Nils Homer

List of Publications by Year
in descending order

15 papers	52,118 citations	687363 13 h-index	996975 15 g-index
16 all docs	16 docs citations	16 times ranked	94984 citing authors

#	Article	IF	Citations
1	An international effort towards developing standards for best practices in analysis, interpretation and reporting of clinical genome sequencing results in the CLARITY Challenge. Genome Biology, 2014, 15, R53.	9.6	101
2	Local alignment of generalized k-base encoded DNA sequence. BMC Bioinformatics, 2010, 11, 347.	2.6	1
3	U87MG Decoded: The Genomic Sequence of a Cytogenetically Aberrant Human Cancer Cell Line. PLoS Genetics, 2010, 6, e1000832.	3.5	229
4	A survey of sequence alignment algorithms for next-generation sequencing. Briefings in Bioinformatics, 2010, 11, 473-483.	6.5	765
5	Improved variant discovery through local re-alignment of short-read next-generation sequencing data using SRMA. Genome Biology, 2010, 11, R99.	8.8	61
6	BFAST: An Alignment Tool for Large Scale Genome Resequencing. PLoS ONE, 2009, 4, e7767.	2.5	444
7	Statistical Comparison Framework and Visualization Scheme for Ranking-Based Algorithms in High-Throughput Genome-Wide Studies. Journal of Computational Biology, 2009, 16, 565-577.	1.6	0
8	Improving the efficiency of genomic loci capture using oligonucleotide arrays for high throughput resequencing. BMC Genomics, 2009, 10, 646.	2.8	34
9	Local alignment of two-base encoded DNA sequence. BMC Bioinformatics, 2009, 10, 175.	2.6	32
10	The Sequence Alignment/Map format and SAMtools. Bioinformatics, 2009, 25, 2078-2079.	4.1	49,124
11	A Genome-wide Analysis Identifies Genetic Variants in the RELN Gene Associated with Otosclerosis. American Journal of Human Genetics, 2009, 84, 328-338.	6.2	66
12	Common sequence variants on 20q11.22 confer melanoma susceptibility. Nature Genetics, 2008, 40, 838-840.	21.4	209
13	Multimarker analysis and imputation of multiple platform pooling-based genome-wide association studies. Bioinformatics, 2008, 24, 1896-1902.	4.1	18
14	Resolving Individuals Contributing Trace Amounts of DNA to Highly Complex Mixtures Using High-Density SNP Genotyping Microarrays. PLoS Genetics, 2008, 4, e1000167.	3.5	892
15	Identification of the Genetic Basis for Complex Disorders by Use of Pooling-Based Genomewide Single-Nucleotideâ€“Polymorphism Association Studies. American Journal of Human Genetics, 2007, 80, 126-139.	6.2	139