

Nils Homer

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/12108621/publications.pdf>

Version: 2024-02-01

15
papers

52,118
citations

686830

13
h-index

996533

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. <i>Genome Biology</i> , 2014, 15, R53.	13.9	101
2	Local alignment of generalized k-base encoded DNA sequence. <i>BMC Bioinformatics</i> , 2010, 11, 347.	1.2	1
3	U87MG Decoded: The Genomic Sequence of a Cytogenetically Aberrant Human Cancer Cell Line. <i>PLoS Genetics</i> , 2010, 6, e1000832.	1.5	229
4	A survey of sequence alignment algorithms for next-generation sequencing. <i>Briefings in Bioinformatics</i> , 2010, 11, 473-483.	3.2	765
5	Improved variant discovery through local re-alignment of short-read next-generation sequencing data using SRMA. <i>Genome Biology</i> , 2010, 11, R99.	3.8	61
6	BFAST: An Alignment Tool for Large Scale Genome Resequencing. <i>PLoS ONE</i> , 2009, 4, e7767.	1.1	444
7	Statistical Comparison Framework and Visualization Scheme for Ranking-Based Algorithms in High-Throughput Genome-Wide Studies. <i>Journal of Computational Biology</i> , 2009, 16, 565-577.	0.8	0
8	Improving the efficiency of genomic loci capture using oligonucleotide arrays for high throughput resequencing. <i>BMC Genomics</i> , 2009, 10, 646.	1.2	34
9	Local alignment of two-base encoded DNA sequence. <i>BMC Bioinformatics</i> , 2009, 10, 175.	1.2	32
10	The Sequence Alignment/Map format and SAMtools. <i>Bioinformatics</i> , 2009, 25, 2078-2079.	1.8	49,124
11	A Genome-wide Analysis Identifies Genetic Variants in the RELN Gene Associated with Otosclerosis. <i>American Journal of Human Genetics</i> , 2009, 84, 328-338.	2.6	66
12	Common sequence variants on 20q11.22 confer melanoma susceptibility. <i>Nature Genetics</i> , 2008, 40, 838-840.	9.4	209
13	Multimarker analysis and imputation of multiple platform pooling-based genome-wide association studies. <i>Bioinformatics</i> , 2008, 24, 1896-1902.	1.8	18
14	Resolving Individuals Contributing Trace Amounts of DNA to Highly Complex Mixtures Using High-Density SNP Genotyping Microarrays. <i>PLoS Genetics</i> , 2008, 4, e1000167.	1.5	892
15	Identification of the Genetic Basis for Complex Disorders by Use of Pooling-Based Genomewide Single-Nucleotide Polymorphism Association Studies. <i>American Journal of Human Genetics</i> , 2007, 80, 126-139.	2.6	139