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EDUCATION

University of California, Berkeley Ph.D. in Biophysics	2008
Princeton University A.B. in Physics with Highest Honors	2004

PROFESSIONAL EXPERIENCE

Associate Member, Fred Hutchinson Cancer Research Center	2015 – present
Assistant Member, Fred Hutchinson Cancer Research Center Computational Biology Program, Public Health Sciences Division Basic Sciences Division	2011 – 2015
Postdoctoral Fellow, Massachusetts Institute of Technology Department of Biology	2009 – 2011
Postdoctoral Associate, University of California, Berkeley Department of Molecular & Cellular Biology and Department of Mathematics	2008 – 2009

HONORS AND AWARDS

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. 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
2. 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.
3. 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.
4. 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
5. 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.
6. Pineda JMB, **Bradley RK** (2018). Most human introns are recognized via multiple and tissue-specific branchpoints. *Genes & Development* 32:577-591.
7. Jagannathan S, **Bradley RK** (2017). Congenital myotonic dystrophy—an RNA-mediated disease across a developmental continuum. *Genes & Development* 31:1067-1068.
8. 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.
9. 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
10. 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.
11. Jagannathan S, **Bradley RK** (2016). Translational plasticity facilitates the accumulation of nonsense genetic variants in the human population. *Genome Research* 26:1639-1650.
12. 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
13. 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

14. 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
Perspective article in Cancer Discovery. Recommended by the Faculty of 1000.
15. 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.
16. The Cancer Genome Atlas Research Network (2015) The molecular taxonomy of primary prostate cancer. *Cell* 163:1011-1025.
17. Hickey TE, Irvine CM, Dvinge H, Tarulli GA, Hanson AR, Ryan NK, Pickering MA, Birrell SN, Hu DG, Mackenzie PI, Russell R, Caldas C, Raj GV, Dehm SM, Plymate SR, **Bradley RK**, Tilley WD, Selth LA (2015) Expression of androgen receptor splice variants in clinical breast cancers. *Oncotarget* 6:44728-44744.
18. Robinson D, Van Allen EM, et al (2015) Integrative clinical genomics of advanced prostate cancer. *Cell* 161:1215-1228.
19. 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
Perspective articles in Nature Reviews Cancer and Cancer Cell.
20. Dvinge H, **Bradley RK** (2015) Widespread intron retention diversifies most cancer transcriptomes. *Genome Medicine* 7:45.
21. 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
Recommended by the Faculty of 1000.
22. 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
23. 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.
Recommended by the Faculty of 1000.
24. 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
Perspective article in Cancer Discovery.

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25. 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.
Recommended by the Faculty of 1000. Perspective articles in EMBO Journal and Circulation Research.
26. 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.
27. 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.
Covered by The Economist and Scientific American.
28. 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.
29. **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.
Perspective article in Genome Biology.
30. **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
Perspective article in PLoS Biology.
31. **Bradley RK**, Holmes I (2009) Evolutionary triplet models of structured RNA. *PLoS Computational Biology* 5:e1000483.
32. **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.
33. **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.
34. Varadarajan A, **Bradley RK**, Holmes I (2008) Tools for simulating evolution of aligned genomic regions with integrated parameter estimation. *Genome Biology* 9:R147.
35. **Bradley RK**, Pachter L, Holmes I (2008) Specific alignment of structured RNA: stochastic grammars and sequence annealing. *Bioinformatics* 24:2677-2683.
36. *Drosophila* 12 Genomes Consortium (2007) Evolution of genes and genomes on the *Drosophila* phylogeny. *Nature* 450:203-218.
37. **Bradley RK**, Holmes I (2007) Transducers: an emerging probabilistic framework for modeling indels on trees. *Bioinformatics* 23:3258-3262.
38. 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.
39. Gubser SS, **Bradley RK** (2005) Degenerate eigenvalues for Hamiltonians with no obvious symmetries. *Adv. Theor. Math. Physics* 9:593-602.