William Ritchie

List of Publications by Year
in descending order

29 papers	2,428 citations	430874 18 h-index	477307 29 g-index
33 all docs	33 docs citations	33 times ranked	4627 citing authors

#	Article	IF	Citations
1	Intron retention and its impact on gene expression and protein diversity: A review and a practical guide. Wiley Interdisciplinary Reviews RNA, 2021, 12, e1631.	6.4	33
2	Identification of CRYAB+ KCNN3+ SOX9+ Astrocyte-Like and EGFR+ PDGFRA+ OLIG1+ Oligodendrocyte-Like Tumoral Cells in Diffuse IDH1-Mutant Gliomas and Implication of NOTCH1 Signalling in Their Genesis. Cancers, 2021, 13, 2107.	3.7	9
3	A cell-to-patient machine learning transfer approach uncovers novel basal-like breast cancer prognostic markers amongst alternative splice variants. BMC Biology, 2021, 19, 70.	3.8	13
4	IRFinder-S: a comprehensive suite to discover and explore intron retention. Genome Biology, 2021, 22, 307.	8.8	19
5	iMOKA: k-mer based software to analyze large collections of sequencing data. Genome Biology, 2020, 21, 261.	8.8	8
6	TALC: Transcript-level Aware Long-read Correction. Bioinformatics, 2020, 36, 5000-5006.	4.1	14
7	Challenges in detecting and quantifying intron retention from next generation sequencing data. Computational and Structural Biotechnology Journal, 2020, 18, 501-508.	4.1	28
8	NF90 modulates processing of a subset of human pri-miRNAs. Nucleic Acids Research, 2020, 48, 6874-6888.	14.5	16
9	Transformation Foci in IDH1-mutated Gliomas Show STAT3 Phosphorylation and Downregulate the Metabolic Enzyme ETNPPL, a Negative Regulator of Glioma Growth. Scientific Reports, 2020, 10, 5504.	3.3	29
10	GECKO is a genetic algorithm to classify and explore high throughput sequencing data. Communications Biology, 2019, 2, 222.	4.4	16
11	An NF90/NF110-mediated feedback amplification loop regulates dicer expression and controls ovarian carcinoma progression. Cell Research, 2018, 28, 556-571.	12.0	24
12	Exploring the Roles of CREBRF and TRIM2 in the Regulation of Angiogenesis by High-Density Lipoproteins. International Journal of Molecular Sciences, 2018, 19, 1903.	4.1	16
13	Identifying microRNA determinants of human myelopoiesis. Scientific Reports, 2018, 8, 7264.	3.3	14
14	Intron retention is regulated by altered MeCP2-mediated splicing factor recruitment. Nature Communications, 2017, 8, 15134.	12.8	92
15	IRFinder: assessing the impact of intron retention on mammalian gene expression. Genome Biology, 2017, 18, 51.	8.8	203
16	Intron retention enhances gene regulatory complexity in vertebrates. Genome Biology, 2017, 18, 216.	8.8	79
17	A dynamic intron retention program in the mammalian megakaryocyte and erythrocyte lineages. Blood, 2016, 127, e24-e34.	1.4	94
18	Intron retention in mRNA: No longer nonsense. BioEssays, 2016, 38, 41-49.	2.5	163

#	ARTICLE	IF	CITATIONS
19	RBM3 regulates temperature sensitive miR-142â€"5p and miR-143 (thermomiRs), which target immune genes and control fever. Nucleic Acids Research, 2016, 44, 2888-2897.	14.5	50
20	ASCT2/SLC1A5 controls glutamine uptake and tumour growth in triple-negative basal-like breast cancer. Oncogene, 2016, 35, 3201-3208.	5.9	430
21	Targeting <scp>ASCT2</scp>â€"mediated glutamine uptake blocks prostate cancer growth and tumour development. Journal of Pathology, 2015, 236, 278-289.	4.5	275
22	Genome-wide characterization of the routes to pluripotency. Nature, 2014, 516, 198-206.	27.8	187
23	Refining microRNA target predictions: Sorting the wheat from the chaff. Biochemical and Biophysical Research Communications, 2014, 445, 780-784.	2.1	31
24	Orchestrated Intron Retention Regulates Normal Granulocyte Differentiation. Cell, 2013, 154, 583-595.	28.9	408
25	Defining and providing robust controls for microRNA prediction. Bioinformatics, 2012, 28, 1058-1061.	4.1	31
26	Integrated miRNA Expression Analysis and Target Prediction. Methods in Molecular Biology, 2012, 822, 289-293.	0.9	3
27	Intron Retention Coupled with Nonsense-Mediated Decay Determines Protein Expression and Nuclear Morphology in Granulopoiesis. Blood, 2012, 120, 112-112.	1.4	9
28	mimiRNA: a microRNA expression profiler and classification resource designed to identify functional correlations between microRNAs and their targets. Bioinformatics, 2010, 26, 223-227.	4.1	75
29	Conserved Expression Patterns Predict microRNA Targets. PLoS Computational Biology, 2009, 5, e1000513.	3.2	49