Cameron P Bracken

List of Publications by Year
in descending order

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	Transcriptional and post-transcriptional control of epithelial-mesenchymal plasticity: why so many regulators?. Cellular and Molecular Life Sciences, 2022, 79, 182.	5.4	18
2	The many regulators of epithelialâˆ’mesenchymal transition. Nature Reviews Molecular Cell Biology, 2022, 23, 89-90.	37.0	27
3	Computational methods for cancer driver discovery: A survey. Theranostics, 2021, 11, 5553-5568.	10.0	19
4	Making use of transcription factor enrichment to identify functional microRNA-regulons. Computational and Structural Biotechnology Journal, 2021, 19, 4896-4903.	4.1	2
5	<i>pDriver</i>: a novel method for unravelling personalized coding and miRNA cancer drivers. Bioinformatics, 2021, 37, 3285-3292.	4.1	8
6	Insufficiently complex unique-molecular identifiers (UMIs) distort small RNA sequencing. Scientific Reports, 2020, 10, 14593.	3.3	9
7	<i>DriverGroup</i>: a novel method for identifying driver gene groups. Bioinformatics, 2020, 36, i583-i591.	4.1	5
8	Extensive transcriptional responses are co-ordinated by microRNAs as revealed by Exonâ€“Intron Split Analysis (EISA). Nucleic Acids Research, 2019, 47, 8606-8619.	14.5	9
9	CBNA: A control theory based method for identifying coding and non-coding cancer drivers. PLoS Computational Biology, 2019, 15, e1007538.	3.2	22
10	miRNA length variation during macrophage stimulation confounds the interpretation of results: implications for miRNA quantification by RT-qPCR. Rna, 2019, 25, 232-238.	3.5	16
11	miR-222 isoforms are differentially regulated by type-I interferon. Rna, 2018, 24, 332-341.	3.5	31
12	MicroRNA-155 expression and function in AML: An evolving paradigm. Experimental Hematology, 2018, 62, 1-6.	0.4	22
13	Combinatorial Targeting by MicroRNAs Co-ordinates Post-transcriptional Control of EMT. Cell Systems, 2018, 7, 77-91.e7.	6.2	92
14	miRâ€200/375 control epithelial plasticityâ€associated alternative splicing by repressing the <scp>RNA</scp> â€binding protein Quaking. EMBO Journal, 2018, 37, .	7.8	82
15	Defects in RNA metabolism in mitochondrial disease. International Journal of Biochemistry and Cell Biology, 2017, 85, 106-113.	2.8	7
16	Naturally existing isoforms of miR-222 have distinct functions. Nucleic Acids Research, 2017, 45, 11371-11385.	14.5	61
17	A network-biology perspective of microRNA function and dysfunction in cancer. Nature Reviews Genetics, 2016, 17, 719-732.	16.3	579
18	p53 Represses the Oncogenic Sno-MiR-28 Derived from a SnoRNA. PLoS ONE, 2015, 10, e0129190.	2.5	55

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19	Network-Based Approaches to Understand the Roles of miR-200 and Other microRNAs in Cancer. Cancer Research, 2015, 75, 2594-2599.	0.9	54
20	Assessing the gene regulatory properties of Argonaute-bound small RNAs of diverse genomic origin. Nucleic Acids Research, 2015, 43, 470-481.	14.5	142
21	Stimulus-dependent differences in signalling regulate epithelial-mesenchymal plasticity and change the effects of drugs in breast cancer cell lines. Cell Communication and Signaling, 2015, 13, 26.	6.5	47
22	Genomeâ€wide identification of miRâ€200 targets reveals a regulatory network controlling cell invasion. EMBO Journal, 2014, 33, 2040-2056.	7.8	126
23	Direct transcriptional regulation by nuclear microRNAs. International Journal of Biochemistry and Cell Biology, 2014, 54, 304-311.	2.8	78
24	On Measuring miRNAs after Transient Transfection of Mimics or Antisense Inhibitors. PLoS ONE, 2013, 8, e55214.	2.5	103
25	IsomiRs â€" the overlooked repertoire in the dynamic microRNAome. Trends in Genetics, 2012, 28, 544-549.	6.7	410
26	Experimental strategies for microRNA target identification. Nucleic Acids Research, 2011, 39, 6845-6853.	14.5	493
27	The Human Mitochondrial Transcriptome. Cell, 2011, 146, 645-658.	28.9	716
28	An autocrine TGF-Î²/ZEB/miR-200 signaling network regulates establishment and maintenance of epithelial-mesenchymal transition. Molecular Biology of the Cell, 2011, 22, 1686-1698.	2.1	505
29	Global analysis of the mammalian RNA degradome reveals widespread miRNA-dependent and miRNA-independent endonucleolytic cleavage. Nucleic Acids Research, 2011, 39, 5658-5668.	14.5	76
30	Regulated post-transcriptional RNA cleavage diversifies the eukaryotic transcriptome. Genome Research, 2010, 20, 1639-1650.	5.5	76
31	Hormonally regulated follicle differentiation and luteinization in the mouse is associated with hypoxia inducible factor activity. Molecular and Cellular Endocrinology, 2010, 327, 47-55.	3.2	42
32	A Double-Negative Feedback Loop between ZEB1-SIP1 and the microRNA-200 Family Regulates Epithelial-Mesenchymal Transition. Cancer Research, 2008, 68, 7846-7854.	0.9	956
33	MicroRNAs as regulators of epithelial-mesenchymal transition. Cell Cycle, 2008, 7, 3112-3117.	2.6	467
34	Regulation of Cyclin D1 RNA Stability by SNIP1. Cancer Research, 2008, 68, 7621-7628.	0.9	86
35	Cell-specific Regulation of Hypoxia-inducible Factor (HIF)-1Î± and HIF-2Î± Stabilization and Transactivation in a Graded Oxygen Environment. Journal of Biological Chemistry, 2006, 281, 22575-22585.	3.4	182
36	SNIP1 Is a Candidate Modifier of the Transcriptional Activity of c-Myc on E Box-Dependent Target Genes. Molecular Cell, 2006, 24, 771-783.	9.7	60

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37	Activity of Hypoxia-inducible Factor 2Î± Is Regulated by Association with the NF-ÎºB Essential Modulator. Journal of Biological Chemistry, 2005, 280, 14240-14251.	3.4	61