

Ryan D Hernandez

List of Publications by Year in descending order

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Version: 2024-02-01

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	Inferring the Joint Demographic History of Multiple Populations from Multidimensional SNP Frequency Data. <i>PLoS Genetics</i> , 2009, 5, e1000695.	3.5	1,522
2	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. <i>Nature</i> , 2021, 590, 290-299.	27.8	1,069
3	Genome-Wide Survey of SNP Variation Uncovers the Genetic Structure of Cattle Breeds. <i>Science</i> , 2009, 324, 528-532.	12.6	746
4	Assessing the Evolutionary Impact of Amino Acid Mutations in the Human Genome. <i>PLoS Genetics</i> , 2008, 4, e1000083.	3.5	586
5	selscan: An Efficient Multithreaded Program to Perform EHH-Based Scans for Positive Selection. <i>Molecular Biology and Evolution</i> , 2014, 31, 2824-2827.	8.9	555
6	Classic Selective Sweeps Were Rare in Recent Human Evolution. <i>Science</i> , 2011, 331, 920-924.	12.6	432
7	Genetic Ancestry and Natural Selection Drive Population Differences in Immune Responses to Pathogens. <i>Cell</i> , 2016, 167, 657-669.e21.	28.9	419
8	Genome-Wide Patterns of Nucleotide Polymorphism in Domesticated Rice. <i>PLoS Genetics</i> , 2007, 3, e163.	3.5	406
9	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. <i>Nature</i> , 2020, 586, 763-768.	27.8	376
10	Proportionally more deleterious genetic variation in European than in African populations. <i>Nature</i> , 2008, 451, 994-997.	27.8	365
11	Simultaneous inference of selection and population growth from patterns of variation in the human genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 7882-7887.	7.1	310
12	Global environmental drivers of influenza. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 13081-13086.	7.1	239
13	A flexible forward simulator for populations subject to selection and demography. <i>Bioinformatics</i> , 2008, 24, 2786-2787.	4.1	197
14	Context Dependence, Ancestral Misidentification, and Spurious Signatures of Natural Selection. <i>Molecular Biology and Evolution</i> , 2007, 24, 1792-1800.	8.9	162
15	Demographic Histories and Patterns of Linkage Disequilibrium in Chinese and Indian Rhesus Macaques. <i>Science</i> , 2007, 316, 240-243.	12.6	161
16	Assessing the contribution of rare variants to complex trait heritability from whole-genome sequence data. <i>Nature Genetics</i> , 2022, 54, 263-273.	21.4	156
17	Dynamic incorporation of multiple in silico functional annotations empowers rare variant association analysis of large whole-genome sequencing studies at scale. <i>Nature Genetics</i> , 2020, 52, 969-983.	21.4	146
18	A continuum of admixture in the Western Hemisphere revealed by the African Diaspora genome. <i>Nature Communications</i> , 2016, 7, 12522.	12.8	136

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19	Evolutionary Processes Acting on Candidate cis-Regulatory Regions in Humans Inferred from Patterns of Polymorphism and Divergence. <i>PLoS Genetics</i> , 2009, 5, e1000592.	3.5	123
20	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
21	Ultrarare variants drive substantial cis heritability of human gene expression. <i>Nature Genetics</i> , 2019, 51, 1349-1355.	21.4	98
22	A <i>Cutibacterium acnes</i> antibiotic modulates human skin microbiota composition in hair follicles. <i>Science Translational Medicine</i> , 2020, 12, .	12.4	83
23	Human demographic history has amplified the effects of background selection across the genome. <i>PLoS Genetics</i> , 2018, 14, e1007387.	3.5	71
24	Association study in African-admixed populations across the Americas recapitulates asthma risk loci in non-African populations. <i>Nature Communications</i> , 2019, 10, 880.	12.8	71
25	De novo mutations across 1,465 diverse genomes reveal mutational insights and reductions in the Amish founder population. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 2560-2569.	7.1	71
26	A high-resolution HLA reference panel capturing global population diversity enables multi-ancestry fine-mapping in HIV host response. <i>Nature Genetics</i> , 2021, 53, 1504-1516.	21.4	69
27	Selection and explosive growth alter genetic architecture and hamper the detection of causal rare variants. <i>Genome Research</i> , 2016, 26, 863-873.	5.5	63
28	Functional Segregation of Overlapping Genes in HIV. <i>Cell</i> , 2016, 167, 1762-1773.e12.	28.9	58
29	Cancer-associated arginine-to-histidine mutations confer a gain in pH sensing to mutant proteins. <i>Science Signaling</i> , 2017, 10, .	3.6	54
30	A genome-wide association and admixture mapping study of bronchodilator drug response in African Americans with asthma. <i>Pharmacogenomics Journal</i> , 2019, 19, 249-259.	2.0	54
31	Population Genetics of Rare Variants and Complex Diseases. <i>Human Heredity</i> , 2012, 74, 118-128.	0.8	53
32	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
33	Context-Dependent Mutation Rates May Cause Spurious Signatures of a Fixation Bias Favoring Higher GC-Content in Humans. <i>Molecular Biology and Evolution</i> , 2007, 24, 2196-2202.	8.9	50
34	Population sequencing data reveal a compendium of mutational processes in the human germ line. <i>Science</i> , 2021, 373, 1030-1035.	12.6	43
35	ROP: dumpster diving in RNA-sequencing to find the source of 1 trillion reads across diverse adult human tissues. <i>Genome Biology</i> , 2018, 19, 36.	8.8	42
36	Statistical inference of a convergent antibody repertoire response to influenza vaccine. <i>Genome Medicine</i> , 2016, 8, 60.	8.2	41

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37	Ancestry-Dependent Enrichment of Deleterious Homozygotes in Runs of Homozygosity. <i>American Journal of Human Genetics</i> , 2019, 105, 747-762.	6.2	36
38	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
39	Genome sequencing unveils a regulatory landscape of platelet reactivity. <i>Nature Communications</i> , 2021, 12, 3626.	12.8	29
40	Prominent features of the amino acid mutation landscape in cancer. <i>PLoS ONE</i> , 2017, 12, e0183273.	2.5	26
41	Robust Forward Simulations of Recurrent Hitchhiking. <i>Genetics</i> , 2014, 197, 221-236.	2.9	24
42	The Temporal Dynamics of Background Selection in Nonequilibrium Populations. <i>Genetics</i> , 2020, 214, 1019-1030.	2.9	23
43	Genetic Simulation Tools for Post-Genome Wide Association Studies of Complex Diseases. <i>Genetic Epidemiology</i> , 2015, 39, 11-19.	1.3	22
44	Population Genetic Simulations of Complex Phenotypes with Implications for Rare Variant Association Tests. <i>Genetic Epidemiology</i> , 2015, 39, 35-44.	1.3	16
45	Whole-genome association analyses of sleep-disordered breathing phenotypes in the NHLBI TOPMed program. <i>Genome Medicine</i> , 2021, 13, 136.	8.2	16
46	Recent shifts in the genomic ancestry of Mexican Americans may alter the genetic architecture of biomedical traits. <i>ELife</i> , 2020, 9, .	6.0	15
47	CauseMap: fast inference of causality from complex time series. <i>PeerJ</i> , 2015, 3, e824.	2.0	12
48	Rock, Paper, Scissors: Harnessing Complementarity in Ortholog Detection Methods Improves Comparative Genomic Inference. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 629-638.	1.8	10
49	Pooled Sequencing of Candidate Genes Implicates Rare Variants in the Development of Asthma Following Severe RSV Bronchiolitis in Infancy. <i>PLoS ONE</i> , 2015, 10, e0142649.	2.5	10
50	Population genetic simulation study of power in association testing across genetic architectures and study designs. <i>Genetic Epidemiology</i> , 2020, 44, 90-103.	1.3	7
51	Singleton Variants Dominate the Genetic Architecture of Human Gene Expression. <i>SSRN Electronic Journal</i> , 2018, , .	0.4	4