science, 2005, , 101-110.	1.3	12
126	South Asian Patient Population Genetics Reveal Strong Founder Effects and High Rates of Homozygosity â€“ New Resources for Precision Medicine. SSRN Electronic Journal, 0, , .	0.4	2