Bryan Howie

List of Publications by Year
in descending order

17 papers	9,569 citations	471509 17 h-index	888059 17 g-index
17 all docs	17 docs citations	17 times ranked	22080 citing authors

#	Article	IF	Citations
1	A new multipoint method for genome-wide association studies by imputation of genotypes. Nature Genetics, 2007, 39, 906-913.	21.4	2,407
2	Fast and accurate genotype imputation in genome-wide association studies through pre-phasing. Nature Genetics, 2012, 44, 955-959.	21.4	1,592
3	Genotype imputation for genome-wide association studies. Nature Reviews Genetics, 2010, 11, 499-511.	16.3	1,408
4	Identification of loci associated with schizophrenia by genome-wide association and follow-up. Nature Genetics, 2008, 40, 1053-1055.	21.4	977
5	Genotype Imputation with Thousands of Genomes. G3: Genes, Genomes, Genetics, 2011, 1, 457-470.	1.8	869
6	Haplotype Estimation Using Sequencing Reads. American Journal of Human Genetics, 2013, 93, 687-696.	6.2	364
7	Genome-wide and fine-resolution association analysis of malaria in West Africa. Nature Genetics, 2009, 41, 657-665.	21.4	345
8	Landscape of immunogenic tumor antigens in successful immunotherapy of virally induced epithelial cancer. Science, 2017, 356, 200-205.	12.6	327
9	Improved imputation of low-frequency and rare variants using the UK10K haplotype reference panel. Nature Communications, 2015, 6, 8111.	12.8	300
10	High-throughput pairing of T cell receptor Î± and Î² sequences. Science Translational Medicine, 2015, 7, 301ra131.	12.4	209
11	The origin, evolution, and functional impact of short insertionâ€“deletion variants identified in 179 human genomes. Genome Research, 2013, 23, 749-761.	5.5	206
12	Tumor- and Neoantigen-Reactive T-cell Receptors Can Be Identified Based on Their Frequency in Fresh Tumor. Cancer Immunology Research, 2016, 4, 734-743.	3.4	163
13	Detection of Minimal Residual Disease in B Lymphoblastic Leukemia by High-Throughput Sequencing of IGH. Clinical Cancer Research, 2014, 20, 4540-4548.	7.0	138
14	1000 Genomes-based imputation identifies novel and refined associations for the Wellcome Trust Case Control Consortium phase 1 Data. European Journal of Human Genetics, 2012, 20, 801-805.	2.8	123
15	Analytical evaluation of the clonoSEQ Assay for establishing measurable (minimal) residual disease in acute lymphoblastic leukemia, chronic lymphocytic leukemia, and multiple myeloma. BMC Cancer, 2020, 20, 612.	2.6	72
16	Comparing Algorithms for Genotype Imputation. American Journal of Human Genetics, 2008, 83, 535-539.	6.2	37
17	Estimating the Ages of Selection Signals from Different Epochs in Human History. Molecular Biology and Evolution, 2016, 33, 657-669.	8.9	32