Christian Fuchsberger

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/5228655/publications.pdf

Version: 2024-02-01

126 papers	45,276 citations	25014 57 h-index	18115 120 g-index
148 all docs	148 docs citations	148 times ranked	62129 citing authors

#	Article	IF	Citations
1	A global reference for human genetic variation. Nature, 2015, 526, 68-74.	13.7	13,998
2	An integrated map of genetic variation from 1,092 human genomes. Nature, 2012, 491, 56-65.	13.7	7,199
3	Next-generation genotype imputation service and methods. Nature Genetics, 2016, 48, 1284-1287.	9.4	2,828
4	A reference panel of 64,976 haplotypes for genotype imputation. Nature Genetics, 2016, 48, 1279-1283.	9.4	2,421
5	Fast and accurate genotype imputation in genome-wide association studies through pre-phasing. Nature Genetics, 2012, 44, 955-959.	9.4	1,592
6	Reference-based phasing using the Haplotype Reference Consortium panel. Nature Genetics, 2016, 48, 1443-1448.	9.4	1,357
7	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299.	13.7	1,069
8	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	13.7	952
9	New loci associated with kidney function and chronic kidney disease. Nature Genetics, 2010, 42, 376-384.	9.4	710
10	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. Diabetes, 2017, 66, 2888-2902.	0.3	615
11	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	9.4	549
12	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
13	The Metabochip, a Custom Genotyping Array for Genetic Studies of Metabolic, Cardiovascular, and Anthropometric Traits. PLoS Genetics, 2012, 8, e1002793.	1.5	448
14	minimac2: faster genotype imputation. Bioinformatics, 2015, 31, 782-784.	1.8	444
15	Loss-of-function mutations in SLC30A8 protect against type 2 diabetes. Nature Genetics, 2014, 46, 357-363.	9.4	428
16	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.	1.5	419
17	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. Nature Communications, 2016, 7, 10023.	5.8	412
18	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. Nature Genetics, 2015, 47, 1415-1425.	9.4	365

#	Article	IF	Citations
19	Common variants at ten loci modulate the QT interval duration in the QTSCD Study. Nature Genetics, 2009, 41, 407-414.	9.4	356
20	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	13.7	353
21	Integrative Annotation of Variants from 1092 Humans: Application to Cancer Genomics. Science, 2013, 342, 1235587.	6.0	341
22	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	9.4	341
23	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.	2.6	326
24	Common variants in 22 loci are associated with QRS duration and cardiac ventricular conduction. Nature Genetics, 2010, 42, 1068-1076.	9.4	308
25	Identification of heart rateâ€“associated loci and their effects on cardiac conduction and rhythm disorders. Nature Genetics, 2013, 45, 621-631.	9.4	282
26	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. Nature Genetics, 2014, 46, 826-836.	9.4	281
27	The GenomeAsia 100K Project enables genetic discoveries across Asia. Nature, 2019, 576, 106-111.	13.7	265
28	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. Nature Genetics, 2019, 51, 1459-1474.	9.4	251
29	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. Nature Genetics, 2022, 54, 560-572.	9.4	250
30	Exome sequencing of 20,791Âcases of type 2 diabetes and 24,440Âcontrols. Nature, 2019, 570, 71-76.	13.7	248
31	Exome array analysis identifies new loci and low-frequency variants influencing insulin processing and secretion. Nature Genetics, 2013, 45, 197-201.	9.4	247
32	Meta-analysis identifies common and rare variants influencing blood pressure and overlapping with metabolic trait loci. Nature Genetics, 2016, 48, 1162-1170.	9.4	223
33	CUBN Is a Gene Locus for Albuminuria. Journal of the American Society of Nephrology: JASN, 2011, 22, 555-570.	3.0	208
34	Whole-Exome Sequencing Identifies Rare and Low-Frequency Coding Variants Associated with LDL Cholesterol. American Journal of Human Genetics, 2014, 94, 233-245.	2.6	193
35	Genome sequencing elucidates Sardinian genetic architecture and augments association analyses for lipid and blood inflammatory markers. Nature Genetics, 2015, 47, 1272-1281.	9.4	193
36	Genome-wide analyses identify a role for SLC17A4 and AADAT in thyroid hormone regulation. Nature Communications, 2018, 9, 4455.	5.8	181

#	Article	IF	Citations
37	Genome-Wide Association and Functional Follow-Up Reveals New Loci for Kidney Function. PLoS Genetics, 2012, 8, e1002584.	1.5	166
38	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.	3.3	152
39	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.	0.4	146
40	mtDNA-Server: next-generation sequencing data analysis of human mitochondrial DNA in the cloud. Nucleic Acids Research, 2016, 44, W64-W69.	6.5	144
41	Genetic Regulation of Adipose Gene Expression and Cardio-Metabolic Traits. American Journal of Human Genetics, 2017, 100, 428-443.	2.6	141
42	Genome-wide association analysis identifies multiple loci related to resting heart rate. Human Molecular Genetics, 2010, 19, 3885-3894.	1.4	133
43	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. Nature Communications, 2019, 10, 4130.	5.8	133
44	Genome-wide Association Studies Identify Genetic Loci Associated With Albuminuria in Diabetes. Diabetes, 2016, 65, 803-817.	0.3	131
45	The Power of Gene-Based Rare Variant Methods to Detect Disease-Associated Variation and Test Hypotheses About Complex Disease. PLoS Genetics, 2015, 11, e1005165.	1.5	124
46	Structural forms of the human amylase locus and their relationships to SNPs, haplotypes and obesity. Nature Genetics, 2015, 47, 921-925.	9.4	120
47	Genome-wide meta-analysis associates HLA-DQA1/DRB1 and LPA and lifestyle factors with human longevity. Nature Communications, 2017, 8, 910.	5.8	118
48	1000 Genomes-based meta-analysis identifies 10 novel loci for kidney function. Scientific Reports, 2017, 7, 45040.	1.6	98
49	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.	1.5	95
50	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
51	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	5.8	84
52	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.	1.8	83
53	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
54	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.	9.4	69

#	Article	IF	Citations
55	Prosaposin is a regulator of progranulin levels and oligomerization. Nature Communications, 2016, 7, 11992.	5.8	68
56	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.	2.6	67
57	Data for Genetic Analysis Workshop 18: human whole genome sequence, blood pressure, and simulated phenotypes in extended pedigrees. BMC Proceedings, 2014, 8, S2.	1.8	65
58	Integration of genome-wide association studies with biological knowledge identifies six novel genes related to kidney function. Human Molecular Genetics, 2012, 21, 5329-5343.	1.4	64
59	The Cooperative Health Research in South Tyrol (CHRIS) study: rationale, objectives, and preliminary results. Journal of Translational Medicine, 2015, 13, 348.	1.8	63
60	Genome-wide association studies of metabolites in Finnish men identify disease-relevant loci. Nature Communications, 2022, 13, 1644.	5.8	63
61	Association of mitochondrial DNA copy number with metabolic syndrome and type 2 diabetes in 14Â176 individuals. Journal of Internal Medicine, 2021, 290, 190-202.	2.7	61
62	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. Nature Communications, 2020, 11, 2542.	5.8	59
63	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
64	Re-sequencing Expands Our Understanding of the Phenotypic Impact of Variants at GWAS Loci. PLoS Genetics, 2014, 10, e1004147.	1.5	50
65	Multiple Hepatic Regulatory Variants at the GALNT2 GWAS Locus Associated with High-Density Lipoprotein Cholesterol. American Journal of Human Genetics, 2015, 97, 801-815.	2.6	49
66	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.	1.5	49
67	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.	1.4	47
68	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.	0.3	47
69	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.	2.6	47
70	GWAtoolbox: an R package for fast quality control and handling of genome-wide association studies meta-analysis data. Bioinformatics, 2012, 28, 444-445.	1.8	46
71	An efficient resampling method for calibrating single and gene-based rare variant association analysis in caseâ€“control studies. Biostatistics, 2016, 17, 1-15.	0.9	46
72	Adipose Tissue Gene Expression Associations Reveal Hundreds of Candidate Genes for Cardiometabolic Traits. American Journal of Human Genetics, 2019, 105, 773-787.	2.6	45

#	Article	IF	Citations
73	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.	1.7	44
74	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.	1.4	41
75	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.	2.2	40
76	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.	3.0	39
77	Loss-of-function genomic variants highlight potential therapeutic targets for cardiovascular disease. Nature Communications, 2020, 11, 6417.	5.8	39
78	Imputation-Aware Tag SNP Selection To Improve Power for Large-Scale, Multi-ethnic Association Studies. G3: Genes, Genomes, Genetics, 2018, 8, 3255-3267.	0.8	36
79	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.	1.1	35
80	Genotype Imputation in Genomeâ€Wide Association Studies. Current Protocols in Human Genetics, 2013, 78, Unit 1.25.	3.5	34
81	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.	3.0	33
82	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Scientific Data, 2017, 4, 170179.	2.4	31
83	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.	1.4	30
84	Sequencing and imputation in GWAS: Costâ€effective strategies to increase power and genomic coverage across diverse populations. Genetic Epidemiology, 2020, 44, 537-549.	0.6	30
85	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.	3.3	28
86	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.	2.0	27
87	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.	1.4	26
88	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.	2.6	24
89	Genes predict village of origin in rural Europe. European Journal of Human Genetics, 2010, 18, 1269-1270.	1.4	22
90	Improving power for rareâ€variant tests by integrating external controls. Genetic Epidemiology, 2017, 41, 610-619.	0.6	18

#	Article	IF	Citations
91	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.	2.6	18
92	Omics-squared: human genomic, transcriptomic and phenotypic data for genetic analysis workshop 19. BMC Proceedings, 2016, 10, 71-77.	1.8	17
93	Reversal of Agingâ€Induced Increases in Aortic Stiffness by Targeting Cytoskeletal Proteinâ€Protein Interfaces. Journal of the American Heart Association, 2018, 7, .	1.6	17
94	Evaluation of the role of STAP1 in Familial Hypercholesterolemia. Scientific Reports, 2019, 9, 11995.	1.6	17
95	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. Communications Biology, 2022, 5, .	2.0	17
96	Identification of African-Specific Admixture between Modern and Archaic Humans. American Journal of Human Genetics, 2019, 105, 1254-1261.	2.6	16
97	Jenti: an efficient tool for mining complex inbred genealogies. Bioinformatics, 2008, 24, 724-726.	1.8	15
98	emeraLD: rapid linkage disequilibrium estimation with massive datasets. Bioinformatics, 2019, 35, 164-166.	1.8	15
99	KCND3 potassium channel gene variant confers susceptibility to electrocardiographic early repolarization pattern. JCI Insight, 2019, 4, .	2.3	15
100	Meta-imputation: An efficient method to combine genotype data after imputation with multiple reference panels. American Journal of Human Genetics, 2022, 109, 1007-1015.	2.6	15
101	Copy number variation and association over T-cell receptor genesâ€"influence of DNA source. Immunogenetics, 2010, 62, 561-567.	1.2	14
102	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.	1.1	14
103	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.	1.1	12
104	Testing Asbru Guidelines and Protocols for Neonatal Intensive Care. Lecture Notes in Computer Science, 2005, , 101-110.	1.0	12
105	Adiponectin GWAS loci harboring extensive allelic heterogeneity exhibit distinct molecular consequences. PLoS Genetics, 2020, 16, e1009019.	1.5	11
106	PedVizApi: a Java API for the interactive, visual analysis of extended pedigrees. Bioinformatics, 2008, 24, 279-281.	1.8	8
107	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.	1.1	8
108	Microbiota, type 2 diabetes and non-alcoholic fatty liver disease: protocol of an observational study. Journal of Translational Medicine, 2019, 17, 408.	1.8	7

#	Article	IF	Citations
109	Influence of blood sampling on protein profiling and pattern analysis using matrix-assisted laser desorption/ionisation mass spectrometry. BJU International, 2007, 99, 658-662.	1.3	6
110	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.	1.5	6
111	Whole Exome Sequencing Enhanced Imputation Identifies 85 Metabolite Associations in the Alpine CHRIS Cohort. Metabolites, 2022, 12, 604.	1.3	6
112	Genetic and Metabolic Determinants of Atrial Fibrillation in a General Population Sample: The CHRIS Study. Biomolecules, 2021, 11, 1663.	1.8	5
113	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.	0.5	4
114	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.	1.0	4
115	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.	0.2	2
116	Combining sequence data from multiple studies: Impact of analysis strategies on rare variant calling and association results. Genetic Epidemiology, 2020, 44, 41-51.	0.6	2
117	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
118	Visual Analytical Methods to Identify Family Clustered Diseases. , 2008, , .		1
119	Independent test assessment using the extreme value distribution theory. BMC Proceedings, 2016, 10, 245-249.	1.8	1
120	Analysis and Visualization of Spatial Proteomic Data for Tissue Characterization. , 2008, , .		0
121	410 LAMIN A/C IS A POTENTIAL DISCRIMINATORY BIOMARKER OF LOW AND HIGH GRADE PROSTATE CANCER. Journal of Urology, 2010, 183, .	0.2	0
122	617 STEROID HORMONES REGULATION OF METASTASIS-ASSOCIATED CHAPERONE PROTEINS AGR2 AND AGR3 IN PROSTATE CANCER CELLS. Journal of Urology, 2011, 185, .	0.2	0
123	Whole Genome and Exome Sequencing of Type 2 Diabetes. Frontiers in Diabetes, 2014, , 29-41.	0.4	0
124	154: Integration of TPSA and High-Throughput Mass Spectrometry Data Improves Prostate Cancer Prediction. Journal of Urology, 2007, 177, 52-53.	0.2	0
125	Abstract 3549: miRNAs and androgen receptor interplay in prostate cancer. , 2014, , .		0
126	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