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EDUCATION

University of California, Berkeley 2008
Ph.D. in Biophysics

Princeton University 2004
A.B. in Physics with Highest Honors

PROFESSIONAL EXPERIENCE

Director, Translational Data Science Integrated Research Center, FHCC 2021 – present
Full Professor, Fred Hutchinson Cancer Center 2020 – present
Associate Professor, Fred Hutchinson Cancer Center 2015 – 2020
Assistant Professor, Fred Hutchinson Cancer Center 2011 – 2015
Computational Biology Program, Public Health Sciences Division and
Basic Sciences Division

Postdoctoral Fellow, Massachusetts Institute of Technology 2009 – 2011
Department of Biology

Postdoctoral Associate, University of California, Berkeley 2008 – 2009
Department of Molecular & Cellular Biology and Department of Mathematics

HONORS AND AWARDS

McIlwain Family Endowed Chair in Data Science 2020 – present

Leukemia & Lymphoma Society Scholar 2017 – 2022

Fred Hutchinson President's Young Investigator Award 2016

Ellison Medical Foundation New Scholar 2013 – 2017

Damon Runyon Cancer Research Foundation Dale F. Frey Scientist 2012 – 2014

Damon Runyon Cancer Research Foundation Postdoctoral Fellow 2009 – 2011

NSF Graduate Research Fellow 2005 – 2008

ITO Foundation Fellow 2004 – 2005

Highest Honors, Princeton University 2004

Kusaka Memorial Prize in Theoretical Physics, Princeton University 2004

Kusaka Memorial Prize in Physics, Princeton University 2003

PUBLICATIONS (reverse chronological order)

1. Wang E^{*†}, Pineda JMB^{*}, Kim WJ^{*}, Chen S, Bourcier J, Stahl M, Hogg SJ, Bewersdorf JP, Han C, Singer ME, Cui D, Erickson CE, Tittley SM, Penson AV, Knorr K, Stanley RF, Rahman J, Krishnamoorthy G, Fagin JA, Creger E, McMillan E, Mak C-C, Jarvis M, Bossard C, Beaupre DM, **Bradley RK[†]**, Abdel-Wahab O[†] (2022). Modulation of RNA splicing enhances response to BCL2 inhibition in leukemia. *Cancer Cell* 41:1-17.
2. Choudhary GS, Pellagatti A, Agianian B, Smith MA, Bhagat TD, Gordon-Mitchell S, Sahu S, Pandey S, Shah N, Aluri S, Aggarwal R, Aminov S, Schwartz L, Steeples V, Booher RN, Ramachandra M, Samson M, Carbajal M, Pradhan K, Bowman TV, Pillai MM, Will B, Wickrema A, Shastri A, **Bradley RK**, Martell RE, Steidl RG, Gavathiotis E, Boulwood J, Starczynowski DT, Verma A (2022). Activation of targetable inflammatory immune signaling is seen in myelodysplastic syndromes with SF3B1 mutations. *eLife* 11:e78136.
3. North K^{*}, Benbarche S^{*}, Liu B, Pangallo P, Chen S, Stahl M, Bewersdorf JP, Stanley RF, Erickson C, Cho H, Pineda JMB, Thomas JD, Polaski JT, Belleville AE, Gabel AM, Udy DB, Humbert O, Kiem H-P, Abdel-Wahab O[†], **Bradley RK[†]** (2022). Synthetic introns enable splicing factor mutation-dependent targeting of cancer cells. *Nature Biotechnology* 40:1103-1113. ^{*}co-first authors; [†]co-corresponding authors
4. Udy DB, **Bradley RK** (2021). Nonsense-mediated mRNA decay uses complementary mechanisms to suppress mRNA and protein accumulation. *Life Science Alliance* doi:10.26508/lsa.202101217.
5. Clough CA, Pangallo J, Sarchi M, Ilagan JO, North K, Bergantinos R, Stolla MC, Naru J, Nugent P, Kim E, Stirewalt DL, Subramaniam AR, Abdel-Wahab O, Abkowitz JL, **Bradley RK[†]**, Doulatov S[†] (2021). Coordinated mis-splicing of TMEM14C and ABCB7 causes ring sideroblast formation in SF3B1-mutant myelodysplastic syndrome. *Blood* doi:10.1182/blood.2021012652 (2021) [†]co-corresponding authors
6. Parrish PCR^{*}, Thomas JD^{*}, Gabel AM, Kamlapurkar S, **Bradley RK**, Berger AH (2021). Discovery of synthetic lethal and tumor suppressor paralog pairs in the human genome. *Cell Reports* 36, 109597. ^{*}co-first authors
7. Vichas A^{*}, AK Riley^{*}, Nkinsi NT, Kamlapurkar S, Parrish PCR, Lo A, Duke F, Chen J, Fung I, Watson J, Rees M, Gabel AM, Thomas JD, **Bradley RK**, Lee JK, Hatch EM, Baine MK, Rekhtman N, Ladanyi M, Piccioni F, Berger AH (2021). Integrative oncogene-dependency mapping identifies RIT1 vulnerabilities and synergies in lung cancer. *Nature Communications* 12:4789. ^{*}co-first authors
8. Beauchamp EM, Leventhal M, Bernard E, Hoppe ER, Todisco G, Creignou M, Galli A, Castellano CA, McConkey M, Tarun A, Wong W, Schenone M, Stanclift C, Tanenbaum B, Malolepsza E, Nilsson B, Bick AG, Weinstock JS, Miller M, Niroula A, Dunford A, Taylor-Weiner A, Wood T, Barbera A, Anand S; Psaty BM, Desai P, Cho MH, Johnson AD, Loos R; MacArthur DG, Lek M; Neuberg DS, Lage K, Carr SA, Hellstrom-Lindberg E, Malcovati L, Papaemmanuil E, Stewart C, Getz G, **Bradley RK**, Jaiswal S, Ebert BL (2021). *ZBTB33* is mutated in clonal hematopoiesis and myelodysplastic syndromes and impacts RNA splicing. *Blood Cancer Discovery* 2:500-517.
9. Lu SX^{*}, De Neef E^{*}, Thomas JD^{*}, Sabio E, Rousseau B, Gigoux M, Knorr DA, Greenbaum B, Elhanati Y, Hogg SJ, Chow A, Ghosh A, Xie A, Zamarin D, Cui D, Erickson C, Singer M, Cho H, Wang E, Lu B, Durham BH, Shah H, Chowell D, Gabel AM, Shen Y, Liu J, Jin J, Rhodes MC, Taylor RE, Molina H, Wolchok JD, Merghoub T, Diaz LA, Abdel-Wahab O[†], **Bradley RK[†]** (2021). Pharmacologic modulation of RNA splicing enhances anti-tumor immunity. *Cell* doi:10.1016/j.cell.2021.05.038. ^{*}co-first authors; [†]co-corresponding authors

10. Li S, Simonia Y, Zhuanga S, Gabel A, Mag S, Cheeg J, Islasa L, Cessnaa A, Creaney J, **Bradley RK**, Redwood A, Robinson BW, Newell EW (2021). Characterization of neoantigen-specific T cells in cancer resistant to immune checkpoint therapies. *PNAS* 118:e2025570118.
11. Inoue D*, Polaski JT*, Taylor J*, Castel P, Chen S, Kobayashi S, Hogg SJ, Hayashi Y, Pineda JMB, El Marabti E, Erickson C, Knorr K, Fukumoto M, Yamazaki H, Tanaka A, Fukui C, Lu SX, Durham BH, Liu B, Wang E, Mehta S, Zakheim D, Garippa R, Penson A, Chew G-L, McCormick F, **Bradley RK**[†], Abdel-Wahab O[†] (2021). Minor intron retention drives clonal hematopoietic disorders and diverse cancer predisposition. *Nature Genetics* 53:707-718. *co-first authors; [†]co-corresponding authors
12. Takao S, Forbes L, Uni M, Cheng S, Pineda JMB, Tarumoto Y, Cifani P, Minuesa G, Chen C, Kharas MG, **Bradley RK**, Vakoc C, Koche RP, Kentsis A (2021). Convergent organization of aberrant MYB complex controls oncogenic gene expression in acute myeloid leukemia. *eLife* 10:e65905.
13. Chew G-L, Bleakley M, **Bradley RK**, Malik HS, Henikoff S, Molaro A, Sarthy J (2021). Short H2A histone variants are expressed in cancer. *Nature Communications* 12:490.
14. Polaski JT, Udy DB, Escobar-Hoyos LF, Askan G, Leach SD, Ventura A, Kannan R[†], **Bradley RK**[†] (2021). The origins and consequences of *UPFI* variants in pancreatic adenocarcinoma. *eLife* 10:e62209. [†]co-corresponding authors
15. Taylor J*, Mi X*, North KD*, Binder M, Penson A, Lasho TL, Knorr K, Haddadin M, Liu B, Pangallo J, Benbarche S, Wiseman DH, Tefferi A, Halene S, Liang Y, Patnaik MM, **Bradley RK**, Abdel-Wahab O (2020). Single-cell genomics reveals the genetic and molecular bases for escape from mutational epistasis in myeloid neoplasms. *Blood* doi:10.1182/blood.2020006868. *co-first authors
16. Escobar-Hoyos LF, Penson A, Kannan R, Cho H, Pan C-H, Singh RK, Apken LH, Hobbs GA, Luo R, Lecomte N, Babu S, Pan FC, Alonso-Curbelo D, Morris JP, Askan G, Grbovic-Huezo O, Ogrodowski P, Bermeo J, Saglimbeni J, Cruz CD, Ho Y-J, Lawrence SA, Melchor JP, Goda GA, Bai K, Pastore A, Hogg SJ, Raghavan S, Bailey P, Chang DK, Biankin A, Shroyer KR, Wolpin BM, Aguirre AJ, Ventura A, Taylor B, Der CJ, Dominguez D, Kümmel D, Oeckinghaus A, Lowe SW, **Bradley RK**[†], Abdel-Wahab O[†], Leach SD[†] (2020). Altered RNA splicing by mutant p53 activates oncogenic RAS signaling in pancreatic cancer. *Cancer Cell* 38:1–14. [†]co-senior authors
17. Jones TI, Chew G-L, Barraza-Flores P, Schreier S, Ramirez M, Wuebbles RD, Burkin DJ, **Bradley RK**, Jones PL (2020). Transgenic mice expressing tunable levels of DUX4 develop characteristic facioscapulohumeral muscular dystrophy-like pathophysiology ranging in severity. *Skeletal Muscle* 10:8.
18. Rahman MA, Lin K-T, **Bradley RK**, Abdel-Wahab O, Krainer AR (2020). Recurrent SRSF2 mutations in MDS affect both splicing and NMD. *Genes & Development* 34:1–15.
19. Pangallo J, Kiladjian J-J, Cassinat B, Renneville A, Taylor J, Polaski JT, North K, Abdel-Wahab O, **Bradley RK** (2020). Rare and private spliceosomal gene mutations drive partial, complete, and dual phenocopies of hotspot alterations. *Blood* doi:10.1182/blood.2019002894.
20. Thomas JD, Polaski JT, Feng Q, De Neef EJ, Hoppe ER, McSharry MV, Pangallo J, Gabel AM, Belleville AE, Watson J, Nkinsi NT, Berger AH, **Bradley RK** (2020). RNA isoform screens uncover the essentiality and tumor suppressor activity of ultraconserved poison exons. *Nature Genetics* 52:84–94.

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21. Inoue D^{*}, Chew G-L^{*}, Liu B, Michel BC, Pangallo J, D'Avino AR, Hitchman T, North K, Lee SC-W, Bitner L, Block A, Moore AR, Yoshimi A, Escobar-Hoyos L, Cho H, Penson A, Lu SX, Taylor J, Chen Y, Kadoch C, Abdel-Wahab O[†], **Bradley RK**[†] (2019). Spliceosomal disruption of the non-canonical BAF complex in cancer. *Nature* 574:432–436. ^{*}co-first authors; [†]co-corresponding authors
22. Yoshimi A, Lin K-T, Wiseman DH, Rahman MA, Pastore A, Wang B, Lee SC-W, Micol J-B, Zhang XJ, de Botton S, Penard-Lacronique V, Stein EM, Cho H, Miles RE, Inoue D, Albrecht TR, Somervaille TCP, Batta K, Amaral F, Simeoni F, Wilks DP, Cargo C, Intlekofer AM, Levine RL, Dvinge H, **Bradley RK**, Wagner EJ, Krainer AR, Abdel-Wahab O. Coordinated alterations in RNA splicing and epigenetic regulation drive leukaemogenesis. *Nature* 574:273–277.
23. Dvinge H[†], Guenthoer J, Porter PL, **Bradley RK**[†] (2019). RNA components of the spliceosome regulate tissue- and cancer-specific alternative splicing. *Genome Research* 29:1591–1604. [†]co-corresponding authors
24. Chew G-L^{*}, Campbell A^{*}, De Neef E, Sutliff NA, Shadle SC, Tapscott SJ[†], **Bradley RK**[†] (2019). DUX4 suppresses MHC class I to promote cancer immune evasion and resistance to checkpoint blockade. *Developmental Cell* 50:1–14. ^{*}co-first authors; [†]co-corresponding authors
25. Palangat M, Anastasakis DG, Fei DL, Lindblad KE, **Bradley RK**, Hourigan CS, Hafner M, Larson DR (2019). The splicing factor U2AF1 contributes to cancer progression through a noncanonical role in translation regulation. *Genes & Development* 33:1–16.
26. Jagannathan S[†], Ogata Y, Gafken PR, Tapscott SJ[†], **Bradley RK**[†] (2019). Quantitative proteomics reveals key roles for post-transcriptional gene regulation in the molecular pathology of FSHD. *eLife* 8:e41740. [†]co-corresponding authors
27. Blazquez L, Emmett W, Faraway R, Pineda JMB, Bajew S, Gohr A, Haberman N, Sibley CR, **Bradley RK**, Irimia M, Ule J (2018). Exon junction complex shapes the transcriptome by repressing recursive splicing. *Molecular Cell* 72:496–509.
28. Fei DL, Zhen T, Durham B, Ferrarone J, Zhang T, Garrett L, Yoshimi A, Abdel-Wahab O, **Bradley RK**, Liu P, and Varmus H (2018). Impaired hematopoiesis and leukemia development in mice with a conditional knock-in allele of a mutant splicing factor gene *U2af1*. *PNAS* doi:10.1073/pnas.1812669115.
29. Lee SC^{*}, North K^{*}, Kim E^{*}, Jang E, Obeng E, Lu SX, Liu B, Inoue D, Yoshimi A, Ki M, Yeo M, Zhang XJ, Kim MK, Cho H, Chung YR, Taylor J, Durham BH, Kim YJ, Pastore A, Monette S, Palacino J, Seiler M, Buonamici S, Smith PG, Ebert BL, **Bradley RK**[†], Abdel-Wahab O[†] (2018). Synthetic lethal and convergent biological effects of cancer-associated spliceosomal gene mutations. *Cancer Cell* 34:225–241. ^{*}co-first authors; [†]co-corresponding authors
30. Chang C-J, Kotini AG, Olszewska M, Georgomanoli M, Teruya-Feldstein J, Sperber H, Sanchez R, DeVita R, Martins TJ, Abdel-Wahab O, **Bradley RK**, Papapetrou EP (2018). Dissecting the contributions of cooperating gene mutations to cancer phenotypes and drug responses with patient-derived iPSCs. *Stem Cell Reports* 10:1610–1624.
31. Pineda JMB, **Bradley RK** (2018). Most human introns are recognized via multiple and tissue-specific branchpoints. *Genes & Development* 32:577–591.
32. Jagannathan S, **Bradley RK** (2017). Congenital myotonic dystrophy—an RNA-mediated disease across a developmental continuum. *Genes & Development* 31:1067–1068.

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33. Feng Q, Jagannathan S, **Bradley RK** (2017). The RNA surveillance factor UPF1 represses myogenesis via its E3 ubiquitin ligase activity. *Molecular Cell* 67:239–251.
34. Fei DL[†], Motowski H, Chatrikhi R, Prasad S, Yu J, Gao S, Kielkopf CL[†], **Bradley RK**[†], Varmus H[†] (2016). Wild-type U2AF1 antagonizes the splicing program characteristic of U2AF1-mutant tumors and is required for cell survival. *PLoS Genetics* 12:e1006384. [†]co-corresponding authors
35. Uo T, Dvinge H, Sprenger CC, **Bradley RK**, Nelson PS, Plymate SR (2016). Systematic and functional characterization of novel androgen receptor variants arising from alternative splicing in the ligand-binding domain. *Oncogene* 36:1440–1450.
36. Jagannathan S, **Bradley RK** (2016). Translational plasticity facilitates the accumulation of nonsense genetic variants in the human population. *Genome Research* 26:1639–1650.
37. Jagannathan S^{*}, Shadle S^{*}, Resnick R, Snider L, Tawil RN, van der Maarel SM, **Bradley RK**[†], Tapscott SJ[†] (2016). Model systems of DUX4 expression recapitulate the transcriptional profile of FSHD cells. *Human Molecular Genetics* 25:4419–4431. ^{*}co-first authors; [†]co-corresponding authors
38. Dvinge H^{*}, Kim E^{*}, Abdel-Wahab O[†], **Bradley RK**[†] (2016) RNA splicing factors as oncoproteins and tumour suppressors. *Nature Reviews Cancer* 16:413–430. ^{*}co-first authors; [†]co-corresponding authors
39. Lee SC^{*}, Dvinge H^{*}, Kim E, Cho H, Micol JB, Chung YR, Durham BH, Yoshimi A, Kim YJ, Thomas M, Lobry C, Chen CW, Pastore A, Taylor J, Wang X, Krivtsov A, Armstrong SA, Palacino J, Buonamici S, Smith PG, **Bradley RK**[†], Abdel-Wahab O[†] (2016) Modulation of splicing catalysis for therapeutic targeting of leukemia with mutations in genes encoding spliceosomal proteins. *Nature Medicine* 22:672–678. ^{*}co-first authors; [†]co-corresponding authors
40. Inoue D, **Bradley RK**, Abdel-Wahab O (2016) Spliceosomal gene mutations in myelodysplasia: molecular links to clonal abnormalities of hematopoiesis. *Genes & Development* 30:989–1001.
41. The Cancer Genome Atlas Research Network (2015) The molecular taxonomy of primary prostate cancer. *Cell* 163:1011–1025.
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43. Robinson D, Van Allen EM, et al (2015) Integrative clinical genomics of advanced prostate cancer. *Cell* 161:1215–1228.
44. Kim E^{*}, Ilagan JO^{*}, Liang Y^{*}, Daubner GM^{*}, Lee SC-W, Ramakrishnan A, Li Y, Chung YR, Micol J-B, Murphy M, Cho H, Kim M-K, Zebari AS, Aumann S, Park CY, Buonamici S, Smith PG, Deeg HJ, Lobry C, Aifantis I, Modis Y, Allain FH-T, Halene S, **Bradley RK**[†], Abdel-Wahab O[†] (2015) *SRSF2* mutations contribute to myelodysplasia through mutant-specific effects on exon recognition. *Cancer Cell* 27:617–630. ^{*}co-first authors; [†]co-corresponding authors
45. Dvinge H, **Bradley RK** (2015) Widespread intron retention diversifies most cancer transcriptomes. *Genome Medicine* 7:45.

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46. Feng Q, Snider L, Jagannathan S, Tawil R, van der Maarel SM, Tapscott SJ[†], **Bradley RK**[†] (2015) A feedback loop between nonsense-mediated decay and the retrogene *DUX4* in facioscapulohumeral muscular dystrophy. *eLife* 4:e04996. [†]co-corresponding authors
47. Ilagan JO^{*}, Ramakrishnan A^{*}, Hayes B, Murphy ME, Zebari AS, Bradley P, **Bradley RK** (2015) *U2AF1* mutations alter splice site recognition in hematological malignancies. *Genome Research* 25:14–26. ^{*}co-first authors
48. Dvinge H, Ries RE, Ilagan JO, Stirewalt DL, Meshinchi S, **Bradley RK** (2014) Sample processing obscures cancer-specific alterations in leukemic transcriptomes. *PNAS* 111:16802–16807.
49. Hubert CG^{*}, **Bradley RK**^{*}, Ding Y, Toledo CM, Herman J, Skutt-Kakaria K, Girard EJ, Davison J, Berndt J, Corrin P, Hardcastle J, Basom R, Delrow JJ, Webb T, Pollard SM, Lee J, Olson JM, Paddison PJ (2013) Genome-wide RNAi screens in human brain tumor isolates reveal a novel viability requirement for PHF5A. *Genes & Development* 27:1032–1045. ^{*}co-first authors
50. Klattenhoff C, Scheuermann JC, Surface LE, **Bradley RK**, Fields PA, Steinhauser ML, Ding H, Butty VL, Torrey L, Haas S, Abo R, Tabebordbar M, Lee RT, Burge CB, Boyer LA (2013) *Braveheart*, a long non-coding RNA required for cardiovascular lineage commitment. *Cell* 152:570–583.
51. Xi Z, Yuguo W, **Bradley RK**, Sugumaran M, Marx CJ, Rest JS, Davis CC (2013) Massive mitochondrial gene transfer in a parasitic flowering plant. *PLoS Genetics* 9:e1003265.
52. Xi Z, **Bradley RK**, Wurdack KJ, Wong KM, Sugumaran M, Bomblies K, Rest JS, Davis CC (2012) Horizontal transfer of expressed genes in a parasitic flowering plant. *BMC Genomics* 13:227.
53. Satija R, **Bradley RK** (2012) The TAGteam motif facilitates binding of 21 sequence-specific transcription factors in the *Drosophila* embryo. *Genome Research* 22:656–665.
54. **Bradley RK**, Merkin JM, Lambert N, Burge CB (2012) Alternative splicing of RNA triplets is often regulated and accelerates proteome evolution. *PLoS Biology* 10:e1001229.
55. **Bradley RK**^{*}, Li XY^{*}, Trapnell C, Davidson S, Pachter L, Chu HC, Tonkin LA, Biggin MD, Eisen MB (2010) Binding site turnover produces pervasive quantitative changes in transcription factor binding between closely related *Drosophila* species. *PLoS Biology* 8:e1000343. ^{*}co-first authors
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57. **Bradley RK**, Roberts A, Smoot M, Juvekar S, Do J, Dewey C, Holmes I, Pachter L (2009) Fast Statistical Alignment. *PLoS Computational Biology* 5:e1000392.
58. **Bradley RK**, Uzilov AV, Skinner ME, Bendana YR, Barquist L, Holmes I (2009) Evolutionary modeling and prediction of non-coding RNAs in *Drosophila*. *PLoS One* 4:e6478.
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61. *Drosophila* 12 Genomes Consortium (2007) Evolution of genes and genomes on the *Drosophila* phylogeny. Nature 450:203–218.
62. **Bradley RK**, Holmes I (2007) Transducers: an emerging probabilistic framework for modeling indels on trees. Bioinformatics 23:3258–3262.
63. Klosterman PS, Uzilov AV, Bendana YR, **Bradley RK**, Chao S, Kosiol C, Goldman N, Holmes I (2006) Xrate: a fast prototyping, training and annotation tool for phylo-grammars. BMC Bioinformatics. 7:428.
64. Gubser SS, **Bradley RK** (2005) Degenerate eigenvalues for Hamiltonians with no obvious symmetries. Adv. Theor. Math. Physics 9:593–602.