Robert K Bradley

List of Publications by Year
in descending order

61 papers	10,530 citations	101384 36 h-index	128067 60 g-index
75 all docs	75 docs citations	75 times ranked	17411 citing authors

#	Article	IF	Citations
1	Integrative Clinical Genomics of Advanced Prostate Cancer. Cell, 2015, 161, 1215-1228.	13.5	2,660
2	Evolution of genes and genomes on the Drosophila phylogeny. Nature, 2007, 450, 203-218.	13.7	1,886
3	Braveheart, a Long Noncoding RNA Required for Cardiovascular Lineage Commitment. Cell, 2013, 152, 570-583.	13.5	839
4	RNA splicing factors as oncoproteins and tumour suppressors. Nature Reviews Cancer, 2016, 16, 413-430.	12.8	549
5	SRSF2 Mutations Contribute to Myelodysplasia by Mutant-Specific Effects on Exon Recognition. Cancer Cell, 2015, 27, 617-630.	7.7	449
6	Fast Statistical Alignment. PLoS Computational Biology, 2009, 5, e1000392.	1.5	302
7	Modulation of splicing catalysis for therapeutic targeting of leukemia with mutations in genes encoding spliceosomal proteins. Nature Medicine, 2016, 22, 672-678.	15.2	301
8	Widespread intron retention diversifies most cancer transcriptomes. Genome Medicine, 2015, 7, 45.	3.6	283
9	U2AF1 mutations alter splice site recognition in hematological malignancies. Genome Research, 2015, 25, 14-26.	2.4	238
10	Binding Site Turnover Produces Pervasive Quantitative Changes in Transcription Factor Binding between Closely Related Drosophila Species. PLoS Biology, 2010, 8, e1000343.	2.6	184
11	Spliceosomal disruption of the non-canonical BAF complex in cancer. Nature, 2019, 574, 432-436.	13.7	163
12	Synthetic Lethal and Convergent Biological Effects of Cancer-Associated Spliceosomal Gene Mutations. Cancer Cell, 2018, 34, 225-241.e8.	7.7	162
13	Coordinated alterations in RNA splicing and epigenetic regulation drive leukaemogenesis. Nature, 2019, 574, 273-277.	13.7	149
14	Pharmacologic modulation of RNA splicing enhances anti-tumor immunity. Cell, 2021, 184, 4032-4047.e31.	13.5	131
15	Massive Mitochondrial Gene Transfer in a Parasitic Flowering Plant Clade. PLoS Genetics, 2013, 9, e1003265.	1.5	115
16	Genome-wide RNAi screens in human brain tumor isolates reveal a novel viability requirement for PHF5A. Genes and Development, 2013, 27, 1032-1045.	2.7	114
17	Altered RNA Splicing by Mutant p53 Activates Oncogenic RAS Signaling in Pancreatic Cancer. Cancer Cell, 2020, 38, 198-211.e8.	7.7	99
18	A feedback loop between nonsense-mediated decay and the retrogene DUX4 in facioscapulohumeral muscular dystrophy. ELife, 2015, 4, .	2.8	97

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19	RNA components of the spliceosome regulate tissue- and cancer-specific alternative splicing. Genome Research, 2019, 29, 1591-1604.	2.4	96
20	Spliceosomal gene mutations in myelodysplasia: molecular links to clonal abnormalities of hematopoiesis. Genes and Development, 2016, 30, 989-1001.	2.7	95
21	Most human introns are recognized via multiple and tissue-specific branchpoints. Genes and Development, 2018, 32, 577-591.	2.7	95
22	Alternative Splicing of RNA Triplets Is Often Regulated and Accelerates Proteome Evolution. PLoS Biology, 2012, 10, e1001229.	2.6	93
23	Horizontal transfer of expressed genes in a parasitic flowering plant. BMC Genomics, 2012, 13, 227.	1.2	90
24	DUX4 Suppresses MHC Class I to Promote Cancer Immune Evasion and Resistance to Checkpoint Blockade. Developmental Cell, 2019, 50, 658-671.e7.	3.1	76
25	Model systems of DUX4 expression recapitulate the transcriptional profile of FSHD cells. Human Molecular Genetics, 2016, 25, ddw271.	1.4	75
26	Exon Junction Complex Shapes the Transcriptome by Repressing Recursive Splicing. Molecular Cell, 2018, 72, 496-509.e9.	4.5	75
27	Sample processing obscures cancer-specific alterations in leukemic transcriptomes. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 16802-16807.	3.3	72
28	Wild-Type U2AF1 Antagonizes the Splicing Program Characteristic of U2AF1-Mutant Tumors and Is Required for Cell Survival. PLoS Genetics, 2016, 12, e1006384.	1.5	72
29	RNA isoform screens uncover the essentiality and tumor-suppressor activity of ultraconserved poison exons. Nature Genetics, 2020, 52, 84-94.	9.4	70
30	Minor intron retention drives clonal hematopoietic disorders and diverse cancer predisposition. Nature Genetics, 2021, 53, 707-718.	9.4	61
31	Impaired hematopoiesis and leukemia development in mice with a conditional knock-in allele of a mutant splicing factor gene U2af1. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E10437-E10446.	3.3	59
32	XRate: a fast prototyping, training and annotation tool for phylo-grammars. BMC Bioinformatics, 2006, 7, 428.	1.2	49
33	Discovery of synthetic lethal and tumor suppressor paralog pairs in the human genome. Cell Reports, 2021, 36, 109597.	2.9	48
34	The RNA Surveillance Factor UPF1 Represses Myogenesis via Its E3ÂUbiquitin Ligase Activity. Molecular Cell, 2017, 67, 239-251.e6.	4.5	47
35	The TAGteam motif facilitates binding of 21 sequence-specific transcription factors in the Drosophila embryo. Genome Research, 2012, 22, 656-665.	2.4	44
36	Recurrent SRSF2 mutations in MDS affect both splicing and NMD. Genes and Development, 2020, 34, 413-427.	2.7	44

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37	Dissecting the Contributions of Cooperating Gene Mutations to Cancer Phenotypes and Drug Responses with Patient-Derived iPSCs. Stem Cell Reports, 2018, 10, 1610-1624.	2.3	43
38	Single-cell genomics reveals the genetic and molecular bases for escape from mutational epistasis in myeloid neoplasms. Blood, 2020, 136, 1477-1486.	0.6	43
39	Transgenic mice expressing tunable levels of DUX4 develop characteristic facioscapulohumeral muscular dystrophy-like pathophysiology ranging in severity. Skeletal Muscle, 2020, 10, 8.	1.9	37
40	Convergent organization of aberrant MYB complex controls oncogenic gene expression in acute myeloid leukemia. ELife, 2021, 10, .	2.8	37
41	Specific alignment of structured RNA: stochastic grammars and sequence annealing. Bioinformatics, 2008, 24, 2677-2683.	1.8	35
42	Quantitative proteomics reveals key roles for post-transcriptional gene regulation in the molecular pathology of facioscapulohumeral muscular dystrophy. ELife, 2019, 8, .	2.8	34
43	Coordinated missplicing of TMEM14C and ABCB7 causes ring sideroblast formation in SF3B1-mutant myelodysplastic syndrome. Blood, 2022, 139, 2038-2049.	0.6	34
44	Transducers: an emerging probabilistic framework for modeling indels on trees. Bioinformatics, 2007, 23, 3258-3262.	1.8	33
45	Translational plasticity facilitates the accumulation of nonsense genetic variants in the human population. Genome Research, 2016, 26, 1639-1650.	2.4	31
46	Characterization of neoantigen-specific T cells in cancer resistant to immune checkpoint therapies. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	30
47	Short H2A histone variants are expressed in cancer. Nature Communications, 2021, 12, 490.	5.8	29
48	Synthetic introns enable splicing factor mutation-dependent targeting of cancer cells. Nature Biotechnology, 2022, 40, 1103-1113.	9.4	24
49	Integrative oncogene-dependency mapping identifies RIT1 vulnerabilities and synergies in lung cancer. Nature Communications, 2021, 12, 4789.	5.8	21
50	Tools for simulating evolution of aligned genomic regions with integrated parameter estimation. Genome Biology, 2008, 9, R147.	13.9	20
51	ZBTB33 Is Mutated in Clonal Hematopoiesis and Myelodysplastic Syndromes and Impacts RNA Splicing. Blood Cancer Discovery, 2021, 2, 500-517.	2.6	17
52	Evolutionary Modeling and Prediction of Non-Coding RNAs in Drosophila. PLoS ONE, 2009, 4, e6478.	1.1	13
53	Nonsense-mediated mRNA decay uses complementary mechanisms to suppress mRNA and protein accumulation. Life Science Alliance, 2022, 5, e202101217.	1.3	13
54	Rare and private spliceosomal gene mutations drive partial, complete, and dual phenocopies of hotspot alterations. Blood, 2020, 135, 1032-1043.	0.6	11

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55	The origins and consequences of UPF1 variants in pancreatic adenosquamous carcinoma. ELife, 2021, 10, .	2.8	8
56	Degenerate eigenvalues for Hamiltonians with no obvious symmetries. Advances in Theoretical and Mathematical Physics, 2005, 9, 593-602.	0.4	7
57	Evolutionary Triplet Models of Structured RNA. PLoS Computational Biology, 2009, 5, e1000483.	1.5	6
58	Coordinated Mis-Splicing of Multiple Mitochondrial Iron Metabolism Genes Causes Ring Sideroblast Formation in SF3B1-Mutant MDS. Blood, 2020, 136, 4-4.	0.6	2
59	Congenital myotonic dystrophyâ€"an RNA-mediated disease across a developmental continuum. Genes and Development, 2017, 31, 1067-1068.	2.7	1
60	ZRSR2 Mutation Induced Minor Intron Retention Drives MDS and Diverse Cancer Predisposition Via Aberrant Splicing of LZTR1. Blood, 2020, 136, 10-11.	0.6	1
61	Probing Aberrant Splicing in a Novel Model of SF3B1-Mutant Myelodysplastic Syndromes. Blood, 2019, 134, 1706-1706.	0.6	0