Ryan D Hernandez

List of Publications by Year
in descending order

51 papers	9,729 citations	117625 34 h-index	168389 53 g-index
68 all docs	68 docs citations	68 times ranked	15541 citing authors

#	Article	IF	Citations
1	Assessing the contribution of rare variants to complex trait heritability from whole-genome sequence data. Nature Genetics, 2022, 54, 263-273.	21.4	156
2	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299.	27.8	1,069
3	Genome sequencing unveils a regulatory landscape of platelet reactivity. Nature Communications, 2021, 12, 3626.	12.8	29
4	Population sequencing data reveal a compendium of mutational processes in the human germ line. Science, 2021, 373, 1030-1035.	12.6	43
5	Whole-genome association analyses of sleep-disordered breathing phenotypes in the NHLBI TOPMed program. Genome Medicine, 2021, 13, 136.	8.2	16
6	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
7	Population genetic simulation study of power in association testing across genetic architectures and study designs. Genetic Epidemiology, 2020, 44, 90-103.	1.3	7
8	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. Nature, 2020, 586, 763-768.	27.8	376
9	A Cutibacterium acnes antibiotic modulates human skin microbiota composition in hair follicles. Science Translational Medicine, 2020, 12, .	12.4	83
10	Dynamic incorporation of multiple in silico functional annotations empowers rare variant association analysis of large whole-genome sequencing studies at scale. Nature Genetics, 2020, 52, 969-983.	21.4	146
11	De novo mutations across 1,465 diverse genomes reveal mutational insights and reductions in the Amish founder population. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 2560-2569.	7.1	71
12	The Temporal Dynamics of Background Selection in Nonequilibrium Populations. Genetics, 2020, 214, 1019-1030.	2.9	23
13	Recent shifts in the genomic ancestry of Mexican Americans may alter the genetic architecture of biomedical traits. ELife, 2020, 9, .	6.0	15
14	Ultrarare variants drive substantial cis heritability of human gene expression. Nature Genetics, 2019, 51, 1349-1355.	21.4	98
15	Ancestry-Dependent Enrichment of Deleterious Homozygotes in Runs of Homozygosity. American Journal of Human Genetics, 2019, 105, 747-762.	6.2	36
16	Association study in African-admixed populations across the Americas recapitulates asthma risk loci in non-African populations. Nature Communications, 2019, 10, 880.	12.8	71
17	A genome-wide association and admixture mapping study of bronchodilator drug response in African Americans with asthma. Pharmacogenomics Journal, 2019, 19, 249-259.	2.0	54
18	An admixture mapping meta-analysis implicates genetic variation at 18q21 with asthma susceptibility in Latinos. Journal of Allergy and Clinical Immunology, 2019, 143, 957-969.	2.9	33

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19	Singleton Variants Dominate the Genetic Architecture of Human Gene Expression. SSRN Electronic Journal, 2018, , .	0.4	4
20	Human demographic history has amplified the effects of background selection across the genome. PLoS Genetics, 2018, 14, e1007387.	3.5	71
21	ROP: dumpster diving in RNA-sequencing to find the source of 1 trillion reads across diverse adult human tissues. Genome Biology, 2018, 19, 36.	8.8	42
22	Cancer-associated arginine-to-histidine mutations confer a gain in pH sensing to mutant proteins. Science Signaling, 2017, 10, .	3.6	54
23	Prominent features of the amino acid mutation landscape in cancer. PLoS ONE, 2017, 12, e0183273.	2.5	26
24	Selection and explosive growth alter genetic architecture and hamper the detection of causal rare variants. Genome Research, 2016, 26, 863-873.	5.5	63
25	Functional Segregation of Overlapping Genes in HIV. Cell, 2016, 167, 1762-1773.e12.	28.9	58
26	A continuum of admixture in the Western Hemisphere revealed by the African Diaspora genome. Nature Communications, 2016, 7, 12522.	12.8	136
27	Genetic Ancestry and Natural Selection Drive Population Differences in Immune Responses to Pathogens. Cell, 2016, 167, 657-669.e21.	28.9	419
28	Global environmental drivers of influenza. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 13081-13086.	7.1	239
29	Statistical inference of a convergent antibody repertoire response to influenza vaccine. Genome Medicine, 2016, 8, 60.	8.2	41
30	Population Genetic Simulations of Complex Phenotypes with Implications for Rare Variant Association Tests. Genetic Epidemiology, 2015, 39, 35-44.	1.3	16
31	Rock, Paper, Scissors: Harnessing Complementarity in Ortholog Detection Methods Improves Comparative Genomic Inference. G3: Genes, Genomes, Genetics, 2015, 5, 629-638.	1.8	10
32	Genome-wide association study and admixture mapping reveal new loci associated with total IgE levels in Latinos. Journal of Allergy and Clinical Immunology, 2015, 135, 1502-1510.	2.9	52
33	Genetic Simulation Tools for Postâ€Genome Wide Association Studies of Complex Diseases. Genetic Epidemiology, 2015, 39, 11-19.	1.3	22
34	Pooled Sequencing of Candidate Genes Implicates Rare Variants in the Development of Asthma Following Severe RSV Bronchiolitis in Infancy. PLoS ONE, 2015, 10, e0142649.	2.5	10
35	CauseMap: fast inference of causality from complex time series. PeerJ, 2015, 3, e824.	2.0	12
36	selscan: An Efficient Multithreaded Program to Perform EHH-Based Scans for Positive Selection. Molecular Biology and Evolution, 2014, 31, 2824-2827.	8.9	555

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37	A genome-wide association study of bronchodilator response in Latinos implicates rare variants. Journal of Allergy and Clinical Immunology, 2014, 133, 370-378.e15.	2.9	105
38	Robust Forward Simulations of Recurrent Hitchhiking. Genetics, 2014, 197, 221-236.	2.9	24
39	Population Genetics of Rare Variants and Complex Diseases. Human Heredity, 2012, 74, 118-128.	0.8	53
40	Classic Selective Sweeps Were Rare in Recent Human Evolution. Science, 2011, 331, 920-924.	12.6	432
41	Evolutionary Processes Acting on Candidate cis-Regulatory Regions in Humans Inferred from Patterns of Polymorphism and Divergence. PLoS Genetics, 2009, 5, e1000592.	3.5	123
42	Inferring the Joint Demographic History of Multiple Populations from Multidimensional SNP Frequency Data. PLoS Genetics, 2009, 5, e1000695.	3.5	1,522
43	Genome-Wide Survey of SNP Variation Uncovers the Genetic Structure of Cattle Breeds. Science, 2009, 324, 528-532.	12.6	746
44	Proportionally more deleterious genetic variation in European than in African populations. Nature, 2008, 451, 994-997.	27.8	365
45	A flexible forward simulator for populations subject to selection and demography. Bioinformatics, 2008, 24, 2786-2787.	4.1	197
46	Assessing the Evolutionary Impact of Amino Acid Mutations in the Human Genome. PLoS Genetics, 2008, 4, e1000083.	3.5	586
47	Genome-Wide Patterns of Nucleotide Polymorphism in Domesticated Rice. PLoS Genetics, 2007, 3, e163.	3.5	406
48	Context Dependence, Ancestral Misidentification, and Spurious Signatures of Natural Selection. Molecular Biology and Evolution, 2007, 24, 1792-1800.	8.9	162
49	Demographic Histories and Patterns of Linkage Disequilibrium in Chinese and Indian Rhesus Macaques. Science, 2007, 316, 240-243.	12.6	161
50	Context-Dependent Mutation Rates May Cause Spurious Signatures of a Fixation Bias Favoring Higher GC-Content in Humans. Molecular Biology and Evolution, 2007, 24, 2196-2202.	8.9	50
51	Simultaneous inference of selection and population growth from patterns of variation in the human genome. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 7882-7887.	7.1	310