Nils Homer

List of Publications by Year in Descending Order

15 papers	33,302 citations	13 h-index	16 g-index
16 ext. papers	45,939 ext. citations	9.7 avg, IF	6.64 L-index

#	Paper	IF	Citations
15	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	18.3	86
14	U87MG decoded: the genomic sequence of a cytogenetically aberrant human cancer cell line. *PLoS Genetics*, **2010**, 6, e1000832	6	195
13	A survey of sequence alignment algorithms for next-generation sequencing. *Briefings in Bioinformatics*, **2010**, 11, 473-83	13.4	632
12	Improved variant discovery through local re-alignment of short-read next-generation sequencing data using SRMA. *Genome Biology*, **2010**, 11, R99	18.3	57
11	Local alignment of generalized k-base encoded DNA sequence. *BMC Bioinformatics*, **2010**, 11, 347	3.6	1
10	BFAST: an alignment tool for large scale genome resequencing. *PLoS ONE*, **2009**, 4, e7767	3.7	394
9	Statistical comparison framework and visualization scheme for ranking-based algorithms in high-throughput genome-wide studies. *Journal of Computational Biology*, **2009**, 16, 565-77	1.7	
8	Improving the efficiency of genomic loci capture using oligonucleotide arrays for high throughput resequencing. *BMC Genomics*, **2009**, 10, 646	4.5	32
7	Local alignment of two-base encoded DNA sequence. *BMC Bioinformatics*, **2009**, 10, 175	3.6	30
6	The Sequence Alignment/Map format and SAMtools. *Bioinformatics*, **2009**, 25, 2078-9	7.2	30805
5	A genome-wide analysis identifies genetic variants in the RELN gene associated with otosclerosis. *American Journal of Human Genetics*, **2009**, 84, 328-38	11	52
4	Common sequence variants on 20q11.22 confer melanoma susceptibility. *Nature Genetics*, **2008**, 40, 838-40	36.3	188
3	Multimarker analysis and imputation of multiple platform pooling-based genome-wide association studies. *Bioinformatics*, **2008**, 24, 1896-902	7.2	15
2	Resolving individuals contributing trace amounts of DNA to highly complex mixtures using high-density SNP genotyping microarrays. *PLoS Genetics*, **2008**, 4, e1000167	6	686
1	Identification of the genetic basis for complex disorders by use of pooling-based genomewide single-nucleotide-polymorphism association studies. *American Journal of Human Genetics*, **2007**, 80, 126-39	11	129