# Nils Homer

List of Publications by Year
in descending order

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

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 1 | The Sequence Alignment/Map format and SAMtools. Bioinformatics, 2009, 25, 2078-2079. | 4.1 | 49,124 |
| 2 | 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 |
| 3 | A survey of sequence alignment algorithms for next-generation sequencing. Briefings in Bioinformatics, 2010, 11, 473-483. | 6.5 | 765 |
| 4 | BFAST: An Alignment Tool for Large Scale Genome Resequencing. PLoS ONE, 2009, 4, e7767. | 2.5 | 444 |
| 5 | U87MG Decoded: The Genomic Sequence of a Cytogenetically Aberrant Human Cancer Cell Line. PLoS Genetics, 2010, 6, e1000832. | 3.5 | 229 |
| 6 | Common sequence variants on 20q11.22 confer melanoma susceptibility. Nature Genetics, 2008, 40, 838-840. | 21.4 | 209 |
| 7 | 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 |
| 8 | 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 |
| 9 | 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 |
| 10 | Improved variant discovery through local re-alignment of short-read next-generation sequencing data using SRMA. Genome Biology, 2010, 11, R99. | 8.8 | 61 |
| 11 | Improving the efficiency of genomic loci capture using oligonucleotide arrays for high throughput resequencing. BMC Genomics, 2009, 10, 646. | 2.8 | 34 |
| 12 | Local alignment of two-base encoded DNA sequence. BMC Bioinformatics, 2009, 10, 175. | 2.6 | 32 |
| 13 | Multimarker analysis and imputation of multiple platform pooling-based genome-wide association studies. Bioinformatics, 2008, 24, 1896-1902. | 4.1 | 18 |
| 14 | Local alignment of generalized k-base encoded DNA sequence. BMC Bioinformatics, 2010, 11, 347. | 2.6 | 1 |
| 15 | 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 |