

Christopher R Gignoux

List of Publications by Year in descending order

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Version: 2024-02-01

87
papers

8,317
citations

108046

37
h-index

73587

79
g-index

104
all docs

104
docs citations

104
times ranked

14417
citing authors

#	ARTICLE	IF	CITATIONS
1	Polygenic prediction of atopic dermatitis improves with atopic training and filaggrin factors. <i>Journal of Allergy and Clinical Immunology</i> , 2022, 149, 145-155.	1.5	11
2	Protein prediction for trait mapping in diverse populations. <i>PLoS ONE</i> , 2022, 17, e0264341.	1.1	13
3	Allele imputation for the killer cell immunoglobulin-like receptor KIR3DL1/S1. <i>PLoS Computational Biology</i> , 2022, 18, e1009059.	1.5	5
4	Predicted gene expression in ancestrally diverse populations leads to discovery of susceptibility loci for lifestyle and cardiometabolic traits. <i>American Journal of Human Genetics</i> , 2022, 109, 669-679.	2.6	5
5	RAREsim: A simulation method for very rare genetic variants. <i>American Journal of Human Genetics</i> , 2022, 109, 680-691.	2.6	1
6	Disentangling Signatures of Selection Before and After European Colonization in Latin Americans. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	16
7	COVID-19 Surveillance in the Biobank at the Colorado Center for Personalized Medicine: Observational Study. <i>JMIR Public Health and Surveillance</i> , 2022, 8, e37327.	1.2	4
8	Opportunities and challenges for the use of common controls in sequencing studies. <i>Nature Reviews Genetics</i> , 2022, 23, 665-679.	7.7	13
9	Clotting factor genes are associated with preeclampsia in high-altitude pregnant women in the Peruvian Andes. <i>American Journal of Human Genetics</i> , 2022, 109, 1117-1139.	2.6	10
10	Type 1 diabetes in diverse ancestries and the use of genetic risk scores. <i>Lancet Diabetes and Endocrinology</i> , 2022, 10, 597-608.	5.5	23
11	Adaptive Admixture of HLA Class I Allotypes Enhanced Genetically Determined Strength of Natural Killer Cells in East Asians. <i>Molecular Biology and Evolution</i> , 2021, 38, 2582-2596.	3.5	17
12	Toward a fine-scale population health monitoring system. <i>Cell</i> , 2021, 184, 2068-2083.e11.	13.5	78
13	Admixed Populations Improve Power for Variant Discovery and Portability in Genome-Wide Association Studies. <i>Frontiers in Genetics</i> , 2021, 12, 673167.	1.1	22
14	Applicability of ancestral genotyping in pharmacogenomic research with hormonal contraception. <i>Clinical and Translational Science</i> , 2021, 14, 1713-1718.	1.5	0
15	Rapid detection of identity-by-descent tracts for mega-scale datasets. <i>Nature Communications</i> , 2021, 12, 3546.	5.8	20
16	Summix: A method for detecting and adjusting for population structure in genetic summary data. <i>American Journal of Human Genetics</i> , 2021, 108, 1270-1282.	2.6	5
17	Current Developments in Detection of Identity-by-Descent Methods and Applications. <i>Frontiers in Genetics</i> , 2021, 12, 722602.	1.1	21
18	Paths and timings of the peopling of Polynesia inferred from genomic networks. <i>Nature</i> , 2021, 597, 522-526.	13.7	31

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19	Host methylation predicts SARS-CoV-2 infection and clinical outcome. <i>Communications Medicine</i> , 2021, 1, 42.	1.9	35
20	Leveraging health systems data to characterize a large effect variant conferring risk for liver disease in Puerto Ricans. <i>American Journal of Human Genetics</i> , 2021, 108, 2099-2111.	2.6	4
21	Population History and Gene Divergence in Native Mexicans Inferred from 76 Human Exomes. <i>Molecular Biology and Evolution</i> , 2020, 37, 994-1006.	3.5	43
22	On the cross-population generalizability of gene expression prediction models. <i>PLoS Genetics</i> , 2020, 16, e1008927.	1.5	41
23	A common variant in PNPLA3 is associated with age at diagnosis of NAFLD in patients from a multi-ethnic biobank. <i>Journal of Hepatology</i> , 2020, 72, 1070-1081.	1.8	35
24	Native American gene flow into Polynesia predating Easter Island settlement. <i>Nature</i> , 2020, 583, 572-577.	13.7	64
25	Development of a small panel of SNPs to infer ancestry in Chileans that distinguishes Aymara and Mapuche components. <i>Biological Research</i> , 2020, 53, 15.	1.5	18
26	On the cross-population generalizability of gene expression prediction models. , 2020, 16, e1008927.		0
27	On the cross-population generalizability of gene expression prediction models. , 2020, 16, e1008927.		0
28	On the cross-population generalizability of gene expression prediction models. , 2020, 16, e1008927.		0
29	On the cross-population generalizability of gene expression prediction models. , 2020, 16, e1008927.		0
30	On the cross-population generalizability of gene expression prediction models. , 2020, 16, e1008927.		0
31	On the cross-population generalizability of gene expression prediction models. , 2020, 16, e1008927.		0
32	Genetic analyses of diverse populations improves discovery for complex traits. <i>Nature</i> , 2019, 570, 514-518.	13.7	679
33	The role of country of birth, and genetic and self-identified ancestry, in obesity susceptibility among African and Hispanic Americans. <i>American Journal of Clinical Nutrition</i> , 2019, 110, 16-23.	2.2	13
34	The Future of Genomic Studies Must Be Globally Representative: Perspectives from PAGE. <i>Annual Review of Genomics and Human Genetics</i> , 2019, 20, 181-200.	2.5	33
35	Conservation, Extensive Heterozygosity, and Convergence of Signaling Potential All Indicate a Critical Role for KIR3DL3 in Higher Primates. <i>Frontiers in Immunology</i> , 2019, 10, 24.	2.2	31
36	An admixture mapping meta-analysis implicates genetic variation at 18q21 with asthma susceptibility in Latinos. <i>Journal of Allergy and Clinical Immunology</i> , 2019, 143, 957-969.	1.5	33

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37	Standardized Biogeographic Grouping System for Annotating Populations in Pharmacogenetic Research. <i>Clinical Pharmacology and Therapeutics</i> , 2019, 105, 1256-1262.	2.3	90
38	A genome-wide association study identifies only two ancestry specific variants associated with spontaneous preterm birth. <i>Scientific Reports</i> , 2018, 8, 226.	1.6	37
39	Different Selected Mechanisms Attenuated the Inhibitory Interaction of KIR2DL1 with C2+ HLA-C in Two Indigenous Human Populations in Southern Africa. <i>Journal of Immunology</i> , 2018, 200, 2640-2655.	0.4	32
40	An ancestry-based approach for detecting interactions. <i>Genetic Epidemiology</i> , 2018, 42, 49-63.	0.6	17
41	Imputation-Aware Tag SNP Selection To Improve Power for Large-Scale, Multi-ethnic Association Studies. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 3255-3267.	0.8	36
42	Whole-genome sequencing of 175 Mongolians uncovers population-specific genetic architecture and gene flow throughout North and East Asia. <i>Nature Genetics</i> , 2018, 50, 1696-1704.	9.4	38
43	Worldwide Frequencies of <i>APOL1</i> Renal Risk Variants. <i>New England Journal of Medicine</i> , 2018, 379, 2571-2572.	13.9	69
44	Rapid evolution of a skin-lightening allele in southern African KhoeSan. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 13324-13329.	3.3	17
45	The clinical imperative for inclusivity: Race, ethnicity, and ancestry (REA) in genomics. <i>Human Mutation</i> , 2018, 39, 1713-1720.	1.1	102
46	Genetic diversity in populations across Latin America: implications for population and medical genetic studies. <i>Current Opinion in Genetics and Development</i> , 2018, 53, 98-104.	1.5	37
47	Identifying tagging SNPs for African specific genetic variation from the African Diaspora Genome. <i>Scientific Reports</i> , 2017, 7, 46398.	1.6	26
48	Human Demographic History Impacts Genetic Risk Prediction across Diverse Populations. <i>American Journal of Human Genetics</i> , 2017, 100, 635-649.	2.6	1,120
49	An Unexpectedly Complex Architecture for Skin Pigmentation in Africans. <i>Cell</i> , 2017, 171, 1340-1353.e14.	13.5	134
50	Genetic identification of a common collagen disease in Puerto Ricans via identity-by-descent mapping in a health system. <i>ELife</i> , 2017, 6, .	2.8	65
51	Admixture mapping in two Mexican samples identifies significant associations of locus ancestry with triglyceride levels in the BUD13/ZNF259/APOA5 region and fine mapping points to rs964184 as the main driver of the association signal. <i>PLoS ONE</i> , 2017, 12, e0172880.	1.1	16
52	Differential methylation between ethnic sub-groups reflects the effect of genetic ancestry and environmental exposures. <i>ELife</i> , 2017, 6, .	2.8	153
53	The Great Migration and African-American Genomic Diversity. <i>PLoS Genetics</i> , 2016, 12, e1006059.	1.5	166
54	Fine-Scale Human Population Structure in Southern Africa Reflects Ecogeographic Boundaries. <i>Genetics</i> , 2016, 204, 303-314.	1.2	93

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55	A continuum of admixture in the Western Hemisphere revealed by the African Diaspora genome. <i>Nature Communications</i> , 2016, 7, 12522.	5.8	136
56	Making Precision Medicine Socially Precise. Take a Deep Breath. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2016, 193, 348-350.	2.5	43
57	Air Pollution and Lung Function in Minority Youth with Asthma in the GALA II (Genes&Environments) Tj ETQq1 1 0.784314 rgBT /Ov	2.5	54
58	Strategies for Enriching Variant Coverage in Candidate Disease Loci on a Multiethnic Genotyping Array. <i>PLoS ONE</i> , 2016, 11, e0167758.	1.1	72
59	Genomic Insights into the Ancestry and Demographic History of South America. <i>PLoS Genetics</i> , 2015, 11, e1005602.	1.5	198
60	Genome-wide association study and admixture mapping reveal new loci associated with total IgE levels in Latinos. <i>Journal of Allergy and Clinical Immunology</i> , 2015, 135, 1502-1510.	1.5	52
61	Genetic ancestry influences asthma susceptibility and lung function among Latinos. <i>Journal of Allergy and Clinical Immunology</i> , 2015, 135, 228-235.	1.5	113
62	Loss and Gain of Natural Killer Cell Receptor Function in an African Hunter-Gatherer Population. <i>PLoS Genetics</i> , 2015, 11, e1005439.	1.5	42
63	A genome-wide association study of bronchodilator response in Latinos implicates rare variants. <i>Journal of Allergy and Clinical Immunology</i> , 2014, 133, 370-378.e15.	1.5	105
64	Dissecting childhood asthma with nasal transcriptomics distinguishes subphenotypes of disease. <i>Journal of Allergy and Clinical Immunology</i> , 2014, 133, 670-678.e12.	1.5	204
65	Genome-wide association study of breast cancer in Latinas identifies novel protective variants on 6q25. <i>Nature Communications</i> , 2014, 5, 5260.	5.8	123
66	Genome-wide association study and admixture mapping identify different asthma-associated loci in Latinos: The Genes-environments & Admixture in Latino Americans study. <i>Journal of Allergy and Clinical Immunology</i> , 2014, 134, 295-305.	1.5	106
67	The genetics of Mexico recapitulates Native American substructure and affects biomedical traits. <i>Science</i> , 2014, 344, 1280-1285.	6.0	420
68	A meta-analysis of genome-wide association studies for serum total IgE in diverse study populations. <i>Journal of Allergy and Clinical Immunology</i> , 2013, 131, 1176-1184.	1.5	58
69	Socioeconomic Status and Childhood Asthma in Urban Minority Youths. The GALA II and SAGE II Studies. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2013, 188, 1202-1209.	2.5	110
70	Reconstructing Native American Migrations from Whole-Genome and Whole-Exome Data. <i>PLoS Genetics</i> , 2013, 9, e1004023.	1.5	185
71	Reconstructing the Population Genetic History of the Caribbean. <i>PLoS Genetics</i> , 2013, 9, e1003925.	1.5	296
72	Gene flow from North Africa contributes to differential human genetic diversity in southern Europe. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 11791-11796.	3.3	174

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73	Integration of Mouse and Human Genome-Wide Association Data Identifies KCNIP4 as an Asthma Gene. PLoS ONE, 2013, 8, e56179.	1.1	28
74	Development of a Panel of Genome-Wide Ancestry Informative Markers to Study Admixture Throughout the Americas. PLoS Genetics, 2012, 8, e1002554.	1.5	212
75	Limited Evidence for Classic Selective Sweeps in African Populations. Genetics, 2012, 192, 1049-1064.	1.2	72
76	Heterogeneity in Genetic Admixture across Different Regions of Argentina. PLoS ONE, 2012, 7, e34695.	1.1	117
77	Case-control admixture mapping in Latino populations enriches for known asthma-associated genes. Journal of Allergy and Clinical Immunology, 2012, 130, 76-82.e12.	1.5	53
78	Genome-wide ancestry association testing identifies a common European variant on 6q14.1 as a risk factor for asthma in African American subjects. Journal of Allergy and Clinical Immunology, 2012, 130, 622-629.e9.	1.5	31
79	Further replication studies of the EVE Consortium meta-analysis identifies 2 asthma risk loci in European Americans. Journal of Allergy and Clinical Immunology, 2012, 130, 1294-1301.	1.5	30
80	Genetic Ancestry-Smoking Interactions and Lung Function in African Americans: A Cohort Study. PLoS ONE, 2012, 7, e39541.	1.1	28
81	Population Genetic Structure and Origins of Native Hawaiians in the Multiethnic Cohort Study. PLoS ONE, 2012, 7, e47881.	1.1	19
82	Cosmopolitan and ethnic-specific replication of genetic risk factors for asthma in 2 Latino populations. Journal of Allergy and Clinical Immunology, 2011, 128, 37-43.e12.	1.5	34
83	Meta-analysis of genome-wide association studies of asthma in ethnically diverse North American populations. Nature Genetics, 2011, 43, 887-892.	9.4	736
84	Rapid, global demographic expansions after the origins of agriculture. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 6044-6049.	3.3	225
85	Hunter-gatherer genomic diversity suggests a southern African origin for modern humans. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 5154-5162.	3.3	394
86	History Shaped the Geographic Distribution of Genomic Admixture on the Island of Puerto Rico. PLoS ONE, 2011, 6, e16513.	1.1	87
87	Characterizing the Time Dependency of Human Mitochondrial DNA Mutation Rate Estimates. Molecular Biology and Evolution, 2008, 26, 217-230.	3.5	111