

# William Ritchie

## List of Publications by Year in descending order

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Version: 2024-02-01

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	ASCT2/SLC1A5 controls glutamine uptake and tumour growth in triple-negative basal-like breast cancer. <i>Oncogene</i> , 2016, 35, 3201-3208.	5.9	430
2	Orchestrated Intron Retention Regulates Normal Granulocyte Differentiation. <i>Cell</i> , 2013, 154, 583-595.	28.9	408
3	Targeting ASCT2-mediated glutamine uptake blocks prostate cancer growth and tumour development. <i>Journal of Pathology</i> , 2015, 236, 278-289.	4.5	275
4	IRFinder: assessing the impact of intron retention on mammalian gene expression. <i>Genome Biology</i> , 2017, 18, 51.	8.8	203
5	Genome-wide characterization of the routes to pluripotency. <i>Nature</i> , 2014, 516, 198-206.	27.8	187
6	Intron retention in mRNA: No longer nonsense. <i>BioEssays</i> , 2016, 38, 41-49.	2.5	163
7	A dynamic intron retention program in the mammalian megakaryocyte and erythrocyte lineages. <i>Blood</i> , 2016, 127, e24-e34.	1.4	94
8	Intron retention is regulated by altered MeCP2-mediated splicing factor recruitment. <i>Nature Communications</i> , 2017, 8, 15134.	12.8	92
9	Intron retention enhances gene regulatory complexity in vertebrates. <i>Genome Biology</i> , 2017, 18, 216.	8.8	79
10	mimiRNA: a microRNA expression profiler and classification resource designed to identify functional correlations between microRNAs and their targets. <i>Bioinformatics</i> , 2010, 26, 223-227.	4.1	75
11	RBM3 regulates temperature sensitive miR-142-5p and miR-143 (thermomiRs), which target immune genes and control fever. <i>Nucleic Acids Research</i> , 2016, 44, 2888-2897.	14.5	50
12	Conserved Expression Patterns Predict microRNA Targets. <i>PLoS Computational Biology</i> , 2009, 5, e1000513.	3.2	49
13	Intron retention and its impact on gene expression and protein diversity: A review and a practical guide. <i>Wiley Interdisciplinary Reviews RNA</i> , 2021, 12, e1631.	6.4	33
14	Defining and providing robust controls for microRNA prediction. <i>Bioinformatics</i> , 2012, 28, 1058-1061.	4.1	31
15	Refining microRNA target predictions: Sorting the wheat from the chaff. <i>Biochemical and Biophysical Research Communications</i> , 2014, 445, 780-784.	2.1	31
16	Transformation Foci in IDH1-mutated Gliomas Show STAT3 Phosphorylation and Downregulate the Metabolic Enzyme ETNPPL, a Negative Regulator of Glioma Growth. <i>Scientific Reports</i> , 2020, 10, 5504.	3.3	29
17	Challenges in detecting and quantifying intron retention from next generation sequencing data. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 501-508.	4.1	28
18	An NF90/NF110-mediated feedback amplification loop regulates dicer expression and controls ovarian carcinoma progression. <i>Cell Research</i> , 2018, 28, 556-571.	12.0	24

#	ARTICLE	IF	CITATIONS
19	IRFinder-S: a comprehensive suite to discover and explore intron retention. <i>Genome Biology</i> , 2021, 22, 307.	8.8	19
20	Exploring the Roles of CREBRF and TRIM2 in the Regulation of Angiogenesis by High-Density Lipoproteins. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1903.	4.1	16
21	GECKO is a genetic algorithm to classify and explore high throughput sequencing data. <i>Communications Biology</i> , 2019, 2, 222.	4.4	16
22	NF90 modulates processing of a subset of human pri-miRNAs. <i>Nucleic Acids Research</i> , 2020, 48, 6874-6888.	14.5	16
23	Identifying microRNA determinants of human myelopoiesis. <i>Scientific Reports</i> , 2018, 8, 7264.	3.3	14
24	TALC: Transcript-level Aware Long-read Correction. <i>Bioinformatics</i> , 2020, 36, 5000-5006.	4.1	14
25	A cell-to-patient machine learning transfer approach uncovers novel basal-like breast cancer prognostic markers amongst alternative splice variants. <i>BMC Biology</i> , 2021, 19, 70.	3.8	13
26	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. <i>Cancers</i> , 2021, 13, 2107.	3.7	9
27	Intron Retention Coupled with Nonsense-Mediated Decay Determines Protein Expression and Nuclear Morphology in Granulopoiesis. <i>Blood</i> , 2012, 120, 112-112.	1.4	9
28	iMOKA: k-mer based software to analyze large collections of sequencing data. <i>Genome Biology</i> , 2020, 21, 261.	8.8	8
29	Integrated miRNA Expression Analysis and Target Prediction. <i>Methods in Molecular Biology</i> , 2012, 822, 289-293.	0.9	3