John Novembre

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/164951/publications.pdf

Version: 2024-02-01

90
papers

18,248
citations

50170
46
h-index

43802
91
g-index

104
all docs

104
docs citations

104
times ranked

26668
citing authors

#	Article	IF	Citations
1	Haplotype-based inference of the distribution of fitness effects. Genetics, 2022, 220, .	1.2	1
2	Ancient genomes from the Himalayas illuminate the genetic history of Tibetans and their Tibeto-Burman speaking neighbors. Nature Communications, 2022, 13, 1203.	5.8	25
3	Properties of 2-locus genealogies and linkage disequilibrium in temporally structured samples. Genetics, 2022, 221, .	1.2	5
4	The background and legacy of Lewontin's apportionment of human genetic diversity. Philosophical Transactions of the Royal Society B: Biological Sciences, 2022, 377, 20200406.	1.8	17
5	Getting genetic ancestry right for science and society. Science, 2022, 376, 250-252.	6.0	93
6	Public attitudes toward genetic risk scoring in medicine and beyond. Social Science and Medicine, 2021, 274, 113796.	1.8	7
7	Fast and flexible estimation of effective migration surfaces. ELife, 2021, 10, .	2.8	28
8	Parental relatedness through time revealed by runs of homozygosity in ancient DNA. Nature Communications, 2021, 12, 5425.	5.8	94
9	Indigenous Ancestry and Admixture in the Uruguayan Population. Frontiers in Genetics, 2021, 12, 733195.	1.1	6
10	Genetic Landscapes Reveal How Human Genetic Diversity Aligns with Geography. Molecular Biology and Evolution, 2020, 37, 943-951.	3.5	40
11	Genetic history from the Middle Neolithic to present on the Mediterranean island of Sardinia. Nature Communications, 2020, 11, 939.	5.8	96
12	Exploring Population Structure with Admixture Models and Principal Component Analysis. Methods in Molecular Biology, 2020, 2090, 67-86.	0.4	23
13	A variant-centric perspective on geographic patterns of human allele frequency variation. ELife, 2020, 9, .	2.8	33
14	De Novo Mutation Rate Estimation in Wolves of Known Pedigree. Molecular Biology and Evolution, 2019, 36, 2536-2547.	3.5	46
15	Estimating recent migration and population-size surfaces. PLoS Genetics, 2019, 15, e1007908.	1.5	76
16	Circuitâ€theory applications to connectivity science and conservation. Conservation Biology, 2019, 33, 239-249.	2.4	216
17	Inference and visualization of DNA damage patterns using a grade of membership model. Bioinformatics, 2019, 35, 1292-1298.	1.8	7
18	Natural Selection and Origin of a Melanistic Allele in North American Gray Wolves. Molecular Biology and Evolution, 2018, 35, 1190-1209.	3.5	45

#	ARTICLE	IF	CITATIONS
19	Tread Lightly Interpreting Polygenic Tests of Selection. Genetics, 2018, 208, 1351-1355.	1.2	98
20	Estimating Time to the Common Ancestor for a Beneficial Allele. Molecular Biology and Evolution, 2018, 35, 1003-1017.	3.5	53
21	The genetic prehistory of the Andean highlands 7000 years BP though European contact. Science Advances, 2018, 4, eaau4921.	4.7	115
22	Using pseudoalignment and base quality to accurately quantify microbial community composition. PLoS Computational Biology, 2018, 14, e1006096.	1.5	20
23	A tribute to a true conservation innovator, Brad McRae, 1966-2017. Conservation Biology, 2018, 33, 480.	2.4	2
24	Genomic history of the Sardinian population. Nature Genetics, 2018, 50, 1426-1434.	9.4	71
25	Detecting past and ongoing natural selection among ethnically Tibetan women at high altitude in Nepal. PLoS Genetics, 2018, 14, e1007650.	1.5	43
26	Brad McRae (1966â€“2017). Molecular Ecology, 2018, 27, 3035-3036.	2.0	1
27	The first horse herders and the impact of early Bronze Age steppe expansions into Asia. Science, 2018, 360, .	6.0	262
28	Visualizing the geography of genetic variants. Bioinformatics, 2017, 33, 594-595.	1.8	94
29	Population- and individual-specific regulatory variation in Sardinia. Nature Genetics, 2017, 49, 700-707.	9.4	38
30	Overexpression of the Cytokine BAFF and Autoimmunity Risk. New England Journal of Medicine, 2017, 376, 1615-1626.	13.9	301
31	Reconstructing genetic history of Siberian and Northeastern European populations. Genome Research, 2017, 27, 1-14.	2.4	87
32	A Temporal Perspective on the Interplay of Demography and Selection on Deleterious Variation in Humans. G3: Genes, Genomes, Genetics, 2017, 7, 1027-1037.	0.8	14
33	Similar genomic proportions of copy number variation within gray wolves and modern dog breeds inferred from whole genome sequencing. BMC Genomics, 2017, 18, 977.	1.2	24
34	A longitudinal cline characterizes the genetic structure of human populations in the Tibetan plateau. PLoS ONE, 2017, 12, e0175885.	1.1	15
35	Conflation of Short Identity-by-Descent Segments Bias Their Inferred Length Distribution. G3: Genes, Genomes, Genetics, 2016, 6, 1287-1296.	0.8	38
36	Pritchard, Stephens, and Donnelly on Population Structure. Genetics, 2016, 204, 391-393.	1.2	85

#	ARTICLE	IF	CITATIONS
37	Targeted capture and resequencing of 1040 genes reveal environmentally driven functional variation in grey wolves. Molecular Ecology, 2016, 25, 357-379.	2.0	47
38	Genetic subdivision and candidate genes under selection in North American grey wolves. Molecular Ecology, 2016, 25, 380-402.	2.0	100
39	Recent advances in the study of fine-scale population structure in humans. Current Opinion in Genetics and Development, 2016, 41, 98-105.	1.5	47
40	Chimpanzee genomic diversity reveals ancient admixture with bonobos. Science, 2016, 354, 477-481.	6.0	230
41	Visualizing spatial population structure with estimated effective migration surfaces. Nature Genetics, 2016, 48, 94-100.	9.4	445
42	Demographically-Based Evaluation of Genomic Regions under Selection in Domestic Dogs. PLoS Genetics, 2016, 12, e1005851.	1.5	77
43	Ancient DNA steps into the language debate. Nature, 2015, 522, 164-165.	13.7	7
44	Fast and accurate site frequency spectrum estimation from low coverage sequence data. Bioinformatics, 2015, 31, 720-727.	1.8	12
45	Power Analysis of Artificial Selection Experiments Using Efficient Whole Genome Simulation of Quantitative Traits. Genetics, 2015, 199, 991-1005.	1.2	54
46	Genome sequencing elucidates Sardinian genetic architecture and augments association analyses for lipid and blood inflammatory markers. Nature Genetics, 2015, 47, 1272-1281.	9.4	193
47	Height-reducing variants and selection for short stature in Sardinia. Nature Genetics, 2015, 47, 1352-1356.	9.4	96
48	Genome Sequencing Highlights the Dynamic Early History of Dogs. PLoS Genetics, 2014, 10, e1004016.	1.5	481
49	Spatial Localization of Recent Ancestors for Admixed Individuals. G3: Genes, Genomes, Genetics, 2014, 4, 2505-2518.	0.8	19
50	Variations on a Common STRUCTURE: New Algorithms for a Valuable Model. Genetics, 2014, 197, 809-811.	1.2	13
51	Analysis of rare variant population structure in Europeans explains differential stratification of gene-based tests. European Journal of Human Genetics, 2014, 22, 1137-1144.	1.4	21
52	Characterizing Bias in Population Genetic Inferences from Low-Coverage Sequencing Data. Molecular Biology and Evolution, 2014, 31, 723-735.	3.5	76
53	Derived immune and ancestral pigmentation alleles in a 7,000-year-old Mesolithic European. Nature, 2014, 507, 225-228.	13.7	328
54	Demographic Events and Evolutionary Forces Shaping European Genetic Diversity. Cold Spring Harbor Perspectives in Biology, 2014, 6, a008516-a008516.	2.3	14

#	ARTICLE	IF	CITATIONS
55	Fast spatial ancestry via flexible allele frequency surfaces. Bioinformatics, 2014, 30, 2915-2922.	1.8	16
56	Novel statistical methods for integrating genetic and stable isotope data to infer individualâ€•level migratory connectivity. Molecular Ecology, 2013, 22, 4163-4176.	2.0	72
57	The influence of genomic context on mutation patterns in the human genome inferred from rare variants. Genome Research, 2013, 23, 1974-1984.	2.4	51
58	Maximum Likelihood Estimation of Frequencies of Known Haplotypes from Pooled Sequence Data. Molecular Biology and Evolution, 2013, 30, 1145-1158.	3.5	63
59	Human population structure and the adaptive response to pathogen-induced selection pressures. Philosophical Transactions of the Royal Society B: Biological Sciences, 2012, 367, 878-886.	1.8	44
60	Commentary on Sokal, Oden, and Thomson's â€œA Problem with Synthetic Mapsâ€•(1999). Human Biology, 2012, 84, 623-626.	0.4	2
61	An Abundance of Rare Functional Variants in 202 Drug Target Genes Sequenced in 14,002 People. Science, 2012, 337, 100-104.	6.0	626
62	A model-based approach for analysis of spatial structure in genetic data. Nature Genetics, 2012, 44, 725-731.	9.4	147
63	Deep sequencing of the<i>LRRK2</i>gene in 14,002 individuals reveals evidence of purifying selection and independent origin of the p.Arg1628Pro mutation in Europe. Human Mutation, 2012, 33, 1087-1098.	1.1	24
64	A genome-wide perspective on the evolutionary history of enigmatic wolf-like canids. Genome Research, 2011, 21, 1294-1305.	2.4	266
65	Perspectives on Human Population Structure at the Cusp of the Sequencing Era. Annual Review of Genomics and Human Genetics, 2011, 12, 245-274.	2.5	69
66	Recombination rates in admixed individuals identified by ancestry-based inference. Nature Genetics, 2011, 43, 847-853.	9.4	111
67	Genetic variation in the Sorbs of eastern Germany in the context of broader European genetic diversity. European Journal of Human Genetics, 2011, 19, 995-1001.	1.4	59
68	Response to Cavalli-Sforza Interview [Human Biology 82(3):245â€"266 (June 2010)]. Human Biology, 2010, 82, 469-470.	0.4	8
69	Principal Component Analysis under Population Genetic Models of Range Expansion and Admixture. Molecular Biology and Evolution, 2010, 27, 1257-1268.	3.5	125
70	Inferring Genetic Ancestry: Opportunities, Challenges, and Implications. American Journal of Human Genetics, 2010, 86, 661-673.	2.6	214
71	Genome-wide SNP and haplotype analyses reveal a rich history underlying dog domestication. Nature, 2010, 464, 898-902.	13.7	635
72	A Simple Genetic Architecture Underlies Morphological Variation in Dogs. PLoS Biology, 2010, 8, e1000451.	2.6	429

#	ARTICLE	IF	CITATIONS
73	Molecular anthropology in the genomic era. Journal of Anthropological Sciences, 2010, 88, 93-112.	0.4	12
74	Global distribution of genomic diversity underscores rich complex history of continental human populations. Genome Research, 2009, 19, 795-803.	2.4	155
75	Fast model-based estimation of ancestry in unrelated individuals. Genome Research, 2009, 19, 1655-1664.	2.4	6,588
76	Spatial patterns of variation due to natural selection in humans. Nature Reviews Genetics, 2009, 10, 745-755.	7.7	180
77	LIKELIHOOD-BASED INFERENCE IN ISOLATION-BY-DISTANCE MODELS USING THE SPATIAL DISTRIBUTION OF LOW-FREQUENCY ALLELES. Evolution; International Journal of Organic Evolution, 2009, 63, 2914-2925.	1.1	20
78	Signals of recent positive selection in a worldwide sample of human populations. Genome Research, 2009, 19, 826-837.	2.4	658
79	The Role of Geography in Human Adaptation. PLoS Genetics, 2009, 5, e1000500.	1.5	358
80	The Population Reference Sample, POPRES: A Resource for Population, Disease, and Pharmacological Genetics Research. American Journal of Human Genetics, 2008, 83, 347-358.	2.6	289
81	Genes mirror geography within Europe. Nature, 2008, 456, 98-101.	13.7	1,287
82	Interpreting principal component analyses of spatial population genetic variation. Nature Genetics, 2008, 40, 646-649.	9.4	515
83	Polymorphisms of the HNF1A Gene Encoding Hepatocyte Nuclear Factor-1Î± are Associated with C-Reactive Protein. American Journal of Human Genetics, 2008, 82, 1193-1201.	2.6	170
84	Ascertainment Bias in Spatially Structured Populations: A Case Study in the Eastern Fence Lizard. Journal of Heredity, 2007, 98, 331-336.	1.0	82
85	Adaptive drool in the gene pool. Nature Genetics, 2007, 39, 1188-1190.	9.4	20
86	The evolutionary history of the CCR5-Î”32 HIV-resistance mutation. Microbes and Infection, 2005, 7, 302-309.	1.0	115
87	The Geographic Spread of the CCR5 Î”32 HIV-Resistance Allele. PLoS Biology, 2005, 3, e339.	2.6	197
88	Codon Usage Patterns in Cytochrome Oxidase I Across Multiple Insect Orders. Journal of Molecular Evolution, 2003, 56, 691-701.	0.8	17
89	Appendix to Paper by Wall and Herbeck. Journal of Molecular Evolution, 2003, 56, 689-690.	0.8	3
90	Finding Haplotype Block Boundaries by Using the Minimum-Description-Length Principle. American Journal of Human Genetics, 2003, 73, 336-354.	2.6	81