

# Cameron P Bracken

## List of Publications by Year in descending order

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Version: 2024-02-01

37  
papers

5,745  
citations

236925

25  
h-index

330143

37  
g-index

40  
all docs

40  
docs citations

40  
times ranked

10419  
citing authors

#	ARTICLE	IF	CITATIONS
1	A Double-Negative Feedback Loop between ZEB1-SIP1 and the microRNA-200 Family Regulates Epithelial-Mesenchymal Transition. <i>Cancer Research</i> , 2008, 68, 7846-7854.	0.9	956
2	The Human Mitochondrial Transcriptome. <i>Cell</i> , 2011, 146, 645-658.	28.9	716
3	A network-biology perspective of microRNA function and dysfunction in cancer. <i>Nature Reviews Genetics</i> , 2016, 17, 719-732.	16.3	579
4	An autocrine TGF- $\beta$ /ZEB/miR-200 signaling network regulates establishment and maintenance of epithelial-mesenchymal transition. <i>Molecular Biology of the Cell</i> , 2011, 22, 1686-1698.	2.1	505
5	Experimental strategies for microRNA target identification. <i>Nucleic Acids Research</i> , 2011, 39, 6845-6853.	14.5	493
6	MicroRNAs as regulators of epithelial-mesenchymal transition. <i>Cell Cycle</i> , 2008, 7, 3112-3117.	2.6	467
7	IsomiRs – the overlooked repertoire in the dynamic microRNAome. <i>Trends in Genetics</i> , 2012, 28, 544-549.	6.7	410
8	Cell-specific Regulation of Hypoxia-inducible Factor (HIF)-1 $\alpha$ and HIF-2 $\alpha$ Stabilization and Transactivation in a Graded Oxygen Environment. <i>Journal of Biological Chemistry</i> , 2006, 281, 22575-22585.	3.4	182
9	Assessing the gene regulatory properties of Argonaute-bound small RNAs of diverse genomic origin. <i>Nucleic Acids Research</i> , 2015, 43, 470-481.	14.5	142
10	Genome-wide identification of miR-200 targets reveals a regulatory network controlling cell invasion. <i>EMBO Journal</i> , 2014, 33, 2040-2056.	7.8	126
11	On Measuring miRNAs after Transient Transfection of Mimics or Antisense Inhibitors. <i>PLoS ONE</i> , 2013, 8, e55214.	2.5	103
12	Combinatorial Targeting by MicroRNAs Co-ordinates Post-transcriptional Control of EMT. <i>Cell Systems</i> , 2018, 7, 77-91.e7.	6.2	92
13	Regulation of Cyclin D1 RNA Stability by SNIP1. <i>Cancer Research</i> , 2008, 68, 7621-7628.	0.9	86
14	miR-200/375 control epithelial plasticity-associated alternative splicing by repressing the <i>scp</i> RNA-binding protein Quaking. <i>EMBO Journal</i> , 2018, 37, .	7.8	82
15	Direct transcriptional regulation by nuclear microRNAs. <i>International Journal of Biochemistry and Cell Biology</i> , 2014, 54, 304-311.	2.8	78
16	Regulated post-transcriptional RNA cleavage diversifies the eukaryotic transcriptome. <i>Genome Research</i> , 2010, 20, 1639-1650.	5.5	76
17	Global analysis of the mammalian RNA degradome reveals widespread miRNA-dependent and miRNA-independent endonucleolytic cleavage. <i>Nucleic Acids Research</i> , 2011, 39, 5658-5668.	14.5	76
18	Activity of Hypoxia-inducible Factor 2 $\alpha$ Is Regulated by Association with the NF- $\kappa$ B Essential Modulator. <i>Journal of Biological Chemistry</i> , 2005, 280, 14240-14251.	3.4	61

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19	Naturally existing isoforms of miR-222 have distinct functions. <i>Nucleic Acids Research</i> , 2017, 45, 11371-11385.	14.5	61
20	SNIP1 Is a Candidate Modifier of the Transcriptional Activity of c-Myc on E Box-Dependent Target Genes. <i>Molecular Cell</i> , 2006, 24, 771-783.	9.7	60
21	p53 Represses the Oncogenic Sno-MiR-28 Derived from a SnoRNA. <i>PLoS ONE</i> , 2015, 10, e0129190.	2.5	55
22	Network-Based Approaches to Understand the Roles of miR-200 and Other microRNAs in Cancer. <i>Cancer Research</i> , 2015, 75, 2594-2599.	0.9	54
23	Stimulus-dependent differences in signalling regulate epithelial-mesenchymal plasticity and change the effects of drugs in breast cancer cell lines. <i>Cell Communication and Signaling</i> , 2015, 13, 26.	6.5	47
24	Hormonally regulated follicle differentiation and luteinization in the mouse is associated with hypoxia inducible factor activity. <i>Molecular and Cellular Endocrinology</i> , 2010, 327, 47-55.	3.2	42
25	miR-222 isoforms are differentially regulated by type-I interferon. <i>Rna</i> , 2018, 24, 332-341.	3.5	31
26	The many regulators of epithelial~mesenchymal transition. <i>Nature Reviews Molecular Cell Biology</i> , 2022, 23, 89-90.	37.0	27
27	MicroRNA-155 expression and function in AML: An evolving paradigm. <i>Experimental Hematology</i> , 2018, 62, 1-6.	0.4	22
28	CBNA: A control theory based method for identifying coding and non-coding cancer drivers. <i>PLoS Computational Biology</i> , 2019, 15, e1007538.	3.2	22
29	Computational methods for cancer driver discovery: A survey. <i>Theranostics</i> , 2021, 11, 5553-5568.	10.0	19
30	Transcriptional and post-transcriptional control of epithelial-mesenchymal plasticity: why so many regulators?. <i>Cellular and Molecular Life Sciences</i> , 2022, 79, 182.	5.4	18
31	miRNA length variation during macrophage stimulation confounds the interpretation of results: implications for miRNA quantification by RT-qPCR. <i>Rna</i> , 2019, 25, 232-238.	3.5	16
32	Extensive transcriptional responses are co-ordinated by microRNAs as revealed by Exon~Intron Split Analysis (EISA). <i>Nucleic Acids Research</i> , 2019, 47, 8606-8619.	14.5	9
33	Insufficiently complex unique-molecular identifiers (UMIs) distort small RNA sequencing. <i>Scientific Reports</i> , 2020, 10, 14593.	3.3	9
34	<i>pDriver</i> : a novel method for unravelling personalized coding and miRNA cancer drivers. <i>Bioinformatics</i> , 2021, 37, 3285-3292.	4.1	8
35	Defects in RNA metabolism in mitochondrial disease. <i>International Journal of Biochemistry and Cell Biology</i> , 2017, 85, 106-113.	2.8	7
36	<i>DriverGroup</i> : a novel method for identifying driver gene groups. <i>Bioinformatics</i> , 2020, 36, i583-i591.	4.1	5

#	ARTICLE	IF	CITATIONS
37	Making use of transcription factor enrichment to identify functional microRNA-regulons. Computational and Structural Biotechnology Journal, 2021, 19, 4896-4903.	4.1	2