

Timothy D O'connor

List of Publications by Year in descending order

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Version: 2024-02-01

46
papers

5,500
citations

331670

21
h-index

233421

45
g-index

50
all docs

50
docs citations

50
times ranked

13571
citing authors

#	ARTICLE	IF	CITATIONS
1	STRIDE: a command-line HMM-based identifier and sub-classifier of Plasmodium falciparum RIFIN and STEVOR variant surface antigen families. BMC Bioinformatics, 2022, 23, 15.	2.6	1
2	Peptide ancestry informative markers in uterine neoplasms from women of European, African, and Asian ancestry. IScience, 2022, 25, 103665.	4.1	5
3	Population genetics of PDE4B (phosphodiesterase-4B) in neglected Native Americans: Implications for cancer pharmacogenetics. Clinical and Translational Science, 2022, , .	3.1	4
4	Abstract 750: Whole exome sequencing of uterine serous carcinomas reveals racial differences in known and novel driver mutations. Cancer Research, 2022, 82, 750-750.	0.9	0
5	Polygenic risk prediction and SNCA haplotype analysis in a Latino Parkinson's disease cohort. Parkinsonism and Related Disorders, 2022, 102, 7-15.	2.2	2
6	Genome-Wide Analysis of Copy Number Variation in Latin American Parkinson's Disease Patients. Movement Disorders, 2021, 36, 434-441.	3.9	12
7	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299.	27.8	1,069
8	The copy number variation and stroke (CaNVAS) risk and outcome study. PLoS ONE, 2021, 16, e0248791.	2.5	2
9	Characterizing the Genetic Architecture of Parkinson's Disease in Latinos. Annals of Neurology, 2021, 90, 353-365.	5.3	48
10	Impact of Amerind ancestry and FADS genetic variation on omega-3 deficiency and cardiometabolic traits in Hispanic populations. Communications Biology, 2021, 4, 918.	4.4	11
11	Population sequencing data reveal a compendium of mutational processes in the human germ line. Science, 2021, 373, 1030-1035.	12.6	43
12	Tracing the Distribution of European Lactase Persistence Genotypes Along the Americas. Frontiers in Genetics, 2021, 12, 671079.	2.3	3
13	Interpreting Clinical Trials With Omega-3 Supplements in the Context of Ancestry and FADS Genetic Variation. Frontiers in Nutrition, 2021, 8, 808054.	3.7	12
14	A positively selected FBN1 missense variant reduces height in Peruvian individuals. Nature, 2020, 582, 234-239.	27.8	39
15	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
16	Detecting geospatial patterns of Plasmodium falciparum parasite migration in Cambodia using optimized estimated effective migration surfaces. International Journal of Health Geographics, 2020, 19, 13.	2.5	2
17	Evolutionary history of modern Samoans. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 9458-9465.	7.1	14
18	The genetic structure and adaptation of Andean highlanders and Amazonians are influenced by the interplay between geography and culture. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 32557-32565.	7.1	28

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19	Inferring the "Primordial Immune Complex" Origins of MHC Class I and Antigen Receptors Revealed by Comparative Genomics. <i>Journal of Immunology</i> , 2019, 203, 1882-1896.	0.8	24
20	Genomic structure and diversity of <i>Plasmodium falciparum</i> in Southeast Asia reveal recent parasite migration patterns. <i>Nature Communications</i> , 2019, 10, 2665.	12.8	46
21	Ancestral characterization of 1018 cancer cell lines highlights disparities and reveals gene expression and mutational differences. <i>Cancer</i> , 2019, 125, 2076-2088.	4.1	16
22	Evolution of Hominin Polyunsaturated Fatty Acid Metabolism: From Africa to the New World. <i>Genome Biology and Evolution</i> , 2019, 11, 1417-1430.	2.5	38
23	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
24	Native American Genomic Diversity through Ancient DNA. <i>Cell</i> , 2018, 175, 1173-1174.	28.9	1
25	Evolutionary genomic dynamics of Peruvians before, during, and after the Inca Empire. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E6526-E6535.	7.1	115
26	Improving Cancer Detection and Treatment with Liquid Biopsies and ptDNA. <i>Trends in Cancer</i> , 2018, 4, 643-654.	7.4	6
27	Insect outbreaks alter nutrient dynamics in a southern African savanna: patchy defoliation of <i>Colophospermum mopane</i> savanna by <i>Imbrasia belina</i> larvae. <i>Biotropica</i> , 2018, 50, 789-796.	1.6	9
28	Identifying tagging SNPs for African specific genetic variation from the African Diaspora Genome. <i>Scientific Reports</i> , 2017, 7, 46398.	3.3	26
29	Accurate and equitable medical genomic analysis requires an understanding of demography and its influence on sample size and ratio. <i>Genome Biology</i> , 2017, 18, 42.	8.8	3
30	Non-human primates avoid the detrimental effects of prenatal androgen exposure in mixed-sex litters: combined demographic, behavioral, and genetic analyses. <i>American Journal of Primatology</i> , 2016, 78, 1304-1315.	1.7	7
31	An integrated genomic and transcriptomic survey of mucormycosis-causing fungi. <i>Nature Communications</i> , 2016, 7, 12218.	12.8	103
32	A continuum of admixture in the Western Hemisphere revealed by the African Diaspora genome. <i>Nature Communications</i> , 2016, 7, 12522.	12.8	136
33	Challenges and disparities in the application of personalized genomic medicine to populations with African ancestry. <i>Nature Communications</i> , 2016, 7, 12521.	12.8	68
34	Rare Variation Facilitates Inferences of Fine-Scale Population Structure in Humans. <i>Molecular Biology and Evolution</i> , 2015, 32, 653-660.	8.9	38
35	AdmixKJump: identifying population structure in recently diverged groups. <i>Source Code for Biology and Medicine</i> , 2015, 10, 2.	1.7	0
36	Photographic evidence of fire-induced shifts from dwarf-shrub- to grass-dominated vegetation in Nama-Karoo. <i>South African Journal of Botany</i> , 2015, 101, 148-152.	2.5	15

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37	Genetic architecture of quantitative traits and complex diseases. <i>Current Opinion in Genetics and Development</i> , 2013, 23, 678-683.	3.3	30
38	Analysis of 6,515 exomes reveals the recent origin of most human protein-coding variants. <i>Nature</i> , 2013, 493, 216-220.	27.8	898
39	Great ape genetic diversity and population history. <i>Nature</i> , 2013, 499, 471-475.	27.8	768
40	Evolutionary Modeling of Genotype-Phenotype Associations, and Application to primate coding and Non-coding mtDNA Rate Variation. <i>Evolutionary Bioinformatics</i> , 2013, 9, EBO.S11600.	1.2	9
41	Fine-Scale Patterns of Population Stratification Confound Rare Variant Association Tests. <i>PLoS ONE</i> , 2013, 8, e65834.	2.5	42
42	Evolution and Functional Impact of Rare Coding Variation from Deep Sequencing of Human Exomes. <i>Science</i> , 2012, 337, 64-69.	12.6	1,535
43	The promise and limitations of population exomics for human evolution studies. <i>Genome Biology</i> , 2011, 12, 127.	9.6	20
44	Analysis of long branch extraction and long branch shortening. <i>BMC Genomics</i> , 2010, 11, S14.	2.8	10
45	Genotype-phenotype associations: substitution models to detect evolutionary associations between phenotypic variables and genotypic evolutionary rate. <i>Bioinformatics</i> , 2009, 25, i94-i100.	4.1	35
46	Patch dieback of <i>Colophospermum mopane</i> in a dysfunctional semi-arid African savanna. <i>Austral Ecology</i> , 2002, 27, 385-395.	1.5	45