

# Bruce S Weir

## List of Publications by Year in descending order

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Version: 2024-02-01

36  
papers

9,793  
citations

304743

22  
h-index

377865

34  
g-index

41  
all docs

41  
docs citations

41  
times ranked

19080  
citing authors

#	ARTICLE	IF	CITATIONS
1	A second generation human haplotype map of over 3.1 million SNPs. <i>Nature</i> , 2007, 449, 851-861.	27.8	4,137
2	A high-performance computing toolset for relatedness and principal component analysis of SNP data. <i>Bioinformatics</i> , 2012, 28, 3326-3328.	4.1	1,939
3	Genetics in geographically structured populations: defining, estimating and interpreting FST. <i>Nature Reviews Genetics</i> , 2009, 10, 639-650.	16.3	1,089
4	Quality control and quality assurance in genotypic data for genome-wide association studies. <i>Genetic Epidemiology</i> , 2010, 34, 591-602.	1.3	389
5	Model-free Estimation of Recent Genetic Relatedness. <i>American Journal of Human Genetics</i> , 2016, 98, 127-148.	6.2	331
6	Genetic relatedness analysis: modern data and new challenges. <i>Nature Reviews Genetics</i> , 2006, 7, 771-780.	16.3	297
7	A Genome-Wide Survey of Hybrid Incompatibility Factors by the Introgression of Marked Segments of <i>Drosophila mauritiana</i> Chromosomes into <i>Drosophila simulans</i> . <i>Genetics</i> , 1996, 142, 819-837.	2.9	270
8	Measures of human population structure show heterogeneity among genomic regions. <i>Genome Research</i> , 2005, 15, 1468-1476.	5.5	250
9	GWASTools: an R/Bioconductor package for quality control and analysis of genome-wide association studies. <i>Bioinformatics</i> , 2012, 28, 3329-3331.	4.1	177
10	A Unified Characterization of Population Structure and Relatedness. <i>Genetics</i> , 2017, 206, 2085-2103.	2.9	135
11	SeqArray—a storage-efficient high-performance data format for WGS variant calls. <i>Bioinformatics</i> , 2017, 33, 2251-2257.	4.1	127
12	How to estimate kinship. <i>Molecular Ecology</i> , 2018, 27, 4121-4135.	3.9	87
13	Public Access to Genome-Wide Data: Five Views on Balancing Research with Privacy and Protection. <i>PLoS Genetics</i> , 2009, 5, e1000665.	3.5	71
14	A genome-wide study of Hardy-Weinberg equilibrium with next generation sequence data. <i>Human Genetics</i> , 2017, 136, 727-741.	3.8	63
15	The rarity of DNA profiles. <i>Annals of Applied Statistics</i> , 2007, 1, 358-370.	1.1	58
16	Detection and quantification of inbreeding depression for complex traits from SNP data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 8602-8607.	7.1	48
17	Mixed model approaches for diallel analysis based on a bio-model. <i>Genetical Research</i> , 1996, 68, 233-240.	0.9	42
18	Estimating $F_{ST}$ -Statistics: A Historical View. <i>Philosophy of Science</i> , 2012, 79, 637-643.	1.0	35

#	ARTICLE	IF	CITATIONS
19	Eigenanalysis of SNP data with an identity by descent interpretation. <i>Theoretical Population Biology</i> , 2016, 107, 65-76.	1.1	35
20	Combating transnational organized crime by linking multiple large ivory seizures to the same dealer. <i>Science Advances</i> , 2018, 4, eaat0625.	10.3	31
21	DNA statistics in the Simpson matter. <i>Nature Genetics</i> , 1995, 11, 365-368.	21.4	30
22	Population Structure With Localized Haplotype Clusters. <i>Genetics</i> , 2010, 185, 1337-1344.	2.9	28
23	Multi-allelic exact tests for Hardy-Weinberg equilibrium that account for gender. <i>Molecular Ecology Resources</i> , 2018, 18, 461-473.	4.8	21
24	Analyzing population structure for forensic STR markers in next generation sequencing data. <i>Forensic Science International: Genetics</i> , 2020, 49, 102364.	3.1	17
25	Matching and partially-matching DNA profiles. <i>Journal of Forensic Sciences</i> , 2004, 49, 1009-14.	1.6	14
26	How HLA diversity is apportioned: influence of selection and relevance to transplantation. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2022, 377, 20200420.	4.0	14
27	Drawing inferences about the coancestry coefficient. <i>Theoretical Population Biology</i> , 2009, 75, 312-319.	1.1	11
28	Statistical genetic issues for genome-wide association studies This article is one of a selection of papers from the conference "Exploiting Genome-wide Association in Oilseed Brassicas: a model for genetic improvement of major OECD crops for sustainable farming". <i>Genome</i> , 2010, 53, 869-875.	2.0	10
29	Rank-invariant estimation of inbreeding coefficients. <i>Heredity</i> , 2022, 128, 1-10.	2.6	9
30	Elephant genotypes reveal the size and connectivity of transnational ivory traffickers. <i>Nature Human Behaviour</i> , 2022, 6, 371-382.	12.0	9
31	Reply to Kardos et al.: Estimation of inbreeding depression from SNP data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E2494-E2495.	7.1	6
32	The transitivity of the Hardy-Weinberg law. <i>Forensic Science International: Genetics</i> , 2022, 58, 102680.	3.1	6
33	Interpreting Whole-Genome Marker Data. <i>Statistics in Biosciences</i> , 2013, 5, 316-329.	1.2	3
34	From Mendel to quantitative genetics in the genome era: the scientific legacy of W. G. Hill. <i>Nature Genetics</i> , 2022, 54, 934-939.	21.4	3
35	Introduction: Transmission/Disequilibrium Test/Association Group. <i>Genetic Epidemiology</i> , 2001, 21, S421.	1.3	0
36	The Summer Institute in Statistical Genetics. <i>Genetics</i> , 2019, 212, 955-957.	2.9	0