

Angela N Brooks

List of Publications by Year in descending order

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Version: 2024-02-01

23
papers

8,291
citations

430874
18
h-index

580821
25
g-index

38
all docs

38
docs citations

38
times ranked

15190
citing authors

#	ARTICLE	IF	CITATIONS
1	A Next Generation Connectivity Map: L1000 Platform and the First 1,000,000 Profiles. <i>Cell</i> , 2017, 171, 1437-1452.e17.	28.9	2,281
2	Visualizing and interpreting cancer genomics data via the Xena platform. <i>Nature Biotechnology</i> , 2020, 38, 675-678.	17.5	2,069
3	Distinct patterns of somatic genome alterations in lung adenocarcinomas and squamous cell carcinomas. <i>Nature Genetics</i> , 2016, 48, 607-616.	21.4	933
4	Nanopore native RNA sequencing of a human poly(A) transcriptome. <i>Nature Methods</i> , 2019, 16, 1297-1305.	19.0	411
5	Genomic basis for RNA alterations in cancer. <i>Nature</i> , 2020, 578, 129-136.	27.8	280
6	Full-length transcript characterization of SF3B1 mutation in chronic lymphocytic leukemia reveals downregulation of retained introns. <i>Nature Communications</i> , 2020, 11, 1438.	12.8	273
7	Conservation of an RNA regulatory map between <i>Drosophila</i> and mammals. <i>Genome Research</i> , 2011, 21, 193-202.	5.5	208
8	The Coupling of Alternative Splicing and Nonsense-Mediated mRNA Decay. <i>Advances in Experimental Medicine and Biology</i> , 2007, 623, 190-211.	1.6	202
9	Transcriptomic Characterization of SF3B1 Mutation Reveals Its Pleiotropic Effects in Chronic Lymphocytic Leukemia. <i>Cancer Cell</i> , 2016, 30, 750-763.	16.8	173
10	High-throughput Phenotyping of Lung Cancer Somatic Mutations. <i>Cancer Cell</i> , 2016, 30, 214-228.	16.8	171
11	A Pan-Cancer Analysis of Transcriptome Changes Associated with Somatic Mutations in U2AF1 Reveals Commonly Altered Splicing Events. <i>PLoS ONE</i> , 2014, 9, e87361.	2.5	168
12	A Pan-cancer Transcriptome Analysis Reveals Pervasive Regulation through Alternative Promoters. <i>Cell</i> , 2019, 178, 1465-1477.e17.	28.9	144
13	Reintroduction of the archaic variant of <i>NOVA1</i> in cortical organoids alters neurodevelopment. <i>Science</i> , 2021, 371, .	12.6	96
14	Regulation of alternative splicing in <i>Drosophila</i> by 56 RNA binding proteins. <i>Genome Research</i> , 2015, 25, 1771-1780.	5.5	77
15	A Murine Model of Chronic Lymphocytic Leukemia Based on B Cell-Restricted Expression of Sf3b1 Mutation and Atm Deletion. <i>Cancer Cell</i> , 2019, 35, 283-296.e5.	16.8	71
16	Splicing modulation sensitizes chronic lymphocytic leukemia cells to venetoclax by remodeling mitochondrial apoptotic dependencies. <i>JCI Insight</i> , 2018, 3, .	5.0	39
17	Proteasome inhibitor-induced modulation reveals the spliceosome as a specific therapeutic vulnerability in multiple myeloma. <i>Nature Communications</i> , 2020, 11, 1931.	12.8	38
18	RBM25 is a global splicing factor promoting inclusion of alternatively spliced exons and is itself regulated by lysine mono-methylation. <i>Journal of Biological Chemistry</i> , 2017, 292, 13381-13390.	3.4	37

#	ARTICLE	IF	CITATIONS
19	Cell Painting predicts impact of lung cancer variants. <i>Molecular Biology of the Cell</i> , 2022, 33, mbcE21110538.	2.1	25
20	Inflammation drives alternative first exon usage to regulate immune genes including a novel iron-regulated isoform of Aim2. <i>ELife</i> , 2021, 10, .	6.0	23
21	Identification and experimental validation of splicing regulatory elements in <i>Drosophila melanogaster</i> reveals functionally conserved splicing enhancers in metazoans. <i>Rna</i> , 2011, 17, 1884-1894.	3.5	14
22	SRSF1 governs progenitor-specific alternative splicing to maintain adult epithelial tissue homeostasis and renewal. <i>Developmental Cell</i> , 2022, 57, 624-637.e4.	7.0	9
23	eVIP2: Expression-based variant impact phenotyping to predict the function of gene variants. <i>PLoS Computational Biology</i> , 2021, 17, e1009132.	3.2	8