Bruce S Weir

List of Publications by Year
in descending order

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	Rank-invariant estimation of inbreeding coefficients. Heredity, 2022, 128, 1-10.	2.6	9
2	Elephant genotypes reveal the size and connectivity of transnational ivory traffickers. Nature Human Behaviour, 2022, 6, 371-382.	12.0	9
3	The transitivity of the Hardy–Weinberg law. Forensic Science International: Genetics, 2022, 58, 102680.	3.1	6
4	How HLA diversity is apportioned: influence of selection and relevance to transplantation. Philosophical Transactions of the Royal Society B: Biological Sciences, 2022, 377, 20200420.	4.0	14
5	From Mendel to quantitative genetics in the genome era: the scientific legacy of W. G. Hill. Nature Genetics, 2022, 54, 934-939.	21.4	3
6	Analyzing population structure for forensic STR markers in next generation sequencing data. Forensic Science International: Genetics, 2020, 49, 102364.	3.1	17
7	The Summer Institute in Statistical Genetics. Genetics, 2019, 212, 955-957.	2.9	0
8	Reply to Kardos et al.: Estimation of inbreeding depression from SNP data. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E2494-E2495.	7.1	6
9	Multi–allelic exact tests for Hardy–Weinberg equilibrium that account for gender. Molecular Ecology Resources, 2018, 18, 461-473.	4.8	21
10	Combating transnational organized crime by linking multiple large ivory seizures to the same dealer. Science Advances, 2018, 4, eaat0625.	10.3	31
11	How to estimate kinship. Molecular Ecology, 2018, 27, 4121-4135.	3.9	87
12	A genome-wide study of Hardy–Weinberg equilibrium with next generation sequence data. Human Genetics, 2017, 136, 727-741.	3.8	63
13	SeqArray–a storage-efficient high-performance data format for WGS variant calls. Bioinformatics, 2017, 33, 2251-2257.	4.1	127
14	A Unified Characterization of Population Structure and Relatedness. Genetics, 2017, 206, 2085-2103.	2.9	135
15	Detection and quantification of inbreeding depression for complex traits from SNP data. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 8602-8607.	7.1	48
16	Eigenanalysis of SNP data with an identity by descent interpretation. Theoretical Population Biology, 2016, 107, 65-76.	1.1	35
17	Model-free Estimation of Recent Genetic Relatedness. American Journal of Human Genetics, 2016, 98, 127-148.	6.2	331
18	Interpreting Whole-Genome Marker Data. Statistics in Biosciences, 2013, 5, 316-329.	1.2	3

#	ARTICLE	IF	CITATIONS
19	Estimating F-Statistics: A Historical View. Philosophy of Science, 2012, 79, 637-643.	1.0	35
20	A high-performance computing toolset for relatedness and principal component analysis of SNP data. Bioinformatics, 2012, 28, 3326-3328.	4.1	1,939
21	GWASTools: an R/Bioconductor package for quality control and analysis of genome-wide association studies. Bioinformatics, 2012, 28, 3329-3331.	4.1	177
22	Quality control and quality assurance in genotypic data for genome‐wide association studies. Genetic Epidemiology, 2010, 34, 591-602.	1.3	389
23	Population Structure With Localized Haplotype Clusters. Genetics, 2010, 185, 1337-1344.	2.9	28
24	Statistical genetic issues for genome-wide association studiesThis 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". Genome, 2010, 53, 869-875.	2.0	10
25	Public Access to Genome-Wide Data: Five Views on Balancing Research with Privacy and Protection. PLoS Genetics, 2009, 5, e1000665.	3.5	71
26	Drawing inferences about the coancestry coefficient. Theoretical Population Biology, 2009, 75, 312-319.	1.1	11
27	Genetics in geographically structured populations: defining, estimating and interpreting FST. Nature Reviews Genetics, 2009, 10, 639-650.	16.3	1,089
28	The rarity of DNA profiles. Annals of Applied Statistics, 2007, 1, 358-370.	1.1	58
29	A second generation human haplotype map of over 3.1 million SNPs. Nature, 2007, 449, 851-861.	27.8	4,137
30	Genetic relatedness analysis: modern data and new challenges. Nature Reviews Genetics, 2006, 7, 771-780.	16.3	297
31	Measures of human population structure show heterogeneity among genomic regions. Genome Research, 2005, 15, 1468-1476.	5.5	250
32	Matching and partially-matching DNA profiles. Journal of Forensic Sciences, 2004, 49, 1009-14.	1.6	14
33	Introduction: Transmission/Disequilibrium Test/Association Group. Genetic Epidemiology, 2001, 21, S421.	1.3	0
34	Mixed model approaches for diallel analysis based on a bio-model. Genetical Research, 1996, 68, 233-240.	0.9	42
35	A Genome-Wide Survey of Hybrid Incompatibility Factors by the Introgression of Marked Segments of *Drosophila mauritiana* Chromosomes into *Drosophila simulans*. Genetics, 1996, 142, 819-837.	2.9	270
36	DNA statistics in the Simpson matter. Nature Genetics, 1995, 11, 365-368.	21.4	30