Robert K Bradley

List of Publications by Year
in descending order

61 papers	10,530 citations	101535 36 h-index	128286 60 g-index
75 all docs	75 docs citations	75 times ranked	17411 citing authors

#	Article	IF	Citations
1	Coordinated missplicing of TMEM14C and ABCB7 causes ring sideroblast formation in SF3B1-mutant myelodysplastic syndrome. Blood, 2022, 139, 2038-2049.	1.4	34
2	Nonsense-mediated mRNA decay uses complementary mechanisms to suppress mRNA and protein accumulation. Life Science Alliance, 2022, 5, e202101217.	2.8	13
3	Synthetic introns enable splicing factor mutation-dependent targeting of cancer cells. Nature Biotechnology, 2022, 40, 1103-1113.	17.5	24
4	The origins and consequences of UPF1 variants in pancreatic adenosquamous carcinoma. ELife, 2021, 10, .	6.0	8
5	Convergent organization of aberrant MYB complex controls oncogenic gene expression in acute myeloid leukemia. ELife, 2021, 10, .	6.0	37
6	Minor intron retention drives clonal hematopoietic disorders and diverse cancer predisposition. Nature Genetics, 2021, 53, 707-718.	21.4	61
7	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, .	7.1	30
8	ZBTB33 Is Mutated in Clonal Hematopoiesis and Myelodysplastic Syndromes and Impacts RNA Splicing. Blood Cancer Discovery, 2021, 2, 500-517.	5.0	17
9	Pharmacologic modulation of RNA splicing enhances anti-tumor immunity. Cell, 2021, 184, 4032-4047.e31.	28.9	131
10	Integrative oncogene-dependency mapping identifies RIT1 vulnerabilities and synergies in lung cancer. Nature Communications, 2021, 12, 4789.	12.8	21
11	Discovery of synthetic lethal and tumor suppressor paralog pairs in the human genome. Cell Reports, 2021, 36, 109597.	6.4	48
12	Short H2A histone variants are expressed in cancer. Nature Communications, 2021, 12, 490.	12.8	29
13	RNA isoform screens uncover the essentiality and tumor-suppressor activity of ultraconserved poison exons. Nature Genetics, 2020, 52, 84-94.	21.4	70
14	Rare and private spliceosomal gene mutations drive partial, complete, and dual phenocopies of hotspot alterations. Blood, 2020, 135, 1032-1043.	1.4	11
15	Altered RNA Splicing by Mutant p53 Activates Oncogenic RAS Signaling in Pancreatic Cancer. Cancer Cell, 2020, 38, 198-211.e8.	16.8	99
16	Single-cell genomics reveals the genetic and molecular bases for escape from mutational epistasis in myeloid neoplasms. Blood, 2020, 136, 1477-1486.	1.4	43
17	Recurrent SRSF2 mutations in MDS affect both splicing and NMD. Genes and Development, 2020, 34, 413-427.	5.9	44
18	Transgenic mice expressing tunable levels of DUX4 develop characteristic facioscapulohumeral muscular dystrophy-like pathophysiology ranging in severity. Skeletal Muscle, 2020, 10, 8.	4.2	37

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19	Coordinated Mis-Splicing of Multiple Mitochondrial Iron Metabolism Genes Causes Ring Sideroblast Formation in SF3B1-Mutant MDS. Blood, 2020, 136, 4-4.	1.4	2
20	ZRSR2 Mutation Induced Minor Intron Retention Drives MDS and Diverse Cancer Predisposition Via Aberrant Splicing of LZTR1. Blood, 2020, 136, 10-11.	1.4	1
21	RNA components of the spliceosome regulate tissue- and cancer-specific alternative splicing. Genome Research, 2019, 29, 1591-1604.	5.5	96
22	DUX4 Suppresses MHC Class I to Promote Cancer Immune Evasion and Resistance to Checkpoint Blockade. Developmental Cell, 2019, 50, 658-671.e7.	7.0	76
23	Coordinated alterations in RNA splicing and epigenetic regulation drive leukaemogenesis. Nature, 2019, 574, 273-277.	27.8	149
24	Spliceosomal disruption of the non-canonical BAF complex in cancer. Nature, 2019, 574, 432-436.	27.8	163
25	Quantitative proteomics reveals key roles for post-transcriptional gene regulation in the molecular pathology of facioscapulohumeral muscular dystrophy. ELife, 2019, 8, .	6.0	34
26	Probing Aberrant Splicing in a Novel Model of SF3B1-Mutant Myelodysplastic Syndromes. Blood, 2019, 134, 1706-1706.	1.4	0
27	Most human introns are recognized via multiple and tissue-specific branchpoints. Genes and Development, 2018, 32, 577-591.	5.9	95
28	Dissecting the Contributions of Cooperating Gene Mutations to Cancer Phenotypes and Drug Responses with Patient-Derived iPSCs. Stem Cell Reports, 2018, 10, 1610-1624.	4.8	43
29	Exon Junction Complex Shapes the Transcriptome by Repressing Recursive Splicing. Molecular Cell, 2018, 72, 496-509.e9.	9.7	75
30	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.	7.1	59
31	Synthetic Lethal and Convergent Biological Effects of Cancer-Associated Spliceosomal Gene Mutations. Cancer Cell, 2018, 34, 225-241.e8.	16.8	162
32	Congenital myotonic dystrophyâ€"an RNA-mediated disease across a developmental continuum. Genes and Development, 2017, 31, 1067-1068.	5.9	1
33	The RNA Surveillance Factor UPF1 Represses Myogenesis via Its E3ÂUbiquitin Ligase Activity. Molecular Cell, 2017, 67, 239-251.e6.	9.7	47
34	Wild-Type U2AF1 Antagonizes the Splicing Program Characteristic of U2AF1-Mutant Tumors and Is Required for Cell Survival. PLoS Genetics, 2016, 12, e1006384.	3.5	72
35	Modulation of splicing catalysis for therapeutic targeting of leukemia with mutations in genes encoding spliceosomal proteins. Nature Medicine, 2016, 22, 672-678.	30.7	301
36	Spliceosomal gene mutations in myelodysplasia: molecular links to clonal abnormalities of hematopoiesis. Genes and Development, 2016, 30, 989-1001.	5.9	95

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37	Model systems of DUX4 expression recapitulate the transcriptional profile of FSHD cells. Human Molecular Genetics, 2016, 25, ddw271.	2.9	75
38	Translational plasticity facilitates the accumulation of nonsense genetic variants in the human population. Genome Research, 2016, 26, 1639-1650.	5.5	31
39	RNA splicing factors as oncoproteins and tumour suppressors. Nature Reviews Cancer, 2016, 16, 413-430.	28.4	549
40	A feedback loop between nonsense-mediated decay and the retrogene DUX4 in facioscapulohumeral muscular dystrophy. ELife, 2015, 4, .	6.0	97
41	Integrative Clinical Genomics of Advanced Prostate Cancer. Cell, 2015, 161, 1215-1228.	28.9	2,660
42	Widespread intron retention diversifies most cancer transcriptomes. Genome Medicine, 2015, 7, 45.	8.2	283
43	SRSF2 Mutations Contribute to Myelodysplasia by Mutant-Specific Effects on Exon Recognition. Cancer Cell, 2015, 27, 617-630.	16.8	449
44	U2AF1 mutations alter splice site recognition in hematological malignancies. Genome Research, 2015, 25, 14-26.	5.5	238
45	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.	7.1	72
46	Braveheart, a Long Noncoding RNA Required for Cardiovascular Lineage Commitment. Cell, 2013, 152, 570-583.	28.9	839
47	Massive Mitochondrial Gene Transfer in a Parasitic Flowering Plant Clade. PLoS Genetics, 2013, 9, e1003265.	3.5	115
48	Genome-wide RNAi screens in human brain tumor isolates reveal a novel viability requirement for PHF5A. Genes and Development, 2013, 27, 1032-1045.	5.9	114
49	The TAGteam motif facilitates binding of 21 sequence-specific transcription factors in the Drosophila embryo. Genome Research, 2012, 22, 656-665.	5.5	44
50	Horizontal transfer of expressed genes in a parasitic flowering plant. BMC Genomics, 2012, 13, 227.	2.8	90
51	Alternative Splicing of RNA Triplets Is Often Regulated and Accelerates Proteome Evolution. PLoS Biology, 2012, 10, e1001229.	5.6	93
52	Binding Site Turnover Produces Pervasive Quantitative Changes in Transcription Factor Binding between Closely Related Drosophila Species. PLoS Biology, 2010, 8, e1000343.	5.6	184
53	Evolutionary Modeling and Prediction of Non-Coding RNAs in Drosophila. PLoS ONE, 2009, 4, e6478.	2.5	13
54	Fast Statistical Alignment. PLoS Computational Biology, 2009, 5, e1000392.	3.2	302

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55	Evolutionary Triplet Models of Structured RNA. PLoS Computational Biology, 2009, 5, e1000483.	3.2	6
56	Tools for simulating evolution of aligned genomic regions with integrated parameter estimation. Genome Biology, 2008, 9, R147.	9.6	20
57	Specific alignment of structured RNA: stochastic grammars and sequence annealing. Bioinformatics, 2008, 24, 2677-2683.	4.1	35
58	Transducers: an emerging probabilistic framework for modeling indels on trees. Bioinformatics, 2007, 23, 3258-3262.	4.1	33
59	Evolution of genes and genomes on the Drosophila phylogeny. Nature, 2007, 450, 203-218.	27.8	1,886
60	XRate: a fast prototyping, training and annotation tool for phylo-grammars. BMC Bioinformatics, 2006, 7, 428.	2.6	49
61	Degenerate eigenvalues for Hamiltonians with no obvious symmetries. Advances in Theoretical and Mathematical Physics, 2005, 9, 593-602.	0.6	7