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List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/1368650/publications.pdf

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25 papers	3,044 citations	471509 17 h-index	580821 25 g-index
26 all docs	26 docs citations	26 times ranked	5492 citing authors

#	Article	IF	Citations
1	Evolution of genes and genomes on the Drosophila phylogeny. Nature, 2007, 450, 203-218.	27.8	1,886
2	Homotypic clusters of transcription factor binding sites are a key component of human promoters and enhancers. Genome Research, 2010, 20, 565-577.	5.5	203
3	Whole-genome sequencing identifies a recurrent functional synonymous mutation in melanoma. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 13481-13486.	7.1	147
4	DiRE: identifying distant regulatory elements of co-expressed genes. Nucleic Acids Research, 2008, 36, W133-W139.	14.5	118
5	Transposable elements as a significant source of transcription regulating signals. Gene, 2006, 365, 104-110.	2.2	116
6	Do transposable elements really contribute to proteomes?. Trends in Genetics, 2006, 22, 260-267.	6.7	81
7	Transposable Elements: Classification, Identification, and Their Use As a Tool For Comparative Genomics. Methods in Molecular Biology, 2019, 1910, 177-207.	0.9	74
8	Recurrent patterns of DNA methylation in theZNF154,CASP8, andVHLpromoters across a wide spectrum of human solid epithelial tumors and cancer cell lines. Epigenetics, 2013, 8, 1355-1372.	2.7	52
9	The functional relevance of somatic synonymous mutations in melanoma and other cancers. Pigment Cell and Melanoma Research, 2015, 28, 673-684.	3.3	47
10	Pan-cancer stratification of solid human epithelial tumors and cancer cell lines reveals commonalities and tissue-specific features of the CpG island methylator phenotype. Epigenetics and Chromatin, 2015, 8, 14.	3.9	42
11	Significant associations between driver gene mutations and DNA methylation alterations across many cancer types. PLoS Computational Biology, 2017, 13, e1005840.	3.2	39
12	Spliceosomal small nuclear RNA genes in 11 insect genomes. Rna, 2006, 13, 5-14.	3.5	33
13	Tissue-Specific and Ubiquitous Expression Patterns from Alternative Promoters of Human Genes. PLoS ONE, 2010, 5, e12274.	2.5	30
14	Genome-wide detection of a TFIID localization element from an initial human disease mutation. Nucleic Acids Research, 2011, 39, 2175-2187.	14.5	26
15	Transposable Elements and Their Identification. Methods in Molecular Biology, 2012, 855, 337-359.	0.9	26
16	Mastering seeds for genomic size nucleotide BLAST searches. Nucleic Acids Research, 2003, 31, 6935-6941.	14.5	25
17	Bidirectional Promoters as Important Drivers for the Emergence of Species-Specific Transcripts. PLoS ONE, 2013, 8, e57323.	2.5	25
18	Assessing predictions of the impact of variants on splicing in CAGI5. Human Mutation, 2019, 40, 1215-1224.	2.5	18

#	Article	IF	Citations
19	Functional analysis of synonymous substitutions predicted to affect splicing of the CFTR gene. Journal of Cystic Fibrosis, 2012, 11, 511-517.	0.7	17
20	A Case of IL-7R Deficiency Caused by a Novel Synonymous Mutation and Implications for Mutation Screening in SCID Diagnosis. Frontiers in Immunology, 2016, 7, 443.	4.8	15
21	CpG island methylator phenotype in adenocarcinomas from the digestive tract: Methods, conclusions, and controversies. World Journal of Gastrointestinal Oncology, 2017, 9, 105.	2.0	9
22	Ascertaining regions affected by GC-biased gene conversion through weak-to-strong mutational hotspots. Genomics, 2014, 103, 349-356.	2.9	5
23	Characterization and clustering of kinase isoform expression in metastatic melanoma. PLoS Computational Biology, 2022, 18, e1010065.	3.2	4
24	A novel role for nucleolin in splice site selection. RNA Biology, 2022, 19, 333-352.	3.1	3
25	CAGI experiments: Modeling sequence variant impact on gene splicing using predictions from computational tools. Human Mutation, 2019, 40, 1252-1260.	2.5	2