Timothy D O'connor

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/2526882/publications.pdf

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 | Evolution and Functional Impact of Rare Coding Variation from Deep Sequencing of Human Exomes. Science, 2012, 337, 64-69. | 12.6 | 1,535 |
| 2 | Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299. | 27.8 | 1,069 |
| 3 | Analysis of 6,515 exomes reveals the recent origin of most human protein-coding variants. Nature, 2013, 493, 216-220. | 27.8 | 898 |
| 4 | Great ape genetic diversity and population history. Nature, 2013, 499, 471-475. | 27.8 | 768 |
| 5 | A continuum of admixture in the Western Hemisphere revealed by the African Diaspora genome. Nature Communications, 2016, 7, 12522. | 12.8 | 136 |
| 6 | Evolutionary genomic dynamics of Peruvians before, during, and after the Inca Empire. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E6526-E6535. | 7.1 | 115 |
| 7 | An integrated genomic and transcriptomic survey of mucormycosis-causing fungi. Nature Communications, 2016, 7, 12218. | 12.8 | 103 |
| 8 | 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 |
| 9 | 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 |
| 10 | Challenges and disparities in the application of personalized genomic medicine to populations with African ancestry. Nature Communications, 2016, 7, 12521. | 12.8 | 68 |
| 11 | Characterizing the Genetic Architecture of Parkinson's Disease in Latinos. Annals of Neurology, 2021, 90, 353-365. | 5.3 | 48 |
| 12 | Genomic structure and diversity of Plasmodium falciparum in Southeast Asia reveal recent parasite migration patterns. Nature Communications, 2019, 10, 2665. | 12.8 | 46 |
| 13 | Patch dieback of Colophospermum mopane in a dysfunctional semi-arid African savanna. Austral Ecology, 2002, 27, 385-395. | 1.5 | 45 |
| 14 | Population sequencing data reveal a compendium of mutational processes in the human germ line. Science, 2021, 373, 1030-1035. | 12.6 | 43 |
| 15 | Fine-Scale Patterns of Population Stratification Confound Rare Variant Association Tests. PLoS ONE, 2013, 8, e65834. | 2.5 | 42 |
| 16 | A positively selected FBN1 missense variant reduces height in Peruvian individuals. Nature, 2020, 582, 234-239. | 27.8 | 39 |
| 17 | Rare Variation Facilitates Inferences of Fine-Scale Population Structure in Humans. Molecular Biology and Evolution, 2015, 32, 653-660. | 8.9 | 38 |
| 18 | Evolution of Hominin Polyunsaturated Fatty Acid Metabolism: From Africa to the New World. Genome Biology and Evolution, 2019, 11, 1417-1430. | 2.5 | 38 |

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|----|---|-----|-----------|
| 19 | Genotype–phenotype associations: substitution models to detect evolutionary associations between phenotypic variables and genotypic evolutionary rate. Bioinformatics, 2009, 25, i94-i100. | 4.1 | 35 |
| 20 | Genetic architecture of quantitative traits and complex diseases. Current Opinion in Genetics and Development, 2013, 23, 678-683. | 3.3 | 30 |
| 21 | 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 |
| 22 | Identifying tagging SNPs for African specific genetic variation from the African Diaspora Genome. Scientific Reports, 2017, 7, 46398. | 3.3 | 26 |
| 23 | Inferring the "Primordial Immune Complex― Origins of MHC Class I and Antigen Receptors Revealed by Comparative Genomics. Journal of Immunology, 2019, 203, 1882-1896. | 0.8 | 24 |
| 24 | The promise and limitations of population exomics for human evolution studies. Genome Biology, 2011, 12, 127. | 9.6 | 20 |
| 25 | Ancestral characterization of 1018 cancer cell lines highlights disparities and reveals gene expression and mutational differences. Cancer, 2019, 125, 2076-2088. | 4.1 | 16 |
| 26 | Photographic evidence of fire-induced shifts from dwarf-shrub- to grass-dominated vegetation in Nama-Karoo. South African Journal of Botany, 2015, 101, 148-152. | 2.5 | 15 |
| 27 | 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 |
| 28 | Genomeâ€Wide Analysis of Copy Number Variation in Latin American Parkinson's Disease Patients. Movement Disorders, 2021, 36, 434-441. | 3.9 | 12 |
| 29 | 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 |
| 30 | 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 |
| 31 | Analysis of long branch extraction and long branch shortening. BMC Genomics, 2010, 11, S14. | 2.8 | 10 |
| 32 | Evolutionary Modeling of Genotype-Phenotype Associations, and Application to primate coding and Non-coding mtDNA Rate Variation. Evolutionary Bioinformatics, 2013, 9, EBO.S11600. | 1.2 | 9 |
| 33 | Insect outbreaks alter nutrient dynamics in a southern African savanna: patchy defoliation of <i>Colophospermum mopane</i> savanna by <i>Imbrasia belina</i> larvae. Biotropica, 2018, 50, 789-796. | 1.6 | 9 |
| 34 | Nonâ€human primates avoid the detrimental effects of prenatal androgen exposure in mixedâ€sex litters: combined demographic, behavioral, and genetic analyses. American Journal of Primatology, 2016, 78, 1304-1315. | 1.7 | 7 |
| 35 | Improving Cancer Detection and Treatment with Liquid Biopsies and ptDNA. Trends in Cancer, 2018, 4, 643-654. | 7.4 | 6 |
| 36 | Peptide ancestry informative markers in uterine neoplasms from women of European, African, and Asian ancestry. IScience, 2022, 25, 103665. | 4.1 | 5 |

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|----|--|------|-----------|
| 37 | Population genetics of <i>PDE4B</i> (phosphodiesteraseâ€4B) in neglected Native Americans: Implications for cancer pharmacogenetics. Clinical and Translational Science, 2022, , . | 3.1 | 4 |
| 38 | Accurate and equitable medical genomic analysis requires an understanding of demography and its influence on sample size and ratio. Genome Biology, 2017, 18, 42. | 8.8 | 3 |
| 39 | Tracing the Distribution of European Lactase Persistence Genotypes Along the Americas. Frontiers in Genetics, 2021, 12, 671079. | 2.3 | 3 |
| 40 | 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 |
| 41 | The copy number variation and stroke (CaNVAS) risk and outcome study. PLoS ONE, 2021, 16, e0248791. | 2.5 | 2 |
| 42 | 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 |
| 43 | Native American Genomic Diversity through Ancient DNA. Cell, 2018, 175, 1173-1174. | 28.9 | 1 |
| 44 | 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 |
| 45 | AdmixKJump: identifying population structure in recently diverged groups. Source Code for Biology and Medicine, 2015, 10, 2. | 1.7 | 0 |
| 46 | 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 |