

Bryan Howie

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11653165/publications.pdf>

Version: 2024-02-01

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