Ankit Malhotra

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/3307807/publications.pdf

Version: 2024-02-01

26	10,395	567281 15	713466 21
papers	citations	h-index	g-index

27	27	27	19655
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. Nature, 2007, 447, 799-816.	27.8	4,709
2	An integrated map of structural variation in 2,504 human genomes. Nature, 2015, 526, 75-81.	27.8	1,994
3	A novel class of small RNAs: tRNA-derived RNA fragments (tRFs). Genes and Development, 2009, 23, 2639-2649.	5.9	914
4	Muscle-specific microRNA miR-206 promotes muscle differentiation. Journal of Cell Biology, 2006, 174, 677-687.	5.2	710
5	Multi-platform discovery of haplotype-resolved structural variation in human genomes. Nature Communications, 2019, 10, 1784.	12.8	636
6	Punctuated bursts in human male demography inferred from 1,244 worldwide Y-chromosome sequences. Nature Genetics, 2016, 48, 593-599.	21.4	273
7	Efficient CRISPR/Cas9-Mediated Genome Editing in Mice by Zygote Electroporation of Nuclease. Genetics, 2015, 200, 423-430.	2.9	231
8	miR-99 Family of MicroRNAs Suppresses the Expression of Prostate-Specific Antigen and Prostate Cancer Cell Proliferation. Cancer Research, 2011, 71, 1313-1324.	0.9	217
9	Breakpoint profiling of 64 cancer genomes reveals numerous complex rearrangements spawned by homology-independent mechanisms. Genome Research, 2013, 23, 762-776.	5.5	155
10	Genomic Study of Replication Initiation in Human Chromosomes Reveals the Influence of Transcription Regulation and Chromatin Structure on Origin Selection. Molecular Biology of the Cell, 2010, 21, 393-404.	2.1	151
11	The tandem duplicator phenotype as a distinct genomic configuration in cancer. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E2373-82.	7.1	103
12	Pan-S replication patterns and chromosomal domains defined by genome-tiling arrays of ENCODE genomic areas. Genome Research, 2007, 17, 865-876.	5.5	94
13	FusorSV: an algorithm for optimally combining data from multiple structural variation detection methods. Genome Biology, 2018, 19, 38.	8.8	46
14	Systems consequences of amplicon formation in human breast cancer. Genome Research, 2014, 24, 1559-1571.	5.5	32
15	Detection of DNA fusion junctions for BCR-ABL translocations by Anchored ChromPET. Genome Medicine, 2010, 2, 70.	8.2	25
16	Targeted Comparative RNA Interference Analysis Reveals Differential Requirement of Genes Essential for Cell Proliferation. Molecular Biology of the Cell, 2006, 17, 4837-4845.	2.1	15
17	Chromosomal structural variations during progression of a prostate epithelial cell line to a malignant metastatic state inactivate the NF2, NIPSNAP1, UGT2B17, and LPIN2 genes. Cancer Biology and Therapy, 2013, 14, 840-852.	3.4	15
18	Yeast genome analysis identifies chromosomal translocation, gene conversion events and several sites of Ty element insertion. Nucleic Acids Research, 2009, 37, 6454-6465.	14.5	12

#	Article	IF	Citations
19	A Bayesian Framework for Generalized Linear Mixed Modeling Identifies New Candidate Loci for Late-Onset Alzheimerâ€™s Disease. Genetics, 2018, 209, 51-64.	2.9	12
20	Ploidy-Seq: inferring mutational chronology by sequencing polyploid tumor subpopulations. Genome Medicine, 2015, 7, 6.	8.2	6
21	Computational inference of a genomic pluripotency signature in human and mouse stem cells. Biology Direct, 2016, 11, 47.	4.6	5
22	Analysis of Structural Chromosome Variants by Next Generation Sequencing Methods. , 2016, , 39-61.		0
23	Genome Informatics. , 2019, , 178-194.		0
24	Identifying determinants of chromosomal domains as defined by time of replication. FASEB Journal, 2009, 23, 489.4.	0.5	0
25	The genomics of DNA replication of human chromosomes. FASEB Journal, 2009, 23, 78.1.	0.5	0
26	Abstract 5054: Inferring mutational chronology in breast cancer by deep-sequencing tumor subpopulations. , 2012, , .		0