UNIVERSITY OF PENNSYLVANIA - PERELMAN SCHOOL OF MEDICINE
Curriculum Vitae

Date: 10/30/2021

Yoseph Barash, Ph.D.

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If you are not a U.S. citizen or holder of a permanent visa, please indicate the type of visa you have:

Education:

1998	B.Sc.	Hebrew University, Jerusalem, Israel. (Computer Science and Physics)
2006	Ph.D.	School of Computer Science & Engineering Hebrew University, Jerusalem, Israel (Machine learning, computational biology)

Postgraduate Training and Fellowship Appointments:

2006-2009	Postdoc, Department of Computer Science, Centre for Cellular and Biomolecular Research, University of Toronto, Advisors: Prof. Brendan Frey, Prof. Ben Blencowe
2009-2011	Senior Research Fellow, University of Toronto

Military Service:

1991-1995	Army Officer (Major), Chief of an operational wing in an air force unit, Commanding officer in a paratroops reconnaissance unit, An infantry officer instructor in the Officer's Academy Israel Defense Forces

Faculty Appointments:

2012-2018	Assistant Professor of Genetics, University of Pennsylvania School of Medicine
2012-2018	Assistant Professor of Computer and Information Science (Secondary), University of Pennsylvania School of Engineering
2018-present	Associate Professor of Genetics, University of Pennsylvania School of Medicine
2018-present	Associate Professor of Computer and Information Science (Secondary), University of Pennsylvania School of Engineering

Hospital and/or Administrative Appointments:

[none]

Other Appointments:

1997-1998	Algorithm and software developer - Java programming, netPost(TM) Inc
2002	Microarray gene expression analysis (joint research), Functional Genomics Unit, Tel Hashomer Hospital

Specialty Certification:

[none]

Licensure:

[none]

Awards, Honors and Membership in Honorary Societies:

1997	Dean's List for undergraduate achievements, Faculty of Science, Hebrew University
1998	Graduated Cum Laude Magna, Hebrew University
2000	Leibniz award for M.Sc. research study, Hebrew University
2002-2004	Levi Eshkol fellowship recipient, Israeli Ministry of Science
2002	Best poster award, the Annual Israeli Bioinformatics Symposium
2005	Best scientific poster award, Hebrew University
2006-2007	Charles H. Best postdoctoral fellowship recipient, University of Toronto
2010	Lap-Chee Tsui Publication Award (Biomedical Research), Canadian Institutes of Health Research

Memberships in Professional and Scientific Societies and Other Professional Activities:

International:

2014	Fondation pour la Recherche Médicale (France) (Ad Hoc Grant Reviewer)
2017-2020	Israeli Science Foundation (ISF) (Ad Hoc Grant Reviewer)
2018	Prostate Cancer UK (Ad Hoc Grant Reviewer)

National:

2016	National Science Foundation (Ad Hoc Grant Reviewer)
2018-2021	National Institute of Health (Ad Hoc Grant Reviewer)
2019	American Heart Association (Ad Hoc Grant Reviewer)

Editorial Positions:

2003-Present	Reviewer, Bioinformatics
2003	Reviewer, Journal of Bioinformatics and Computational Biology

2004-Present	International Conference on Intelligent Systems for Molecular Biology (ISMB)
2005-2006	Reviewer, International Conference on Computational Molecular Biology (RECOMB)
2008	Reviewer, Genes and Development
2008	Reviewer, Nature
2008	Reviewer, Journal of Machine Learning Research (JMLR)
2010-Present	Reviewer, Nucleic Acid Research (NAR)
2010	BMC Bioinformatics
2010-2017	Reviewer, Nature Methods
2010-Present	Reviewer, Genome Biology
2011-2016	Reviewer, PLoS Computational Biology
2012-Present	International Conference for Neural Information Processing Systems (NIPS)
2012	Reviewer, BMC Genomics
2014	Reviewer, RNA
2014-2020	Reviewer, Cell Reports
2014	Reviewer, Human Molecular Genetics
2015-Present	Reviewer, eLife
2016	Reviewer Human Genetics
2016-Present	Reviewer, Nature Communications
2017-Present	International Conference on Learning Representations (ICLR)
2017	Reviewer, BMC Medical Genomics
2017-Present	International Conference on Machine Learning (ICML)
2018	Reviewer, Nature Communications Biology
2018	Reviewer, Nature Biotechnology
2018-2020	Reviewer, Genetics in Medicine
2021	Reviewer, Genetics
2021	Frontiers

Academic and Institutional Committees:

[none]

Major Academic and Clinical Teaching Responsibilities:

2000-2002	Teaching Assistant (frontal), Data Structures, Algorithms, Java OOD Programming, Hebrew University
2002	Teaching Assistant (frontal), Information Theory Course, Hebrew University
2002-2005	Student Supervisor, Hebrew University
	Supervised numerous undergraduates in their final computational biology (CSLS) projects. Several of these (Noa Shefi, Gali Niv and Omri Peleg) later extended their work to M.Sc. and Ph.D. research in Computational Biology and machine learning.

2002	Project for programming skills improvement, Hebrew University Initiated, in conjunction with Prof. Danny Dolev, head of the CSE school at the Hebrew University, a project to update the curriculum for B.Sc. in CS. Aiming to improve the level of programming skills, we researched the curriculum in other leading universities in the U.S. and interviewed academy and industry figures. Conclusions from this project were adopted in following years.
2003	Teaching Assistant (frontal), Programming Lab, OOD, STL, C++-, Hebrew University
2004-2005	Lecturer, Introduction to Computational Biology Course, Hebrew University
2008-2011	Student Supervisor, University of Toronto: PhD students Hui Xiong, Boyko Kakradov in the PSI lab
2012	Independent Study for students and postdocs - Gabe Otte, Alon Witztum, Axel Bernal
2012	"Predictive Modeling for Splicing", Children Hospital of Philadelphia, Philadelphia, PA
2014-Present	Lecturer, GCB 752 Seminar in Genomics
2014-Present	Mentor rotation students, undergrads, and high school interns (total 17) - Alex Amile Wolf, Matt Paul, Scott Norton, Caleb Radens, Qin Zhu, Osvaldo Rivera, David Lee, David Wang, Joseph Aicher, Lev Litchevski, Kevin Yang, Raehoon Jeong, Nick Page, William Wu, Lev Litichevskiy, Moein Elzubier, Viviana Perry
2014-Present	Mentor PhD Students and postdoc (total 15) - Anupama Jha, Scott Norton, Caleb Radens, Osvaldo Rivera, David Lee, Joseph Aicher, David Wang, Matthew Gazzara, Mathieu Quesnel-Vallieres, Barry Slaff, Deependra Singh, Kevin Yang, Di Wu, Farica Zhuang, Danielle Gutman
2015-2019	Course co-director, lecturer, GCB 537 Advanced Computational Biology
2016	Lecture, UPenn Math Bio Seminar "Modeling RNA local splicing variations from large heterogeneous datasets"
2016	Lecture, PICS Symposium, "Big Data for RNA processing - From computational modeling through the wet lab to patients"
2016	Guest class moderator, CAMB 608 "Advanced discussions of eukaryotic gene regulation"
2016	Organizer/Director, CIS 701 "Topics in Deep Learning"
2017	Penn RNA Group RNA-Seq analysis Workshop organizer/presenter
2018	Organizer/Director CIS 800 course "Peeking into the black box of Deep Learning models"
2019-Present	Lecturer, GCB 533 Statistics for Genomics and Biomedical Informatics

Lectures by Invitation (Last 5 years):

Jul, 2016	"Predictive models for RNA splicing regulation - the next generation", SINGARNA Meeting, Singapore
Sep, 2016	"Integrating Big Data for RNA processing - From computational modeling, through the wet lab, to patients", Festival Of Genomics, San Diego, CA
Nov, 2016	"Integrating Big Data for RNA processing - From computational modeling, through the wet lab, to patients", Rush Medical Center, Chicago, IL
Apr, 2017	"Integrating Big Data for RNA processing - From computational modeling, through the wet lab, to patients", RNA-Seq Conference, San Francisco, CA
Apr, 2017	"Detection, quantification, and visualization of splicing variations from RNA-Seq data", RNA-Seq Workshop, San Francisco, CA
Jul, 2017	"Outlier detection for improved differential splicing quantification from RNA-Seq experiments with replicates", 25th International Conference on Intelligent Systems in Molecular Biology (ISMB), Prague, Czech Republic
Oct, 2017	"Alternative Splicing and Disease: Why should we care and what can we do about it", Pfizer Inc., Boston, US
Oct, 2017	"Big data, small data: Getting from genotype to phenotype through transcriptome variations identification, prediction, and design", BioGen Inc., Boston, US
Oct, 2017	"Building a new view of Transcriptome Variations", Microsoft Research Symposium on Computational Aspects of Biological Information (CABI), Boston, US
Feb, 2018	"Big data, small data: Getting from genotype to phenotype through transcriptome variations identification, prediction, and design", 3rd Annual NGS data analysis & informatics, San Diego, CA, USA
May, 2018	"Computational modeling of alternative splicing - applications for the study of gene regulation and disease", Department of Molecular Genetics Seminar Series, UC Irvine Medical School, Irvine, CA, USA
Oct, 2018	"Big RNA Splicing Data for studying human disease - Challenges, advancements, and lessons learned", Penn State Medical School, USA
Nov, 2018	"Big RNA Splicing Data for studying human disease: Challenges, advancements, and lessons learned", EMBL-EBI Industry Programme workshop, Boston, USA
Dec, 2018	"Big RNA Splicing Data for studying human disease: Challenges, advancements, and lessons learned", Hebrew University, Israel
Dec, 2018	"Big RNA Splicing Data for studying human disease: Challenges, advancements, and lessons learned", Tel Aviv University, Israel
Dec, 2018	"Big RNA Splicing Data for studying human disease: Challenges, advancements, and lessons learned", Weizmann Institute, Israel

Mar, 2019	"Big data, small data: Getting from genotype to phenotype through transcriptome variations identification and prediction", Stanford, USA
Sep, 2019	"Using RNA-seq to map transcriptome variations for disease studies and clinical diagnosis", The 20th Annual Ribo-Club meeting, Quebec, Canada
Sep, 2019	"A tale of two tales: Using RNASeq to map transcriptome variations for disease studies & What do air fights have to do with G-Quads?", The Crick Institue, London, UK
Nov, 2019	"Modeling RNA Splicing - from 'Big Data' RNASeq quantifications to interpreting predictive deep learning models", Northeastern University, Boston, USA
Nov, 2019	"Using RNA-seq to map transcriptome variations for disease studies and clinical diagnosis", Pfizer, Boston
Dec, 2019	"Modeling RNA Splicing - from 'Big Data' RNASeq quantifications to interpreting predictive deep learning models", UCLA, USA
Jan, 2020	"Big data, small data: studying human disease through the lense of RNA Splicing", McGill University Meeting on Clinical implementation of Genomics and Epigenomics, Barbados, 2020
Nov, 2020	"Tools and evaluation for RNA-seq splicing quantification for suspected Mendelian disorders across tissues", Kaiser Permanente, USA (virtual)
Nov, 2020	"Tools and evaluation for RNA-seq splicing quantification for suspected Mendelian disorders across tissues", Boston Children's Hospital, Boston, USA (virtual)
Jan, 2021	"RNA Splicing analysis - How to get the signal out of the noise?" Universität Stuttgart, Germany (virtual)
Feb, 2021	"RNA Splicing analysis - How to get the signal out of the noise?" Arrakis Theraputics, Boston, USA (virtual)
Oct, 2021	"Tools and evaluation for RNA-seq splicing quantification for suspected Mendelian disorders across tissues", Murdoch Children's Research Institute, University of Melbourne, Australia (virtual)

Organizing Roles in Scientific Meetings:

Jul, 2011	Co-organizer, 8th SIG Meeting on Alternative Splicing Vienna, Austria
Jul, 2012	Co-organizer, 9th SIG Meeting on Alternative Splicing Long Beach, CA
Jul, 2013	Co-organizer, 10th SIG Meeting on Integrative RNA Analysis and Disease Berlin, Germany
Apr, 2014	Session Chair, 5th International Conference on Visualizing Biological Data (VIZBI) EMBL, Heidelberg, Germany

Jul, 2014	Co-organizer, 11th SIG Meeting on Integrative RNA Analysis and Disease Boston, MA
Jul, 2015	Co-organizer, 12th SIG Meeting on Integrative RNA Analysis and Disease Dublin, Ireland
Jun, 2016	Co-organizer, Workshop on computational methods for RNA data analysis, International RNA Society Meeting Kyoto, Japan
Jul, 2016	Co-organizer, 13th SIG Meeting on Integrative RNA Analysis and Disease Orlando, Florida
Jul, 2017	Co-organizer, 14th SIG Meeting on RNA at the International Conference on Intelligent Systems in Molecular Biology (ISMB) Prague, Czech Republic
Mar, 2018	Session Chair, 9th International Conference on Visualizing Biological Data (VIZBI) The Broad Institute, Boston, USA
Jul, 2018	Co-organizer, 15th Meeting on Integrative RNA Biology (iRNA) at the International Conference on Intelligent Systems in Molecular Biology (ISMB), Chicago, USA
Jun, 2019	Workshop on Computational Methods for RNA data analysis, International RNA Society Meeting. Krakow, Poland
Jul, 2019	Co-organizer, 16th Meeting on Integrative RNA Biology (iRNA) at the International Conference on Intelligent Systems in Molecular Biology (ISMB), Basel, Switzerland
Nov, 2019	Co-organizer, 3rd Meeting on RNA Informatics Wellcome Genome Campus, Cambridge, UK
Jul, 2020	Co-organizer, 17th Meeting on Integrative RNA Biology (iRNA) at the International Conference on Intelligent Systems in Molecular Biology (ISMB) – Virtual
June, 2021	APAeval Community Challenge and Computational Workshop at the RNA Society Meeting 2021 - Virtual
July, 2021	Co-organizer, 18th Meeting on Integrative RNA Biology (iRNA) at the International Conference on Intelligent Systems in Molecular Biology (ISMB) – Virtual
June, 2022	APAeval Community Challenge (Results) at the RNA Society Meeting 2022
July, 2022	Co-organizer, 19th Meeting on Integrative RNA Biology (iRNA) at the International Conference on Intelligent Systems in Molecular Biology (ISMB)

Bibliography:

Research Publications, peer reviewed (print or other media):

1. Barash, Y. and Friedman,, N.: Context-Specifin Bayesian Clustering for Gene Expression Data. Proceedings of the 5th International Conference on Computational Molecular Biology (RECOMB). ACM, 2001.

2. Barash, Yoseph, Bejerano, Gill, Friedman, Nir: A Simple Hyper-Geometric Approach for Discovering Putative Transcription Factor Binding Sites. Algorithms in Bioinformatics. Springer Berlin / Heidelberg, 2149: 278-293, 2001.

3. Barash, Y., Friedman, N.: Context-specific Bayesian clustering for gene expression data. Journal of computational biology 9(2): 169-91, 2002.

4. Segal, E., Barash, Y., Simon, I., Friedman, N, Koller, D.: From Promoter Sequence to Expression: A Probabilistic Framework. Proceedings of the 6th International Conference on Computational Molecular Biology (RECOMB). ACM, Page: 28-37, 2002.

5. Barash, Y*., Elidan, G.*, Kaplan*, T., Friedman, N.: Modeling Dependencies in Protein-DNA Binding Sites. Proceedings of the Seventh Annual International Conference on Computational Molecular Biology (RECOMB). ACM, Page: 28-37, 2003.

6. Barash, Y., Dehan, E., Krupsky, M., Franklin, W., Geraci, M., Friedman, N., Kaminski, N.: Comparative analysis of algorithms for signal quantitation from oligonucleotide microarrays. Bioinformatics 20(6): 839-46, 2004.

7. Marion, R. M., Regev, A., Segal, E., Barash, Y., Koller, D., Friedman, N., O'Shea, E. K.: Sfp1 is a stress- and nutrient-sensitive regulator of ribosomal protein gene expression. Proceedings of the National Academy of Sciences of the United States of America 101(40): 14315-22, 2004.

8. Barash, Y., Elidan, G., Kaplan, T., Friedman, N.: CIS: compound importance sampling method for protein-DNA binding site p-value estimation. Bioinformatics 21(5): 596-600, 2005.

9. Fagnani, M.*, Barash, Y.*, Ip, J. Y., Misquitta, C., Pan, Q., Saltzman, A. L., Shai, O., Lee, L., Rozenhek, A., Mohammad, N., Willaime-Morawek, S., Babak, T., Zhang, W., Hughes, T. R., van der Kooy, D., Frey, B. J., Blencowe, B. J.: Functional coordination of alternative splicing in the mammalian central nervous system. Genome biology 8(6): R108, 2007 Notes: co-corresponding first author.

10. Aznarez, I.*, Barash, Y.*, Shai, O., He, D., Zielenski, J., Tsui, L. C., Parkinson, J., Frey, B. J., Rommens, J. M., Blencowe, B. J.: A systematic analysis of intronic sequences downstream of 5" splice sites reveals a widespread role for U-rich motifs and TIA1/TIAL1 proteins in alternative splicing regulation. Genome research 18(8): 1247-58, 2008

11. Barash, Y., Blencowe, B. J., Frey, B. J.: Model-based detection of alternative splicing signals. Bioinformatics 26(12): i325-33, 2010.

12. Barash, Y., Calarco, J. A., Gao, W., Pan, Q., Wang, X., Shai, O., Blencowe, B. J., Frey, B. J.: Deciphering the splicing code. Nature 465(7294): 53-9, 2010.

13. Xiong, Hui Yuan*, Barash, Yoseph*, Frey, Brendan J.: Bayesian prediction of tissue-regulated splicing using RNA sequence and cellular context. Bioinformatics 27(18): 2554-2562, 2011.

14. Yoseph Barash, Jorge Vaquero-Garcia, Juan González-Vallinas, Hui Yuan Xiong, Weijun Gao, Leo J Lee and Brendan J Frey: AVISPA: a web tool for the prediction and analysis of alternative splicing. Genome Biology 14(10), 2013

15. Gazzara Matthew R, Vaquero-Garcia Jorge, Lynch Kristen W, Barash Yoseph: In silico to in vivo splicing analysis using splicing code models. Methods (San Diego, Calif.) 67(1): 3-12, May 2014.

16. Xiong Hui Y, Alipanahi Babak, Lee Leo J, Bretschneider Hannes, Merico Daniele, Yuen Ryan K C, Hua Yimin, Gueroussov Serge, Najafabadi Hamed S, Hughes Timothy R, Morris Quaid, Barash Yoseph, Krainer Adrian R, Jojic Nebojsa, Scherer Stephen W, Blencowe Benjamin J, Frey Brendan J: The human splicing code reveals new insights into the genetic determinants of disease. Science 347(6218): 1254806, Jan 2015

17. Martinez N, Agosto L., Qiu J., Mallory M., Gazarra M., Barash Y., Fu X., Lynch K.: Widespread JNK-dependent alternative splicing induces a positive feedback loop through CELF2-mediated regulation of MKK7 during T-cell activation. Genes & Development 29(19), 2015

18. Sotillo E., Barrett D., Black K., Bagashev A., Oldridge D., Wu G., Sussman R., Lanauze C., Gazzara M, Martinez N., Ruella M., Harrington C., Chung E., Perazzelli J., Hofmann T., Maude S., Raman P., Barrera A., Gill S., Lacey S., Melenhorst J., Allman D., Jacoby E., Fry T., Mackall C., Barash Y., Lynch K., Maris J, Grupp S.,Thomas-Tikhonenko A.: Convergence of acquired mutations and alternative splicing of CD19 enables resistance to CART-19 immunotherapy. Cancer Discovery 5(12): 1282-95, December 2015

19. Vaquero-Garcia J., Barrera A., Gazzara, M. González-Vallinas J., Lahens N., Hogenesch J., Lynch K., Barash Y.: A new view of transcriptome complexity and regulation through the lens of local splicing variations. ELife 5: e11752, Feb 2016.

20. Ehrmann, Ingrid, Gazzara, Matthew R., Pagliarini, Vittoria, Dalgliesh, Caroline, Kheirollahi-Chadegani, Mahsa, Xu, Yaobo, Cesari, Eleonora, Danilenko, Marina, Maclennan, Marie, Lowdon, Kate, Vogel, Tanja, Keskivali-Bond, Piia, Wells, Sara, Cater, Heather, Fort, Philippe, Santibanez-Koref, Mauro, Middei, Silvia, Sette, Claudio, Clowry, Gavin J.*, Barash, Yoseph*, Cunningham, Mark O.*, Elliott, David J.*: A SLM2 Feedback Pathway Controls Cortical Network Activity and Mouse Behavior. Cell Reports. Elsevier, 17(12): 3269-3280, December 2016

21. Gazzara, M.R., Mallory, M.J., Roytenberg, R., Lindberg, J., Jha, A., Lynch, K.W., and Barash, Y. (2017).: Ancient antagonism between CELF and RBFOX families tunes mRNA splicing outcomes. Genome Research Page: gr. 220517.117, June 2017

22. Jha, A., Gazzara, M.R., and Barash, Y.: Integrative Deep Models for Alternative Splicing. Bioinformatics Page: 104869, July 2017.

23. Jorge Vaquero-Garcia, Emilie Lalonde, Kathryn G. Ewens, Jessica Ebrahimzadeh,Jennifer Richard-Yutz, Carol L. Shields, Alejandro Barrera, Christopher J. Green, Yoseph Barash*, Arupa Ganguly*: PRiMeUM: a Model for Predicting Risk of Metastasis in Uveal Melanoma. Investigative ophthalmology & visual science 58(10): 4096-4105, August 2017

24. Brady Lauren K, Wang Hejia, Radens Caleb M, Bi Yue, Radovich Milan, Maity Amit, Ivan Cristina, Ivan Mircea, Barash Yoseph, Koumenis Constantinos: Transcriptome analysis of hypoxic cancer cells uncovers intron retention in EIF2B5 as a mechanism to inhibit translation. PLoS biology. 15(9): e2002623, Sep 2017.

25. Green, Christopher, Gazzara, Matthew R., Barash, Yoseph: MAJIQ-SPEL: Web-Tool To Interrogate Classical And Complex Splicing Variations From RNA-Seq Data. Bioinformatics Page: 136077, September 2017.

26. Rohacek Alex M, Bebee Thomas W, Tilton Richard K, Radens Caleb M, McDermott-Roe Chris, Peart Natoya, Kaur Maninder, Zaykaner Michael, Cieply Benjamin, Musunuru Kiran, Barash Yoseph, Germiller John A, Krantz Ian D, Carstens Russ P, Epstein Douglas J: ESRP1 Mutations Cause Hearing Loss due to Defects in Alternative Splicing that Disrupt Cochlear Development. Developmental cell. 43(3): 318-331.e5, Nov 2017.

27. Shinde Mansi Y, Sidoli Simone, Kulej Katarzyna, Mallory Michael J, Radens Caleb M, Reicherter Amanda L, Myers Rebecca L, Barash Yoseph, Lynch Kristen W, Garcia Benjamin A, Klein Peter S: Phosphoproteomics reveals that glycogen synthase kinase-3 phosphorylates multiple splicing factors and is associated with alternative splicing. The Journal of biological chemistry 292(44): 18240-18255, Nov 2017 Notes: The paper was selected as JBC Editor's pick.

28. Norton, Scott, Vaquero-Garcia, Jorge, Barash, Yoseph: Outlier detection for improved differential splicing quantification from RNA-Seq experiments with replicates. Bioinformatics 1: 1-10, December 2017.

29. Ghanem LR, Kromer A, Silverman IM, Ji X, Gazzara M, Nguyen N, Aguilar G, Martinelli M, Barash Y, Liebhaber SA.: Poly(C)-Binding Protein Pcbp2 Enables Differentiation of Definitive Erythropoiesis by Directing Functional Splicing of the Runx1 Transcript. Molecular and Cellular Biology July 2018

30. Ehrmann I, Crichton JH, Gazzara MR, James K, Liu Y, Grellscheid SN, Curk T, de Rooij D, Steyn JS, Cockell S, Adams IR, Barash Y*, Elliott DJ*: An ancient germ cell-specific RNA-binding protein protects the germline from cryptic splice site poisoning. Elife January 2019

31. Kathryn L. Black, Ammar S. Naqvi, Katharina E. Hayer, Scarlett Y. Yang, Elisabeth Gillespie, Asen Bagashev, Vinodh Pillai, Sarah Tasian, Matthew R. Gazzara, Martin Carroll, Deanne Taylor, Kristen W. Lynch, Yoseph Barash, Andrei Thomas-Tikhonenko: Aberrant splicing in B-cell acute lymphoblastic leukemia. Nucleic Acids Research 47(2): 1043, January 2019.

32. Mukta Asnani, Katharina Hayer, Ammar Naqvi, Sisi Zheng, Scarlett Yang, Derek Oldridge, Fadia Ibrahim, Manolis Maragkakis, Matthew Gazzara, Kathryn Black, Asen Bagashev, Deanne Taylor, Zissimos Mourelatos, Stephan Grupp, David Barrett, John Maris, Elena Sotillo, Yoseph Barash, and Andrei Thomas-Tikhonenko: Retention of CD19 intron 2 contributes to CART-19 resistance in leukemias with subclonal frameshift mutations in CD19. Leukemia October 2019.

33. Sarah K. Fiordaliso, Aiko Iwata-Otsubo, Alyssa L. Ritter, Mathieu Quesnel-Vallieres,Katsunori Fujiki, Eriko Nishi, Miroslava Hancarova, Noriko Miyake, Jenny E.V. Morton, Sangmoon Lee, Karl Hackmann, Masashige Bando, Koji Masuda, Ryuichiro Nakato, Michiko Arakawa, Elizabeth Bhoj, Dong Li, Hakon Hakonarson, Ryojun Takeda, Margaret Harr, Beth Keena, Elaine H. Zackai, Nobuhiko Okamoto, Seiji Mizuno, Jung Min Ko, Alica Valachova, Darina Prchalova, Marketa Vlckova, Tommaso Pippucci, Christoph Seiler, Murim Choi, Naomichi Matsumoto, Nataliya DiDonato, Yoseph Barash, Zdenek Sedlacek, Katsuhiko Shirahige, Kosuke Izumi1: Missense Mutations in NKAP Cause a Disorder of Transcriptional Regulation Characterized by Marfanoid Habitus and Cognitive Impairment. American Journal of Human Genetics October 2019.

34. Zheng, S., Naqvi, A.S., Bolton-Gillespie, E., Asnani, M., Hayer, K., Barash, Y., Thomas-Tikhonenko, A., 2019. Pipeline for Discovering Neoepitopes Generated By Alternative Splicing in B-ALL. Blood 134, 1342–1342. https://doi.org/10.1182/blood-2019-131277

35. Asnani, M., Hayer, K.E., Naqvi, A.S., Zheng, S., Yang, S.Y., Oldridge, D., Ibrahim, F., Maragkakis, M., Gazzara, M.R., Black, K.L., Bagashev, A., Taylor, D., Mourelatos, Z., Grupp, S.A., Barrett, D., Maris, J.M., Sotillo, E., Barash, Y., Thomas-Tikhonenko, A., 2019. Retention of CD19 intron 2 contributes to CART-19 resistance in leukemias with subclonal frameshift mutations in CD19. Leukemia 1–6. https://doi.org/10.1038/s41375-019-0580-z

36. Barbieri, E., Hill, C., Quesnel-Vallières, M., Zucco, A.J., Barash, Y., Gardini, A., 2020b. Rapid and Scalable Profiling of Nascent RNA with fastGRO. Cell Reports 33, 108373. https://doi.org/10.1016/j.celrep.2020.108373

37. Aicher, J.K., Jewell, P., Vaquero-Garcia, J., Barash, Y., Bhoj, E.J., 2020. Mapping RNA splicing variations in clinically accessible and nonaccessible tissues to facilitate Mendelian disease diagnosis using RNA-seq. Genetics in Medicine 22, 1181–1190. https://doi.org/10.1038/s41436-020-0780-y

38. Jha, A., K. Aicher, J., R. Gazzara, M., Singh, D., Barash, Y., 2020. Enhanced Integrated Gradients: improving interpretability of deep learning models using splicing codes as a case study. Genome Biology 21, 149. https://doi.org/10.1186/s13059-020-02055-7

39. Nurnberg, S.T., Guerraty, M.A., Wirka, R.C., Rao, H.S., Pjanic, M., Norton, S., Serrano, F., Perisic, L., Elwyn, S., Pluta, J., Zhao, W., Testa, S., Park, Y., Nguyen, T., Ko, Y.-A., Wang, T., Hedin, U., Sinha, S., Barash, Y., Brown, C.D., Quertermous, T., Rader, D.J., 2020. Genomic profiling of human vascular cells identifies TWIST1 as a causal gene for common vascular diseases. PLOS Genetics 16, e1008538. https://doi.org/10.1371/journal.pgen.1008538

40. Lee, D.S.M., Ghanem, L.R., Barash, Y., 2020. Integrative analysis reveals RNA G-quadruplexes in UTRs are selectively constrained and enriched for functional associations. Nature Communications 11, 1–12. https://doi.org/10.1038/s41467-020-14404-y

41. Rivera, O.D., Mallory, M.J., Quesnel-Vallières, M., Chatrikhi, R., Schultz, D.C., Carroll, M., Barash, Y.*, Cherry, S.*, Lynch, K.W.*, 2021. Alternative splicing redefines landscape of commonly mutated genes in acute myeloid leukemia. Proc Natl Acad Sci USA 118, e2014967118. https://doi.org/10.1073/pnas.2014967118

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45. Lahens, N.F., Brooks, T.G., Sarantopoulou, D., Nayak, S., Lawrence, C., Mrčela, A., Srinivasan, A., Schug, J., Hogenesch, J.B., Barash, Y., Grant, G.R., 2021. CAMPAREE: a robust and configurable RNA expression simulator. BMC Genomics 22, 692. https://doi.org/10.1186/s12864-021-07934-2

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1. Joseph K Aicher, Elizabeth J Bhoj, Yoseph Barash: Tools and evaluation for RNA-seq splicing quantification for suspected Mendelian disorders across tissues. Wellcome Genomics of Rare Disease Meeting March 2019 Notes: Selected for oral presentation.

2. Mathieu Quesnel-Vallières, Jordi Vaquero-Garcia, Barry Slaff, Scott Norton, David Wang, Kristen Lynch, Yoseph Barash: Methods for RNA splicing analysis using large heterogeneous datasets. International RNA Society Meeting June 2019 Notes: Selected for oral presentation.

3. Barry Slaff, Yoseph Barash: Adjusting for known and unknown confounding factors in RNASeq based splicing analysis. The annual international conference on Intelligent Systems for Molecular Biology (ISMB), Basel, Switzerland July 2019 Notes: Selected for oral presentation.

4. David S.M Lee, Louis Ghanem, Yoseph Barash: Integrative analysis of untranslated regions in human messenger RNAs uncovers G-quadruplexes as constrained regulatory features The annual international conference on Intelligent Systems for Molecular Biology (ISMB), Basel, Switzerland July 2019 Notes: Selected for oral presentation.

5. Jha A., Aicher J.K, Singh D. and Barash Y.: Interpretation of deep learning models in genomics: splicing codes as a case study. The annual international conference on Intelligent Systems for Molecular Biology (ISMB), Basel, Switzerland July 2019.

6. Jorge Vaquero-Garcia, Scott Norton, Nicholas Lahens, Greg Grant, Yoseph Barash: RNA Splicing Analysis for Large Heterogeneous Datasets. The annual international conference on Intelligent Systems for Molecular Biology (ISMB), Basel, Switzerland July 2019 Notes: Poster presentation.

7. Joseph K. Aicher, Elizabeth J. Bhoj, Yoseph Barash: RNA-seq for identifying splicing variants in Mendelian disease: tools and evaluation. The annual international conference on Intelligent Systems for Molecular Biology (ISMB), Basel, Switzerland July 2019 Notes: Poster presentation.

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9. Mathieu Quesnel-Vallières, David C Schultz, Yancy Lo, Brinda Kamalia, Martin Carroll, Yoseph Barash*, Sara Cherry*, Kristen K Lynch*. RNA Society Meeting 2020 (Selected for Talk)

10. Osvaldo D. Rivera, Michael Mallory, Mathieu Quesnel-Vallières, David C. Schultz, Martin Carroll, Yoseph Barash* , Sara Cherry* and Kristen W. Lynch* Splicing aberrations contribute to the functional dysregulation of genes in acute myeloid leukemia. RNA Society Meeting 2020 (Selected for Talk)

11. David Wang, Mathieu Quesnel-Vallieres, Yoseph Barash. A Non-Parametric Bayesian Framework for Detecting Coregulated Splicing Signals in Heterogeneous RNA Datasets with Applications to Acute Myeloid Leukemia. Machine Learning for Systems and Computational Biology (MLSCB) Meeting at ISMB 2020 (Selected for Talk)

12. Anupama Jha, Matthew R. Gazzara, Caleb M. Radens, Paul R. Jewell, Yoseph Barash RBP-Pokedex: Prediction of RBP knockdown effect via DNN experiment modeling. Integrative RNA Biology (iRNA) Meeting at ISMB 2020 (Selected for Talk)

13. Osvaldo D. Rivera, Michael Mallory, Mathieu Quesnel-Vallières, David C. Schultz, Martin Carroll, Yoseph Barash* , Sara Cherry* and Kristen W. Lynch* Splicing variations contribute to the functional dysregulation of genes in acute myeloid leukemia. Integrative RNA Biology (iRNA) Meeting at ISMB 2020 (Selected for Talk)

14. Barry Slaff, Caleb M. Radens, Paul R. Jewell, Anupama Jha, Nicholas Lahens, Gregory Grant, Andrei Thomas-Tikhonenko, Kristen Lynch, Yoseph Barash MOCCASIN: A method for correcting known and unknown confounders in RNA-Seq-based splicing analysis. Integrative RNA Biology (iRNA) Meeting at ISMB 2020 (Poster presentation)

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16. Mathieu Quesnel-Vallieres, Anupama Jha, Andrei Thomas-Tikhonenko, Kristen Lynch, Yoseph Barash. Identifying universal cancer transcriptome patterns by interpreting deep learning models. Integrative RNA Biology (iRNA) Meeting at ISMB 2021 (Selected for Talk)

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<u>Editorials, Reviews, Chapters, including participation in committee reports (print or other media):</u>

1. Barash, Y., Wang, X.: An illuminated view of molecular biology. <u>Genome biology</u> 11(8): 307, 2010.

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1. Barash, Y.: Radio Interview. BBC, The Naked Scientists 2010

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