

# Panagiotis Papasaikas

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3180920/publications.pdf>

Version: 2024-02-01

22  
papers

2,338  
citations

567281

15  
h-index

610901

24  
g-index

29  
all docs

29  
docs citations

29  
times ranked

5142  
citing authors

#	ARTICLE	IF	CITATIONS
1	Epigenomic analysis detects widespread gene-body DNA hypomethylation in chronic lymphocytic leukemia. <i>Nature Genetics</i> , 2012, 44, 1236-1242.	21.4	525
2	Self-organization and symmetry breaking in intestinal organoid development. <i>Nature</i> , 2019, 569, 66-72.	27.8	362
3	Cell Types of the Human Retina and Its Organoids at Single-Cell Resolution. <i>Cell</i> , 2020, 182, 1623-1640.e34.	28.9	359
4	The Spliceosome: The Ultimate RNA Chaperone and Sculptor. <i>Trends in Biochemical Sciences</i> , 2016, 41, 33-45.	7.5	215
5	Transcriptome characterization by RNA sequencing identifies a major molecular and clinical subdivision in chronic lymphocytic leukemia. <i>Genome Research</i> , 2014, 24, 212-226.	5.5	175
6	Functional Splicing Network Reveals Extensive Regulatory Potential of the Core Spliceosomal Machinery. <i>Molecular Cell</i> , 2015, 57, 7-22.	9.7	140
7	UNR/CSDE1 Drives a Post-transcriptional Program to Promote Melanoma Invasion and Metastasis. <i>Cancer Cell</i> , 2016, 30, 694-707.	16.8	131
8	Genome-Wide Identification of Fas/CD95 Alternative Splicing Regulators Reveals Links with Iron Homeostasis. <i>Molecular Cell</i> , 2015, 57, 23-38.	9.7	76
9	PRED-GPCR: GPCR recognition and family classification server. <i>Nucleic Acids Research</i> , 2004, 32, W380-W382.	14.5	49
10	A method for the prediction of GPCRs coupling specificity to G-proteins using refined profile Hidden Markov Models. <i>BMC Bioinformatics</i> , 2005, 6, 104.	2.6	44
11	A Novel method for GPCR recognition and family classification from sequence alone using signatures derived from profile hidden Markov models. <i>SAR and QSAR in Environmental Research</i> , 2003, 14, 413-420.	2.2	35
12	Relationship between nucleosome positioning and progesterone-induced alternative splicing in breast cancer cells. <i>Rna</i> , 2015, 21, 360-374.	3.5	31
13	The RNA hairpin binder TRIM71 modulates alternative splicing by repressing MBNL1. <i>Genes and Development</i> , 2019, 33, 1221-1235.	5.9	31
14	Smu1 and RED are required for activation of spliceosomal B complexes assembled on short introns. <i>Nature Communications</i> , 2019, 10, 3639.	12.8	26
15	Fine-mapping reveals novel alternative splicing of the dopamine transporter. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2010, 153B, 1434-1447.	1.7	18
16	A unique bipartite Polycomb signature regulates stimulus-response transcription during development. <i>Nature Genetics</i> , 2021, 53, 379-391.	21.4	16
17	Functional Network Analysis Reveals the Relevance of SKIIP in the Regulation of Alternative Splicing by p38 SAPK. <i>Cell Reports</i> , 2019, 27, 847-859.e6.	6.4	15
18	Splicing in 4D. <i>Science</i> , 2012, 338, 1547-1548.	12.6	14

#	ARTICLE	IF	CITATIONS
19	Mechanical oscillations orchestrate axial patterning through Wnt activation in <i>Hydra</i> . <i>Science Advances</i> , 2021, 7, eabj6897.	10.3	14
20	Dynamics of alternative splicing during somatic cell reprogramming reveals functions for RNA-binding proteins CPSF3, hnRNP UL1, and TIA1. <i>Genome Biology</i> , 2021, 22, 171.	8.8	12
21	Cooperation between HDAC3 and DAX1 mediates lineage restriction of embryonic stem cells. <i>EMBO Journal</i> , 2021, 40, e106818.	7.8	9
22	Reconstruction of composite regulator-target splicing networks from high-throughput transcriptome data. <i>BMC Genomics</i> , 2015, 16, S7.	2.8	8