

Valer Gotea

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

24
papers

2,484
citations

16
h-index

26
g-index

26
ext. papers

2,835
ext. citations

8.4
avg, IF

4.02
L-index

#	Paper	IF	Citations
24	Evolution of genes and genomes on the Drosophila phylogeny. <i>Nature</i> , 2007 , 450, 203-18	50.4	1586
23	Homotypic clusters of transcription factor binding sites are a key component of human promoters and enhancers. <i>Genome Research</i> , 2010 , 20, 565-77	9.7	167
22	Whole-genome sequencing identifies a recurrent functional synonymous mutation in melanoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 13481-6	11.5	127
21	DiRE: identifying distant regulatory elements of co-expressed genes. <i>Nucleic Acids Research</i> , 2008 , 36, W133-9	20.1	106
20	Transposable elements as a significant source of transcription regulating signals. <i>Gene</i> , 2006 , 365, 104-108	10.8	104
19	Do transposable elements really contribute to proteomes?. <i>Trends in Genetics</i> , 2006 , 22, 260-7	8.5	73
18	Recurrent patterns of DNA methylation in the ZNF154, CASP8, and VHL promoters across a wide spectrum of human solid epithelial tumors and cancer cell lines. <i>Epigenetics</i> , 2013 , 8, 1355-72	5.7	40
17	The functional relevance of somatic synonymous mutations in melanoma and other cancers. <i>Pigment Cell and Melanoma Research</i> , 2015 , 28, 673-84	4.5	36
16	Pan-cancer stratification of solid human epithelial tumors and cancer cell lines reveals commonalities and tissue-specific features of the CpG island methylator phenotype. <i>Epigenetics and Chromatin</i> , 2015 , 8, 14	5.8	27
15	Transposable Elements: Classification, Identification, and Their Use As a Tool For Comparative Genomics. <i>Methods in Molecular Biology</i> , 2019 , 1910, 177-207	1.4	27
14	Spliceosomal small nuclear RNA genes in 11 insect genomes. <i>Rna</i> , 2007 , 13, 5-14	5.8	27
13	Tissue-specific and ubiquitous expression patterns from alternative promoters of human genes. <i>PLoS ONE</i> , 2010 , 5, e12274	3.7	25
12	Significant associations between driver gene mutations and DNA methylation alterations across many cancer types. <i>PLoS Computational Biology</i> , 2017 , 13, e1005840	5	21
11	Transposable elements and their identification. <i>Methods in Molecular Biology</i> , 2012 , 855, 337-59	1.4	21
10	Bidirectional promoters as important drivers for the emergence of species-specific transcripts. <i>PLoS ONE</i> , 2013 , 8, e57323	3.7	20
9	Mastering seeds for genomic size nucleotide BLAST searches. <i>Nucleic Acids Research</i> , 2003 , 31, 6935-41	20.1	17
8	Functional analysis of synonymous substitutions predicted to affect splicing of the CFTR gene. <i>Journal of Cystic Fibrosis</i> , 2012 , 11, 511-7	4.1	14

7	Genome-wide detection of a TFIID localization element from an initial human disease mutation. <i>Nucleic Acids Research</i> , 2011 , 39, 2175-87	20.1	14
6	A Case of IL-7R Deficiency Caused by a Novel Synonymous Mutation and Implications for Mutation Screening in SCID Diagnosis. <i>Frontiers in Immunology</i> , 2016 , 7, 443	8.4	11
5	Assessing predictions of the impact of variants on splicing in CAG15. <i>Human Mutation</i> , 2019 , 40, 1215-1224	4.7	8
4	Ascertaining regions affected by GC-biased gene conversion through weak-to-strong mutational hotspots. <i>Genomics</i> , 2014 , 103, 349-56	4.3	4
3	Characterization and clustering of kinase isoform expression in metastatic melanoma.. <i>PLoS Computational Biology</i> , 2022 , 18, e1010065	5	1
2	CAGI experiments: Modeling sequence variant impact on gene splicing using predictions from computational tools. <i>Human Mutation</i> , 2019 , 40, 1252-1260	4.7	0
1	A novel role for nucleolin in splice site selection.. <i>RNA Biology</i> , 2022 , 19, 333-352	4.8	0