

Carlos D Bustamante

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3776653/publications.pdf>

Version: 2024-02-01

90
papers

12,121
citations

47006

47
h-index

49909

87
g-index

93
all docs

93
docs citations

93
times ranked

22087
citing authors

#	ARTICLE	IF	CITATIONS
1	REVEL: An Ensemble Method for Predicting the Pathogenicity of Rare Missense Variants. American Journal of Human Genetics, 2016, 99, 877-885.	6.2	1,555
2	Human Demographic History Impacts Genetic Risk Prediction across Diverse Populations. American Journal of Human Genetics, 2017, 100, 635-649.	6.2	1,120
3	Genomics for the world. Nature, 2011, 475, 163-165.	27.8	523
4	The genome of a Late Pleistocene human from a Clovis burial site in western Montana. Nature, 2014, 506, 225-229.	27.8	500
5	Genome Sequencing Highlights the Dynamic Early History of Dogs. PLoS Genetics, 2014, 10, e1004016.	3.5	481
6	Genomic evidence for the Pleistocene and recent population history of Native Americans. Science, 2015, 349, aab3884.	12.6	449
7	The genetics of Mexico recapitulates Native American substructure and affects biomedical traits. Science, 2014, 344, 1280-1285.	12.6	420
8	Genetic Control of Chromatin States in Humans Involves Local and Distal Chromosomal Interactions. Cell, 2015, 162, 1051-1065.	28.9	304
9	Pulling out the 1%: Whole-Genome Capture for the Targeted Enrichment of Ancient DNA Sequencing Libraries. American Journal of Human Genetics, 2013, 93, 852-864.	6.2	284
10	Punctuated bursts in human male demography inferred from 1,244 worldwide Y-chromosome sequences. Nature Genetics, 2016, 48, 593-599.	21.4	273
11	Spectrum and prevalence of genetic predisposition in medulloblastoma: a retrospective genetic study and prospective validation in a clinical trial cohort. Lancet Oncology, The, 2018, 19, 785-798.	10.7	268
12	Effect of predicted protein-truncating genetic variants on the human transcriptome. Science, 2015, 348, 666-669.	12.6	252
13	The ancestry and affiliations of Kennewick Man. Nature, 2015, 523, 455-458.	27.8	241
14	Estimating the mutation load in human genomes. Nature Reviews Genetics, 2015, 16, 333-343.	16.3	233
15	Distance from sub-Saharan Africa predicts mutational load in diverse human genomes. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E440-9.	7.1	224
16	Comprehensive transcriptome analysis using synthetic long-read sequencing reveals molecular co-association of distant splicing events. Nature Biotechnology, 2015, 33, 736-742.	17.5	205
17	The African Turquoise Killifish Genome Provides Insights into Evolution and Genetic Architecture of Lifespan. Cell, 2015, 163, 1539-1554.	28.9	200
18	Genetic Recombination Is Targeted towards Gene Promoter Regions in Dogs. PLoS Genetics, 2013, 9, e1003984.	3.5	198

#	ARTICLE	IF	CITATIONS
19	Genomic Insights into the Ancestry and Demographic History of South America. <i>PLoS Genetics</i> , 2015, 11, e1005602.	3.5	198
20	Genetic structure in village dogs reveals a Central Asian domestication origin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 13639-13644.	7.1	192
21	Dispersals and genetic adaptation of Bantu-speaking populations in Africa and North America. <i>Science</i> , 2017, 356, 543-546.	12.6	188
22	Reconstructing Native American Migrations from Whole-Genome and Whole-Exome Data. <i>PLoS Genetics</i> , 2013, 9, e1004023.	3.5	185
23	The Great Migration and African-American Genomic Diversity. <i>PLoS Genetics</i> , 2016, 12, e1006059.	3.5	166
24	Privacy Risks from Genomic Data-Sharing Beacons. <i>American Journal of Human Genetics</i> , 2015, 97, 631-646.	6.2	161
25	A continuum of admixture in the Western Hemisphere revealed by the African Diaspora genome. <i>Nature Communications</i> , 2016, 7, 12522.	12.8	136
26	An Unexpectedly Complex Architecture for Skin Pigmentation in Africans. <i>Cell</i> , 2017, 171, 1340-1353.e14.	28.9	134
27	Ancient genomes from North Africa evidence prehistoric migrations to the Maghreb from both the Levant and Europe. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 6774-6779.	7.1	131
28	Compact genome of the Antarctic midge is likely an adaptation to an extreme environment. <i>Nature Communications</i> , 2014, 5, 4611.	12.8	128
29	The phylogenetic and geographic structure of Y-chromosome haplogroup R1a. <i>European Journal of Human Genetics</i> , 2015, 23, 124-131.	2.8	122
30	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
31	Genome-wide ancestry of 17th-century enslaved Africans from the Caribbean. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 3669-3673.	7.1	110
32	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
33	Polygenic risk scores: a biased prediction?. <i>Genome Medicine</i> , 2018, 10, 100.	8.2	104
34	Genetic Mapping and Biochemical Basis of Yellow Feather Pigmentation in Budgerigars. <i>Cell</i> , 2017, 171, 427-439.e21.	28.9	101
35	Multidimensional structure-function relationships in human β -cardiac myosin from population-scale genetic variation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 6701-6706.	7.1	98
36	The Time Scale of Recombination Rate Evolution in Great Apes. <i>Molecular Biology and Evolution</i> , 2016, 33, 928-945.	8.9	92

#	ARTICLE	IF	CITATIONS
37	An Efficient Multiple-Testing Adjustment for eQTL Studies that Accounts for Linkage Disequilibrium between Variants. <i>American Journal of Human Genetics</i> , 2016, 98, 216-224.	6.2	91
38	Patterns of genomic and phenomic diversity in wine and table grapes. <i>Horticulture Research</i> , 2017, 4, 17035.	6.3	87
39	Population Genomic Analysis of Ancient and Modern Genomes Yields New Insights into the Genetic Ancestry of the Tyrolean Iceman and the Genetic Structure of Europe. <i>PLoS Genetics</i> , 2014, 10, e1004353.	3.5	86
40	The Divergence of Neandertal and Modern Human Y Chromosomes. <i>American Journal of Human Genetics</i> , 2016, 98, 728-734.	6.2	81
41	Demographically-Based Evaluation of Genomic Regions under Selection in Domestic Dogs. <i>PLoS Genetics</i> , 2016, 12, e1005851.	3.5	77
42	Extreme selective sweeps independently targeted the X chromosomes of the great apes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 6413-6418.	7.1	75
43	Population genomic analyses of the chocolate tree, <i>Theobroma cacao</i> L., provide insights into its domestication process. <i>Communications Biology</i> , 2018, 1, 167.	4.4	73
44	Strategies for Enriching Variant Coverage in Candidate Disease Loci on a Multiethnic Genotyping Array. <i>PLoS ONE</i> , 2016, 11, e0167758.	2.5	72
45	Mechanisms Underlying Adaptation to Life in Hydrogen Sulfide-Rich Environments. <i>Molecular Biology and Evolution</i> , 2016, 33, 1419-1434.	8.9	69
46	Origins and genetic legacies of the Caribbean Taino. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 2341-2346.	7.1	64
47	Genetic variant in folate homeostasis is associated with lower warfarin dose in African Americans. <i>Blood</i> , 2014, 124, 2298-2305.	1.4	57
48	Xrare: a machine learning method jointly modeling phenotypes and genetic evidence for rare disease diagnosis. <i>Genetics in Medicine</i> , 2019, 21, 2126-2134.	2.4	56
49	Inference of Gorilla Demographic and Selective History from Whole-Genome Sequence Data. <i>Molecular Biology and Evolution</i> , 2015, 32, 600-612.	8.9	55
50	Mitogenomes illuminate the origin and migration patterns of the indigenous people of the Canary Islands. <i>PLoS ONE</i> , 2019, 14, e0209125.	2.5	54
51	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
52	Clinical Genetics Lacks Standard Definitions and Protocols for the Collection and Use of Diversity Measures. <i>American Journal of Human Genetics</i> , 2020, 107, 72-82.	6.2	52
53	Transcriptome Sequencing from Diverse Human Populations Reveals Differentiated Regulatory Architecture. <i>PLoS Genetics</i> , 2014, 10, e1004549.	3.5	49
54	Comparative performance of two whole-genome capture methodologies on ancient DNA Illumina libraries. <i>Methods in Ecology and Evolution</i> , 2015, 6, 725-734.	5.2	43

#	ARTICLE	IF	CITATIONS
55	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
56	Toward Genetics-Driven Early Intervention in Dilated Cardiomyopathy. <i>Circulation: Cardiovascular Genetics</i> , 2017, 10, .	5.1	41
57	Genomic Evidence for Local Adaptation of Hunter-Gatherers to the African Rainforest. <i>Current Biology</i> , 2019, 29, 2926-2935.e4.	3.9	40
58	Discovery and functional characterization of a neomorphic PTEN mutation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 13976-13981.	7.1	38
59	Efficient analysis of large datasets and sex bias with ADMIXTURE. <i>BMC Bioinformatics</i> , 2016, 17, 218.	2.6	38
60	The Genome of the Self-Fertilizing Mangrove Rivulus Fish, <i>Kryptolebias marmoratus</i> : A Model for Studying Phenotypic Plasticity and Adaptations to Extreme Environments. <i>Genome Biology and Evolution</i> , 2016, 8, 2145-2154.	2.5	38
61	A research roadmap for next-generation sequencing informatics. <i>Science Translational Medicine</i> , 2016, 8, 335ps10.	12.4	37
62	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
63	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
64	ClinGen Variant Curation Interface: a variant classification platform for the application of evidence criteria from ACMG/AMP guidelines. <i>Genome Medicine</i> , 2022, 14, 6.	8.2	34
65	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
66	Phylogenetic applications of whole Y-chromosome sequences and the Near Eastern origin of Ashkenazi Levites. <i>Nature Communications</i> , 2013, 4, 2928.	12.8	31
67	GBStools: A Statistical Method for Estimating Allelic Dropout in Reduced Representation Sequencing Data. <i>PLoS Genetics</i> , 2016, 12, e1005631.	3.5	30
68	Genetic variation drives seasonal onset of hibernation in the 13-lined ground squirrel. <i>Communications Biology</i> , 2019, 2, 478.	4.4	28
69	FasTag: Automatic text classification of unstructured medical narratives. <i>PLoS ONE</i> , 2020, 15, e0234647.	2.5	23
70	Gene expression imputation identifies candidate genes and susceptibility loci associated with cutaneous squamous cell carcinoma. <i>Nature Communications</i> , 2018, 9, 4264.	12.8	21
71	In-solution Y-chromosome capture-enrichment on ancient DNA libraries. <i>BMC Genomics</i> , 2018, 19, 608.	2.8	20
72	Whole-genome sequencing of Atacama skeleton shows novel mutations linked with dysplasia. <i>Genome Research</i> , 2018, 28, 423-431.	5.5	19

#	ARTICLE	IF	CITATIONS
73	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
74	DeepTag: inferring diagnoses from veterinary clinical notes. <i>Npj Digital Medicine</i> , 2018, 1, 60.	10.9	17
75	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
76	Whole-genome sequencing reveals the extent of heterozygosity in a preferentially self-fertilizing hermaphroditic vertebrate. <i>Genome</i> , 2018, 61, 241-247.	2.0	15
77	Inexpensive and Highly Reproducible Cloud-Based Variant Calling of 2,535 Human Genomes. <i>PLoS ONE</i> , 2015, 10, e0129277.	2.5	14
78	A genetic counseling needs assessment of Mexico. <i>Molecular Genetics & Genomic Medicine</i> , 2019, 7, e668.	1.2	12
79	Structural Variation Detection by Proximity Ligation from Formalin-Fixed, Paraffin-Embedded Tumor Tissue. <i>Journal of Molecular Diagnostics</i> , 2019, 21, 375-383.	2.8	10
80	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
81	PATH-SCAN: A REPORTING TOOL FOR IDENTIFYING CLINICALLY ACTIONABLE VARIANTS. , 2013, , .		9
82	The inference of sex-biased human demography from whole-genome data. <i>PLoS Genetics</i> , 2019, 15, e1008293.	3.5	7
83	IMPUTATION-BASED ASSESSMENT OF NEXT GENERATION RARE EXOME VARIANT ARRAYS. , 2013, , .		6
84	Using genotype array data to compare multi- and single-sample variant calls and improve variant call sets from deep coverage whole-genome sequencing data. <i>Bioinformatics</i> , 2016, 33, btw786.	4.1	3
85	Identification of a Novel Somatic Mutation Leading to Allele Dropout for EGFR L858R Genotyping in Non-Small Cell Lung Cancer. <i>Molecular Diagnosis and Therapy</i> , 2017, 21, 431-436.	3.8	2
86	Discovering prescription patterns in pediatric acute-onset neuropsychiatric syndrome patients. <i>Journal of Biomedical Informatics</i> , 2021, 113, 103664.	4.3	2
87	Bayesian model comparison for rare-variant association studies. <i>American Journal of Human Genetics</i> , 2021, 108, 2354-2367.	6.2	2
88	Beyond the reference genome. <i>Nature Biotechnology</i> , 2015, 33, 605-606.	17.5	1
89	Reply to Wang et al.: Sequencing datasets do not refute Central Asian domestication origin of dogs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E2556-E2557.	7.1	1
90	Data mining of digitized health records in a resource-constrained setting reveals that timely immunophenotyping is associated with improved breast cancer outcomes. <i>BMC Cancer</i> , 2018, 18, 933.	2.6	1