Robert K Bradley

List of Publications by Year in Descending Order

66 papers	7,369 citations	31 h-index	75 g-index
75 ext. papers	9,159 ext. citations	15.8 avg, IF	5.6 L-index

#	Paper	IF	Citations
66	Nonsense-mediated mRNA decay uses complementary mechanisms to suppress mRNA and protein accumulation. *Life Science Alliance*, **2022**, 5,	5.8	1
65	Synthetic introns enable splicing factor mutation-dependent targeting of cancer cells.. *Nature Biotechnology*, **2022**,	44.5	2
64	Coordinated mis-splicing of TMEM14C and ABCB7 causes ring sideroblast formation in SF3B1-mutant myelodysplastic syndrome. *Blood*, **2021**,	2.2	2
63	Minor intron retention drives clonal hematopoietic disorders and diverse cancer predisposition. *Nature Genetics*, **2021**, 53, 707-718	36.3	13
62	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,	11.5	8
61	is mutated in clonal hematopoiesis and myelodysplastic syndromes and impacts RNA splicing. *Blood Cancer Discovery*, **2021**, 2, 500-517	7	0
60	Pharmacologic modulation of RNA splicing enhances anti-tumor immunity. *Cell*, **2021**, 184, 4032-4047.e31	36.2	25
59	The origins and consequences of variants in pancreatic adenosquamous carcinoma. *ELife*, **2021**, 10,	8.9	2
58	Convergent organization of aberrant MYB complex controls oncogenic gene expression in acute myeloid leukemia. *ELife*, **2021**, 10,	8.9	12
57	Integrative oncogene-dependency mapping identifies RIT1 vulnerabilities and synergies in lung cancer. *Nature Communications*, **2021**, 12, 4789	17.4	4
56	Discovery of synthetic lethal and tumor suppressor paralog pairs in the human genome. *Cell Reports*, **2021**, 36, 109597	10.6	8
55	Short H2A histone variants are expressed in cancer. *Nature Communications*, **2021**, 12, 490	17.4	12
54	Rare and private spliceosomal gene mutations drive partial, complete, and dual phenocopies of hotspot alterations. *Blood*, **2020**, 135, 1032-1043	2.2	8
53	Altered RNA Splicing by Mutant p53 Activates Oncogenic RAS Signaling in Pancreatic Cancer. *Cancer Cell*, **2020**, 38, 198-211.e8	24.3	38
52	Single-cell genomics reveals the genetic and molecular bases for escape from mutational epistasis in myeloid neoplasms. *Blood*, **2020**, 136, 1477-1486	2.2	21
51	Recurrent SRSF2 mutations in MDS affect both splicing and NMD. *Genes and Development*, **2020**, 34, 413-427	7.6	19
50	ZRSR2 Mutation Induced Minor Intron Retention Drives MDS and Diverse Cancer Predisposition Via Aberrant Splicing of LZTR1. *Blood*, **2020**, 136, 10-11	2.2	0

49	Coordinated Mis-Splicing of Multiple Mitochondrial Iron Metabolism Genes Causes Ring Sideroblast Formation in SF3B1-Mutant MDS. *Blood*, **2020**, 136, 4-4	2.2	1
48	RNA isoform screens uncover the essentiality and tumor-suppressor activity of ultraconserved poison exons. *Nature Genetics*, **2020**, 52, 84-94	36.3	30
47	Transgenic mice expressing tunable levels of DUX4 develop characteristic facioscapulohumeral muscular dystrophy-like pathophysiology ranging in severity. *Skeletal Muscle*, **2020**, 10, 8	5.1	18
46	RNA components of the spliceosome regulate tissue- and cancer-specific alternative splicing. *Genome Research*, **2019**, 29, 1591-1604	9.7	53
45	DUX4 Suppresses MHC Class I to Promote Cancer Immune Evasion and Resistance to Checkpoint Blockade. *Developmental Cell*, **2019**, 50, 658-671.e7	10.2	37
44	Quantitative proteomics reveals key roles for post-transcriptional gene regulation in the molecular pathology of facioscapulohumeral muscular dystrophy. *ELife*, **2019**, 8,	8.9	12
43	Probing Aberrant Splicing in a Novel Model of SF3B1-Mutant Myelodysplastic Syndromes. *Blood*, **2019**, 134, 1706-1706	2.2	
42	Coordinated alterations in RNA splicing and epigenetic regulation drive leukaemogenesis. *Nature*, **2019**, 574, 273-277	50.4	76
41	Spliceosomal disruption of the non-canonical BAF complex in cancer. *Nature*, **2019**, 574, 432-436	50.4	80
40	Most human introns are recognized via multiple and tissue-specific branchpoints. *Genes and Development*, **2018**, 32, 577-591	12.6	49
39	Dissecting the Contributions of Cooperating Gene Mutations to Cancer Phenotypes and Drug Responses with Patient-Derived iPSCs. *Stem Cell Reports*, **2018**, 10, 1610-1624	8	30
38	Synthetic Lethal and Convergent Biological Effects of Cancer-Associated Spliceosomal Gene Mutations. *Cancer Cell*, **2018**, 34, 225-241.e8	24.3	96
37	Exon Junction Complex Shapes the Transcriptome by Repressing Recursive Splicing. *Molecular Cell*, **2018**, 72, 496-509.e9	17.6	43
36	Impaired hematopoiesis and leukemia development in mice with a conditional knock-in allele of a mutant splicing factor gene. *Proceedings of the National Academy of Sciences of the United States of America*, **2018**, 115, E10437-E10446	11.5	38
35	Congenital myotonic dystrophy-an RNA-mediated disease across a developmental continuum. *Genes and Development*, **2017**, 31, 1067-1068	12.6	1
34	The RNA Surveillance Factor UPF1 Represses Myogenesis via Its E3 Ubiquitin Ligase Activity. *Molecular Cell*, **2017**, 67, 239-251.e6	17.6	33
33	Model systems of DUX4 expression recapitulate the transcriptional profile of FSHD cells. *Human Molecular Genetics*, **2016**, 25, 4419-4431	5.6	49
32	Translational plasticity facilitates the accumulation of nonsense genetic variants in the human population. *Genome Research*, **2016**, 26, 1639-1650	9.7	24

31	RNA splicing factors as oncoproteins and tumour suppressors. *Nature Reviews Cancer*, **2016**, 16, 413-30	31.3	383
30	Wild-Type U2AF1 Antagonizes the Splicing Program Characteristic of U2AF1-Mutant Tumors and Is Required for Cell Survival. *PLoS Genetics*, **2016**, 12, e1006384	6	57
29	Modulation of splicing catalysis for therapeutic targeting of leukemia with mutations in genes encoding spliceosomal proteins. *Nature Medicine*, **2016**, 22, 672-8	50.5	227
28	Spliceosomal gene mutations in myelodysplasia: molecular links to clonal abnormalities of hematopoiesis. *Genes and Development*, **2016**, 30, 989-1001	12.6	73
27	SRSF2 Mutations Contribute to Myelodysplasia by Mutant-Specific Effects on Exon Recognition. *Cancer Cell*, **2015**, 27, 617-30	24.3	337
26	U2AF1 mutations alter splice site recognition in hematological malignancies. *Genome Research*, **2015**, 25, 14-26	9.7	174
25	A feedback loop between nonsense-mediated decay and the retrogene DUX4 in facioscapulohumeral muscular dystrophy. *ELife*, **2015**, 4,	8.9	73
24	Integrative clinical genomics of advanced prostate cancer. *Cell*, **2015**, 161, 1215-1228	56.2	1765
23	Widespread intron retention diversifies most cancer transcriptomes. *Genome Medicine*, **2015**, 7, 45	14.4	188
22	Sample processing obscures cancer-specific alterations in leukemic transcriptomes. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 16802-7	11.5	50
21	Braveheart, a long noncoding RNA required for cardiovascular lineage commitment. *Cell*, **2013**, 152, 570-83	32	701
20	Massive mitochondrial gene transfer in a parasitic flowering plant clade. *PLoS Genetics*, **2013**, 9, e1003265	6	86
19	Genome-wide RNAi screens in human brain tumor isolates reveal a novel viability requirement for PHF5A. *Genes and Development*, **2013**, 27, 1032-45	12.6	88
18	Horizontal transfer of expressed genes in a parasitic flowering plant. *BMC Genomics*, **2012**, 13, 227	4.5	73
17	The TAGteam motif facilitates binding of 21 sequence-specific transcription factors in the Drosophila embryo. *Genome Research*, **2012**, 22, 656-65	9.7	38
16	Alternative splicing of RNA triplets is often regulated and accelerates proteome evolution. *PLoS Biology*, **2012**, 10, e1001229	9.7	74
15	Binding site turnover produces pervasive quantitative changes in transcription factor binding between closely related Drosophila species. *PLoS Biology*, **2010**, 8, e1000343	9.7	154
14	Evolutionary modeling and prediction of non-coding RNAs in Drosophila. *PLoS ONE*, **2009**, 4, e6478	3.7	10

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13	Fast statistical alignment. *PLoS Computational Biology*, **2009**, 5, e1000392	5	252
12	Evolutionary triplet models of structured RNA. *PLoS Computational Biology*, **2009**, 5, e1000483	5	4
11	Tools for simulating evolution of aligned genomic regions with integrated parameter estimation. *Genome Biology*, **2008**, 9, R147	18.3	18
10	Specific alignment of structured RNA: stochastic grammars and sequence annealing. *Bioinformatics*, **2008**, 24, 2677-83	7.2	31
9	Evolution of genes and genomes on the Drosophila phylogeny. *Nature*, **2007**, 450, 203-18	50.4	1586
8	Transducers: an emerging probabilistic framework for modeling indels on trees. *Bioinformatics*, **2007**, 23, 3258-62	7.2	29
7	XRate: a fast prototyping, training and annotation tool for phylo-grammars. *BMC Bioinformatics*, **2006**, 7, 428	3.6	40
6	Degenerate eigenvalues for Hamiltonians with no obvious symmetries. *Advances in Theoretical and Mathematical Physics*, **2005**, 9, 593-602	1.3	4
5	Discovery of synthetic lethal and tumor suppressive paralog pairs in the human genome		1
4	RNA components of the spliceosome regulate tissue- and cancer-specific alternative splicing		3
3	Transgenic mice expressing tunable levels of DUX4 develop characteristic facioscapulohumeral muscular dystrophy-like pathophysiology ranging in severity		1
2	Wild-type U2AF1 antagonizes the splicing program characteristic of U2AF1-mutant tumors and is required for cell survival		3
1	Nonsense-mediated mRNA decay utilizes complementary mechanisms to suppress mRNA and protein accumulation		1