

# John Novembre

## List of Publications by Year in descending order

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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	Fast model-based estimation of ancestry in unrelated individuals. <i>Genome Research</i> , 2009, 19, 1655-1664.	2.4	6,588
2	Genes mirror geography within Europe. <i>Nature</i> , 2008, 456, 98-101.	13.7	1,287
3	Signals of recent positive selection in a worldwide sample of human populations. <i>Genome Research</i> , 2009, 19, 826-837.	2.4	658
4	Genome-wide SNP and haplotype analyses reveal a rich history underlying dog domestication. <i>Nature</i> , 2010, 464, 898-902.	13.7	635
5	An Abundance of Rare Functional Variants in 202 Drug Target Genes Sequenced in 14,002 People. <i>Science</i> , 2012, 337, 100-104.	6.0	626
6	Interpreting principal component analyses of spatial population genetic variation. <i>Nature Genetics</i> , 2008, 40, 646-649.	9.4	515
7	Genome Sequencing Highlights the Dynamic Early History of Dogs. <i>PLoS Genetics</i> , 2014, 10, e1004016.	1.5	481
8	Visualizing spatial population structure with estimated effective migration surfaces. <i>Nature Genetics</i> , 2016, 48, 94-100.	9.4	445
9	A Simple Genetic Architecture Underlies Morphological Variation in Dogs. <i>PLoS Biology</i> , 2010, 8, e1000451.	2.6	429
10	The Role of Geography in Human Adaptation. <i>PLoS Genetics</i> , 2009, 5, e1000500.	1.5	358
11	Derived immune and ancestral pigmentation alleles in a 7,000-year-old Mesolithic European. <i>Nature</i> , 2014, 507, 225-228.	13.7	328
12	Overexpression of the Cytokine BAFF and Autoimmunity Risk. <i>New England Journal of Medicine</i> , 2017, 376, 1615-1626.	13.9	301
13	The Population Reference Sample, POPRES: A Resource for Population, Disease, and Pharmacological Genetics Research. <i>American Journal of Human Genetics</i> , 2008, 83, 347-358.	2.6	289
14	A genome-wide perspective on the evolutionary history of enigmatic wolf-like canids. <i>Genome Research</i> , 2011, 21, 1294-1305.	2.4	266
15	The first horse herders and the impact of early Bronze Age steppe expansions into Asia. <i>Science</i> , 2018, 360, .	6.0	262
16	Chimpanzee genomic diversity reveals ancient admixture with bonobos. <i>Science</i> , 2016, 354, 477-481.	6.0	230
17	Circuit theory applications to connectivity science and conservation. <i>Conservation Biology</i> , 2019, 33, 239-249.	2.4	216
18	Inferring Genetic Ancestry: Opportunities, Challenges, and Implications. <i>American Journal of Human Genetics</i> , 2010, 86, 661-673.	2.6	214

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19	The Geographic Spread of the CCR5 $\Delta$ 32 HIV-Resistance Allele. <i>PLoS Biology</i> , 2005, 3, e339.	2.6	197
20	Genome sequencing elucidates Sardinian genetic architecture and augments association analyses for lipid and blood inflammatory markers. <i>Nature Genetics</i> , 2015, 47, 1272-1281.	9.4	193
21	Spatial patterns of variation due to natural selection in humans. <i>Nature Reviews Genetics</i> , 2009, 10, 745-755.	7.7	180
22	Polymorphisms of the HNF1A Gene Encoding Hepatocyte Nuclear Factor-1 $\alpha$ are Associated with C-Reactive Protein. <i>American Journal of Human Genetics</i> , 2008, 82, 1193-1201.	2.6	170
23	Global distribution of genomic diversity underscores rich complex history of continental human populations. <i>Genome Research</i> , 2009, 19, 795-803.	2.4	155
24	A model-based approach for analysis of spatial structure in genetic data. <i>Nature Genetics</i> , 2012, 44, 725-731.	9.4	147
25	Principal Component Analysis under Population Genetic Models of Range Expansion and Admixture. <i>Molecular Biology and Evolution</i> , 2010, 27, 1257-1268.	3.5	125
26	The evolutionary history of the CCR5- $\Delta$ 32 HIV-resistance mutation. <i>Microbes and Infection</i> , 2005, 7, 302-309.	1.0	115
27	The genetic prehistory of the Andean highlands 7000 years BP though European contact. <i>Science Advances</i> , 2018, 4, eaau4921.	4.7	115
28	Recombination rates in admixed individuals identified by ancestry-based inference. <i>Nature Genetics</i> , 2011, 43, 847-853.	9.4	111
29	Genetic subdivision and candidate genes under selection in North American grey wolves. <i>Molecular Ecology</i> , 2016, 25, 380-402.	2.0	100
30	Tread Lightly Interpreting Polygenic Tests of Selection. <i>Genetics</i> , 2018, 208, 1351-1355.	1.2	98
31	Height-reducing variants and selection for short stature in Sardinia. <i>Nature Genetics</i> , 2015, 47, 1352-1356.	9.4	96
32	Genetic history from the Middle Neolithic to present on the Mediterranean island of Sardinia. <i>Nature Communications</i> , 2020, 11, 939.	5.8	96
33	Visualizing the geography of genetic variants. <i>Bioinformatics</i> , 2017, 33, 594-595.	1.8	94
34	Parental relatedness through time revealed by runs of homozygosity in ancient DNA. <i>Nature Communications</i> , 2021, 12, 5425.	5.8	94
35	Getting genetic ancestry right for science and society. <i>Science</i> , 2022, 376, 250-252.	6.0	93
36	Reconstructing genetic history of Siberian and Northeastern European populations. <i>Genome Research</i> , 2017, 27, 1-14.	2.4	87

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37	Pritchard, Stephens, and Donnelly on Population Structure. <i>Genetics</i> , 2016, 204, 391-393.	1.2	85
38	Ascertainment Bias in Spatially Structured Populations: A Case Study in the Eastern Fence Lizard. <i>Journal of Heredity</i> , 2007, 98, 331-336.	1.0	82
39	Finding Haplotype Block Boundaries by Using the Minimum-Description-Length Principle. <i>American Journal of Human Genetics</i> , 2003, 73, 336-354.	2.6	81
40	Demographically-Based Evaluation of Genomic Regions under Selection in Domestic Dogs. <i>PLoS Genetics</i> , 2016, 12, e1005851.	1.5	77
41	Characterizing Bias in Population Genetic Inferences from Low-Coverage Sequencing Data. <i>Molecular Biology and Evolution</i> , 2014, 31, 723-735.	3.5	76
42	Estimating recent migration and population-size surfaces. <i>PLoS Genetics</i> , 2019, 15, e1007908.	1.5	76
43	Novel statistical methods for integrating genetic and stable isotope data to infer individual-level migratory connectivity. <i>Molecular Ecology</i> , 2013, 22, 4163-4176.	2.0	72
44	Genomic history of the Sardinian population. <i>Nature Genetics</i> , 2018, 50, 1426-1434.	9.4	71
45	Perspectives on Human Population Structure at the Cusp of the Sequencing Era. <i>Annual Review of Genomics and Human Genetics</i> , 2011, 12, 245-274.	2.5	69
46	Maximum Likelihood Estimation of Frequencies of Known Haplotypes from Pooled Sequence Data. <i>Molecular Biology and Evolution</i> , 2013, 30, 1145-1158.	3.5	68
47	Genetic variation in the Sorbs of eastern Germany in the context of broader European genetic diversity. <i>European Journal of Human Genetics</i> , 2011, 19, 995-1001.	1.4	59
48	Power Analysis of Artificial Selection Experiments Using Efficient Whole Genome Simulation of Quantitative Traits. <i>Genetics</i> , 2015, 199, 991-1005.	1.2	54
49	Estimating Time to the Common Ancestor for a Beneficial Allele. <i>Molecular Biology and Evolution</i> , 2018, 35, 1003-1017.	3.5	53
50	The influence of genomic context on mutation patterns in the human genome inferred from rare variants. <i>Genome Research</i> , 2013, 23, 1974-1984.	2.4	51
51	Targeted capture and resequencing of 1040 genes reveal environmentally driven functional variation in grey wolves. <i>Molecular Ecology</i> , 2016, 25, 357-379.	2.0	47
52	Recent advances in the study of fine-scale population structure in humans. <i>Current Opinion in Genetics and Development</i> , 2016, 41, 98-105.	1.5	47
53	De Novo Mutation Rate Estimation in Wolves of Known Pedigree. <i>Molecular Biology and Evolution</i> , 2019, 36, 2536-2547.	3.5	46
54	Natural Selection and Origin of a Melanistic Allele in North American Gray Wolves. <i>Molecular Biology and Evolution</i> , 2018, 35, 1190-1209.	3.5	45

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55	Human population structure and the adaptive response to pathogen-induced selection pressures. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2012, 367, 878-886.	1.8	44
56	Detecting past and ongoing natural selection among ethnically Tibetan women at high altitude in Nepal. <i>PLoS Genetics</i> , 2018, 14, e1007650.	1.5	43
57	Genetic Landscapes Reveal How Human Genetic Diversity Aligns with Geography. <i>Molecular Biology and Evolution</i> , 2020, 37, 943-951.	3.5	40
58	Conflation of Short Identity-by-Descent Segments Bias Their Inferred Length Distribution. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 1287-1296.	0.8	38
59	Population- and individual-specific regulatory variation in Sardinia. <i>Nature Genetics</i> , 2017, 49, 700-707.	9.4	38
60	A variant-centric perspective on geographic patterns of human allele frequency variation. <i>ELife</i> , 2020, 9, .	2.8	33
61	Fast and flexible estimation of effective migration surfaces. <i>ELife</i> , 2021, 10, .	2.8	28
62	Ancient genomes from the Himalayas illuminate the genetic history of Tibetans and their Tibeto-Burman speaking neighbors. <i>Nature Communications</i> , 2022, 13, 1203.	5.8	25
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. <i>Human Mutation</i> , 2012, 33, 1087-1098.	1.1	24
64	Similar genomic proportions of copy number variation within gray wolves and modern dog breeds inferred from whole genome sequencing. <i>BMC Genomics</i> , 2017, 18, 977.	1.2	24
65	Exploring Population Structure with Admixture Models and Principal Component Analysis. <i>Methods in Molecular Biology</i> , 2020, 2090, 67-86.	0.4	23
66	Analysis of rare variant population structure in Europeans explains differential stratification of gene-based tests. <i>European Journal of Human Genetics</i> , 2014, 22, 1137-1144.	1.4	21
67	Adaptive drift in the gene pool. <i>Nature Genetics</i> , 2007, 39, 1188-1190.	9.4	20
68	LIKELIHOOD-BASED INFERENCE IN ISOLATION-BY-DISTANCE MODELS USING THE SPATIAL DISTRIBUTION OF LOW-FREQUENCY ALLELES. <i>Evolution; International Journal of Organic Evolution</i> , 2009, 63, 2914-2925.	1.1	20
69	Using pseudoalignment and base quality to accurately quantify microbial community composition. <i>PLoS Computational Biology</i> , 2018, 14, e1006096.	1.5	20
70	Spatial Localization of Recent Ancestors for Admixed Individuals. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 2505-2518.	0.8	19
71	Codon Usage Patterns in Cytochrome Oxidase I Across Multiple Insect Orders. <i>Journal of Molecular Evolution</i> , 2003, 56, 691-701.	0.8	17
72	The background and legacy of Lewontin's apportionment of human genetic diversity. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2022, 377, 20200406.	1.8	17

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73	Fast spatial ancestry via flexible allele frequency surfaces. <i>Bioinformatics</i> , 2014, 30, 2915-2922.	1.8	16
74	A longitudinal cline characterizes the genetic structure of human populations in the Tibetan plateau. <i>PLoS ONE</i> , 2017, 12, e0175885.	1.1	15
75	Demographic Events and Evolutionary Forces Shaping European Genetic Diversity. <i>Cold Spring Harbor Perspectives in Biology</i> , 2014, 6, a008516-a008516.	2.3	14
76	A Temporal Perspective on the Interplay of Demography and Selection on Deleterious Variation in Humans. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 1027-1037.	0.8	14
77	Variations on a Common STRUCTURE: New Algorithms for a Valuable Model. <i>Genetics</i> , 2014, 197, 809-811.	1.2	13
78	Fast and accurate site frequency spectrum estimation from low coverage sequence data. <i>Bioinformatics</i> , 2015, 31, 720-727.	1.8	12
79	Molecular anthropology in the genomic era. <i>Journal of Anthropological Sciences</i> , 2010, 88, 93-112.	0.4	12
80	Response to Cavalli-Sforza Interview [ <i>Human Biology</i> 82(3):245â€“266 (June 2010)]. <i>Human Biology</i> , 2010, 82, 469-470.	0.4	8
81	Ancient DNA steps into the language debate. <i>Nature</i> , 2015, 522, 164-165.	13.7	7
82	Inference and visualization of DNA damage patterns using a grade of membership model. <i>Bioinformatics</i> , 2019, 35, 1292-1298.	1.8	7
83	Public attitudes toward genetic risk scoring in medicine and beyond. <i>Social Science and Medicine</i> , 2021, 274, 113796.	1.8	7
84	Indigenous Ancestry and Admixture in the Uruguayan Population. <i>Frontiers in Genetics</i> , 2021, 12, 733195.	1.1	6
85	Properties of 2-locus genealogies and linkage disequilibrium in temporally structured samples. <i>Genetics</i> , 2022, 221, .	1.2	5
86	Appendix to Paper by Wall and Herbeck. <i>Journal of Molecular Evolution</i> , 2003, 56, 689-690.	0.8	3
87	Commentary on Sokal, Oden, and Thomson's "A Problem with Synthetic Maps" (1999). <i>Human Biology</i> , 2012, 84, 623-626.	0.4	2
88	A tribute to a true conservation innovator, Brad McRae, 1966-2017. <i>Conservation Biology</i> , 2018, 33, 480.	2.4	2
89	Brad McRae (1966â€“2017). <i>Molecular Ecology</i> , 2018, 27, 3035-3036.	2.0	1
90	Haplotype-based inference of the distribution of fitness effects. <i>Genetics</i> , 2022, 220, .	1.2	1