

# Valer Gotea

## List of Publications by Year in descending order

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Version: 2024-02-01

25  
papers

3,044  
citations

471061

17  
h-index

580395

25  
g-index

26  
all docs

26  
docs citations

26  
times ranked

5492  
citing authors

#	ARTICLE	IF	CITATIONS
1	A novel role for nucleolin in splice site selection. <i>RNA Biology</i> , 2022, 19, 333-352.	1.5	3
2	Characterization and clustering of kinase isoform expression in metastatic melanoma. <i>PLoS Computational Biology</i> , 2022, 18, e1010065.	1.5	4
3	Assessing predictions of the impact of variants on splicing in CAG15. <i>Human Mutation</i> , 2019, 40, 1215-1224.	1.1	18
4	Transposable Elements: Classification, Identification, and Their Use As a Tool For Comparative Genomics. <i>Methods in Molecular Biology</i> , 2019, 1910, 177-207.	0.4	74
5	CAGI experiments: Modeling sequence variant impact on gene splicing using predictions from computational tools. <i>Human Mutation</i> , 2019, 40, 1252-1260.	1.1	2
6	Significant associations between driver gene mutations and DNA methylation alterations across many cancer types. <i>PLoS Computational Biology</i> , 2017, 13, e1005840.	1.5	39
7	CpG island methylator phenotype in adenocarcinomas from the digestive tract: Methods, conclusions, and controversies. <i>World Journal of Gastrointestinal Oncology</i> , 2017, 9, 105.	0.8	9
8	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.	2.2	15
9	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.	1.8	42
10	The functional relevance of somatic synonymous mutations in melanoma and other cancers. <i>Pigment Cell and Melanoma Research</i> , 2015, 28, 673-684.	1.5	47
11	Ascertaining regions affected by GC-biased gene conversion through weak-to-strong mutational hotspots. <i>Genomics</i> , 2014, 103, 349-356.	1.3	5
12	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, 13481-13486.	3.3	147
13	Recurrent patterns of DNA methylation in the <i>ZNF154</i> , <i>CASP8</i> , and <i>VHL</i> promoters across a wide spectrum of human solid epithelial tumors and cancer cell lines. <i>Epigenetics</i> , 2013, 8, 1355-1372.	1.3	52
14	Bidirectional Promoters as Important Drivers for the Emergence of Species-Specific Transcripts. <i>PLoS ONE</i> , 2013, 8, e57323.	1.1	25
15	Transposable Elements and Their Identification. <i>Methods in Molecular Biology</i> , 2012, 855, 337-359.	0.4	26
16	Functional analysis of synonymous substitutions predicted to affect splicing of the CFTR gene. <i>Journal of Cystic Fibrosis</i> , 2012, 11, 511-517.	0.3	17
17	Genome-wide detection of a TFIIID localization element from an initial human disease mutation. <i>Nucleic Acids Research</i> , 2011, 39, 2175-2187.	6.5	26
18	Homotypic clusters of transcription factor binding sites are a key component of human promoters and enhancers. <i>Genome Research</i> , 2010, 20, 565-577.	2.4	203

#	ARTICLE	IF	CITATIONS
19	Tissue-Specific and Ubiquitous Expression Patterns from Alternative Promoters of Human Genes. PLoS ONE, 2010, 5, e12274.	1.1	30
20	DiRE: identifying distant regulatory elements of co-expressed genes. Nucleic Acids Research, 2008, 36, W133-W139.	6.5	118
21	Evolution of genes and genomes on the Drosophila phylogeny. Nature, 2007, 450, 203-218.	13.7	1,886
22	Transposable elements as a significant source of transcription regulating signals. Gene, 2006, 365, 104-110.	1.0	116
23	Do transposable elements really contribute to proteomes?. Trends in Genetics, 2006, 22, 260-267.	2.9	81
24	Spliceosomal small nuclear RNA genes in 11 insect genomes. Rna, 2006, 13, 5-14.	1.6	33
25	Mastering seeds for genomic size nucleotide BLAST searches. Nucleic Acids Research, 2003, 31, 6935-6941.	6.5	25