

Christopher R Gignoux

List of Publications by Year in descending order

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Version: 2024-02-01

87
papers

8,317
citations

94433

37
h-index

64796

79
g-index

104
all docs

104
docs citations

104
times ranked

13104
citing authors

#	ARTICLE	IF	CITATIONS
1	Human Demographic History Impacts Genetic Risk Prediction across Diverse Populations. <i>American Journal of Human Genetics</i> , 2017, 100, 635-649.	6.2	1,120
2	Meta-analysis of genome-wide association studies of asthma in ethnically diverse North American populations. <i>Nature Genetics</i> , 2011, 43, 887-892.	21.4	736
3	Genetic analyses of diverse populations improves discovery for complex traits. <i>Nature</i> , 2019, 570, 514-518.	27.8	679
4	The genetics of Mexico recapitulates Native American substructure and affects biomedical traits. <i>Science</i> , 2014, 344, 1280-1285.	12.6	420
5	Hunter-gatherer genomic diversity suggests a southern African origin for modern humans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 5154-5162.	7.1	394
6	Reconstructing the Population Genetic History of the Caribbean. <i>PLoS Genetics</i> , 2013, 9, e1003925.	3.5	296
7	Rapid, global demographic expansions after the origins of agriculture. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 6044-6049.	7.1	225
8	Development of a Panel of Genome-Wide Ancestry Informative Markers to Study Admixture Throughout the Americas. <i>PLoS Genetics</i> , 2012, 8, e1002554.	3.5	212
9	Dissecting childhood asthma with nasal transcriptomics distinguishes subphenotypes of disease. <i>Journal of Allergy and Clinical Immunology</i> , 2014, 133, 670-678.e12.	2.9	204
10	Genomic Insights into the Ancestry and Demographic History of South America. <i>PLoS Genetics</i> , 2015, 11, e1005602.	3.5	198
11	Reconstructing Native American Migrations from Whole-Genome and Whole-Exome Data. <i>PLoS Genetics</i> , 2013, 9, e1004023.	3.5	185
12	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.	7.1	174
13	The Great Migration and African-American Genomic Diversity. <i>PLoS Genetics</i> , 2016, 12, e1006059.	3.5	166
14	Differential methylation between ethnic sub-groups reflects the effect of genetic ancestry and environmental exposures. <i>ELife</i> , 2017, 6, .	6.0	153
15	A continuum of admixture in the Western Hemisphere revealed by the African Diaspora genome. <i>Nature Communications</i> , 2016, 7, 12522.	12.8	136
16	An Unexpectedly Complex Architecture for Skin Pigmentation in Africans. <i>Cell</i> , 2017, 171, 1340-1353.e14.	28.9	134
17	Genome-wide association study of breast cancer in Latinas identifies novel protective variants on 6q25. <i>Nature Communications</i> , 2014, 5, 5260.	12.8	123
18	Heterogeneity in Genetic Admixture across Different Regions of Argentina. <i>PLoS ONE</i> , 2012, 7, e34695.	2.5	117

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19	Genetic ancestry influences asthma susceptibility and lung function among Latinos. <i>Journal of Allergy and Clinical Immunology</i> , 2015, 135, 228-235.	2.9	113
20	Characterizing the Time Dependency of Human Mitochondrial DNA Mutation Rate Estimates. <i>Molecular Biology and Evolution</i> , 2008, 26, 217-230.	8.9	111
21	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.	5.6	110
22	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.	2.9	106
23	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.	2.9	105
24	The clinical imperative for inclusivity: Race, ethnicity, and ancestry (REA) in genomics. <i>Human Mutation</i> , 2018, 39, 1713-1720.	2.5	102
25	Fine-Scale Human Population Structure in Southern Africa Reflects Ecogeographic Boundaries. <i>Genetics</i> , 2016, 204, 303-314.	2.9	93
26	Standardized Biogeographic Grouping System for Annotating Populations in Pharmacogenetic Research. <i>Clinical Pharmacology and Therapeutics</i> , 2019, 105, 1256-1262.	4.7	90
27	History Shaped the Geographic Distribution of Genomic Admixture on the Island of Puerto Rico. <i>PLoS ONE</i> , 2011, 6, e16513.	2.5	87
28	Toward a fine-scale population health monitoring system. <i>Cell</i> , 2021, 184, 2068-2083.e11.	28.9	78
29	Limited Evidence for Classic Selective Sweeps in African Populations. <i>Genetics</i> , 2012, 192, 1049-1064.	2.9	72
30	Strategies for Enriching Variant Coverage in Candidate Disease Loci on a Multiethnic Genotyping Array. <i>PLoS ONE</i> , 2016, 11, e0167758.	2.5	72
31	Worldwide Frequencies of <i>APOL1</i> Renal Risk Variants. <i>New England Journal of Medicine</i> , 2018, 379, 2571-2572.	27.0	69
32	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
33	Native American gene flow into Polynesia predating Easter Island settlement. <i>Nature</i> , 2020, 583, 572-577.	27.8	64
34	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.	2.9	58
35	Air Pollution and Lung Function in Minority Youth with Asthma in the GALA II (Genes"Environments) Tj ETQq1 1 0.784314 rgBT /Over	5.6	54
36	Case-control admixture mapping in Latino populations enriches for known asthma-associated genes. <i>Journal of Allergy and Clinical Immunology</i> , 2012, 130, 76-82.e12.	2.9	53

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37	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.	2.9	52
38	Making Precision Medicine Socially Precise. Take a Deep Breath. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2016, 193, 348-350.	5.6	43
39	Population History and Gene Divergence in Native Mexicans Inferred from 76 Human Exomes. <i>Molecular Biology and Evolution</i> , 2020, 37, 994-1006.	8.9	43
40	Loss and Gain of Natural Killer Cell Receptor Function in an African Hunter-Gatherer Population. <i>PLoS Genetics</i> , 2015, 11, e1005439.	3.5	42
41	On the cross-population generalizability of gene expression prediction models. <i>PLoS Genetics</i> , 2020, 16, e1008927.	3.5	41
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.	21.4	38
43	A genome-wide association study identifies only two ancestry specific variants associated with spontaneous preterm birth. <i>Scientific Reports</i> , 2018, 8, 226.	3.3	37
44	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.	3.3	37
45	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.	1.8	36
46	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.	3.7	35
47	Host methylation predicts SARS-CoV-2 infection and clinical outcome. <i>Communications Medicine</i> , 2021, 1, 42.	4.2	35
48	Cosmopolitan and ethnic-specific replication of genetic risk factors for asthma in 2 Latino populations. <i>Journal of Allergy and Clinical Immunology</i> , 2011, 128, 37-43.e12.	2.9	34
49	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.	6.2	33
50	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.	2.9	33
51	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.	0.8	32
52	Genome-wide ancestry association testing identifies a common European variant on 6q14.1 as a risk factor for asthma in African American subjects. <i>Journal of Allergy and Clinical Immunology</i> , 2012, 130, 622-629.e9.	2.9	31
53	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.	4.8	31
54	Paths and timings of the peopling of Polynesia inferred from genomic networks. <i>Nature</i> , 2021, 597, 522-526.	27.8	31

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55	Further replication studies of the EVE Consortium meta-analysis identifies 2 asthma risk loci in European Americans. <i>Journal of Allergy and Clinical Immunology</i> , 2012, 130, 1294-1301.	2.9	30
56	Integration of Mouse and Human Genome-Wide Association Data Identifies KCNP4 as an Asthma Gene. <i>PLoS ONE</i> , 2013, 8, e56179.	2.5	28
57	Genetic Ancestry-Smoking Interactions and Lung Function in African Americans: A Cohort Study. <i>PLoS ONE</i> , 2012, 7, e39541.	2.5	28
58	Identifying tagging SNPs for African specific genetic variation from the African Diaspora Genome. <i>Scientific Reports</i> , 2017, 7, 46398.	3.3	26
59	Type 1 diabetes in diverse ancestries and the use of genetic risk scores. <i>Lancet Diabetes and Endocrinology</i> , 2022, 10, 597-608.	11.4	23
60	Admixed Populations Improve Power for Variant Discovery and Portability in Genome-Wide Association Studies. <i>Frontiers in Genetics</i> , 2021, 12, 673167.	2.3	22
61	Current Developments in Detection of Identity-by-Descent Methods and Applications. <i>Frontiers in Genetics</i> , 2021, 12, 722602.	2.3	21
62	Rapid detection of identity-by-descent tracts for mega-scale datasets. <i>Nature Communications</i> , 2021, 12, 3546.	12.8	20
63	Population Genetic Structure and Origins of Native Hawaiians in the Multiethnic Cohort Study. <i>PLoS ONE</i> , 2012, 7, e47881.	2.5	19
64	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.	3.4	18
65	An ancestry-based approach for detecting interactions. <i>Genetic Epidemiology</i> , 2018, 42, 49-63.	1.3	17
66	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.	7.1	17
67	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.	8.9	17
68	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.	2.5	16
69	Disentangling Signatures of Selection Before and After European Colonization in Latin Americans. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	16
70	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.	4.7	13
71	Protein prediction for trait mapping in diverse populations. <i>PLoS ONE</i> , 2022, 17, e0264341.	2.5	13
72	Opportunities and challenges for the use of common controls in sequencing studies. <i>Nature Reviews Genetics</i> , 2022, 23, 665-679.	16.3	13

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73	Polygenic prediction of atopic dermatitis improves with atopic training and filaggrin factors. <i>Journal of Allergy and Clinical Immunology</i> , 2022, 149, 145-155.	2.9	11
74	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.	6.2	10
75	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.	6.2	5
76	Allele imputation for the killer cell immunoglobulin-like receptor KIR3DL1/S1. <i>PLoS Computational Biology</i> , 2022, 18, e1009059.	3.2	5
77	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.	6.2	5
78	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.	6.2	4
79	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.	2.6	4
80	RAREsim: A simulation method for very rare genetic variants. <i>American Journal of Human Genetics</i> , 2022, 109, 680-691.	6.2	1
81	Applicability of ancestral genotyping in pharmacogenomic research with hormonal contraception. <i>Clinical and Translational Science</i> , 2021, 14, 1713-1718.	3.1	0
82	On the cross-population generalizability of gene expression prediction models. , 2020, 16, e1008927.		0
83	On the cross-population generalizability of gene expression prediction models. , 2020, 16, e1008927.		0
84	On the cross-population generalizability of gene expression prediction models. , 2020, 16, e1008927.		0
85	On the cross-population generalizability of gene expression prediction models. , 2020, 16, e1008927.		0
86	On the cross-population generalizability of gene expression prediction models. , 2020, 16, e1008927.		0
87	On the cross-population generalizability of gene expression prediction models. , 2020, 16, e1008927.		0