

**Sheng Li, Ph.D.**  
**Assistant Professor**

### **Contact Information**

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### **Education**

2009 – 2014 Ph.D. **Cornell University** in Computational Biology, New York, USA  
2005 – 2009 B.S. **Sun Yat-sen University** in Biotechnology, Guangzhou, China

### **Professional Appointments**

2019 – Assistant Professor, Department of Computer Science and Engineering,  
University of Connecticut School of Engineering, Storrs, CT  
2017 – Assistant Professor, Department of Genetics and Genome Sciences,  
University of Connecticut School of Medicine, Farmington, CT  
2016 – Assistant Professor, The Jackson Laboratory Cancer Center, Bar Harbor, ME  
2016 – Assistant Professor, The Jackson Laboratory for Genomic Medicine,  
Farmington, CT  
2014 – 2016 Instructor of Bioinformatics, Weill Cornell Medicine, New York, NY

### **Honors and Awards**

2021 Encyclopedia of DNA Elements (ENCODE) Consortium Meeting Team  
Contribution Award, NIH-NHGRI  
2019 Maximizing Investigators' Research Award, NIH-NIGMS  
2014 – 2016 Ty Louis Campbell Fellow  
2013 National Science Foundation travel fellow  
2012, 2013 Travel grant for MipTec, the leading European event for drug discovery  
2009 Outstanding undergraduate thesis award, Sun Yat-sen University  
2005 – 2008 Excellent student scholarship  
2006 Lin-zhi Xiao scholarship

### **Editorial**

2020 – Associate Editor, Science Advances

### **Publications**

\* denotes co-corresponding authors

† denotes co-first authors

1. Chen X, Ashoor H, Musich R, Wang J, Zhang M, Zhang C, Lu M, **Li S**. 2021. *epihet* for intra-tumoral epigenetic heterogeneity analysis and visualization. *Sci Rep*. 11(1):376. doi: 10.1038/s41598-020-79627-x. PMID: 33432081.
2. **Li S**<sup>\*,†</sup>, Chen X<sup>†</sup>, Wang J, Meydan C, Glass JL, Shih AH, Delwel R, Levine RL, Mason CE, Melnick AM\*. 2020. Somatic mutations drive specific, but reversible epigenetic heterogeneity states in AML. *Cancer Discov*. 10(12):1934-1949. doi: 10.1158/2159-8290.CD-19-0897. PMID: 32938585.
3. Rosikiewicz W<sup>†</sup>, Chen X<sup>†</sup>, Dominguez PM, Ghamlouch H, Aoufouchi S, Bernard OA, Melnick A\*, **Li S**\*. 2020. TET2 deficiency reprograms the germinal center B cell epigenome and silences genes linked to lymphomagenesis. *Sci Adv*. 6(25). PMID: PMC7299612.
4. Ashoor H, Chen X, Rosikiewicz W, Wang J, Cheng A, Wang P, Ruan Y, **Li S**. 2020. Graph embedding and unsupervised learning predict genomic sub-compartments from HiC chromatin interaction data. *Nat Commun*. 3;11(1):1173. PMID: PMC7054322.
5. Lee B, Wang J, Cai L, Kim M, Namburi S, Tjong H, Feng Y, Wang P, Tang Z, Abbas A, Wei CL\*, Ruan Y\*, **Li S**\*. 2020. ChIA-PIPE: A fully automated pipeline for comprehensive ChIA-PET data analysis and visualization. *Sci Adv*. 6(28):eaay2078. PMID: PMC7439456.
6. Zhao Y, Pan Z, Namburi S, Pattison A, Posner A, Balachander S, Paisie CA, Reddi HV, Rueter J, Gill AJ, Fox S, Raghav KPS, Flynn WF, Tothill RW\*, **Li S**\*, Karuturi RKM\*, George J\*. 2020. CUP-AI-Dx: A tool for inferring cancer tissue of origin and molecular subtype using RNA gene-expression data and artificial intelligence. *EBioMedicine*. 8;61:103030. PMID: PMC7553237.  
*Publication was highlighted as the **best paper of oncology** in Commentary 2020: A year to remember (doi: 10.1016/j.ebiom.2020.103185)*
7. Li P, Lu M, Shi J, Gong Z, Hua L, Li Q, Lim B, Zhang XH, Chen X, **Li S**, Shultz LD, Ren G. 2020. Lung mesenchymal cells elicit lipid storage in neutrophils that fuel breast cancer lung metastasis. *Nat Immunol*. 21(11):1444-1455. PMID: PMC7584447.
8. Karlebach G, Hansen P, Veiga DF, Steinhaus R, Danis D, **Li S**, Anczukow O, Robinson PN. 2020. HBA-DEALS: accurate and simultaneous identification of differential expression and splicing using hierarchical Bayesian analysis. *Genome Biol*. 21(1):171. PMID: PMC7358203.
9. Du M, Jillette N, Zhu JJ, **Li S**, Cheng AW. CRISPR artificial splicing factors. 2020. *Nat Commun*. 12;11(1):2973. PMID: PMC7293279.
10. Zhang Z, Zhou C, Li X, Barnes SD, Deng S, Hoover E, Chen CC, Lee YS, Zhang Y, Wang C, Metang LA, Wu C, Tirado CR, Johnson NA, Wongvipat J, Navrazhina K, Cao Z, Choi D, Huang CH, Linton E, Chen X, Liang Y, Mason CE, de Stanchina E, Abida W, Lujambio A, **Li S**, Lowe SW, Mendell JT, Malladi VS, Sawyers CL, Mu P. 2020. Loss of CHD1 Promotes Heterogeneous Mechanisms of Resistance to AR-Targeted Therapy via Chromatin Dysregulation. *Cancer Cell*. 13;37(4):584-598. PMID: PMC7292228.

11. Parsa S, Ortega-Molina A, Ying HY, Jiang M, Teater M, Wang J, Zhao C, Reznik E, Pasion JP, Kuo D, Mohan P, Wang S, Camarillo JM, Thomas PM, Jain N, Garcia-Bermudez J, Cho BK, Tam W, Kelleher NL, Socci N, Dogan A, De Stanchina E, Ciriello G, Green M.R., **Li S**, Birsoy K, Melnick AM, Wendel HG. 2020. The serine hydroxymethyltransferase-2 (SHMT2) initiates lymphoma development through epigenetic tumor suppressor silencing. *Nat Cancer*. **1**, 653–664. <https://doi.org/10.1038/s43018-020-0080-0>
12. Malkani S, Chin CR, Cekanaviciute E, Mortreux M, Okinula H, Tarbier M, Schreurs AS, Shirazi-Fard Y, Tahimic CGT, Rodriguez DN, Sexton BS, Butler D, Verma A, Bezdán D, Durmaz C, MacKay M, Melnick A, Meydan C, **Li S**, Garrett-Bakelman F, Fromm B, Afshinnekoo E, Langhorst BW, Dimalanta ET, Cheng-Campbell M, Blaber E, Schisler JC, Vanderburg C, Friedländer MR, McDonald JT, Costes SV, Rutkove S, Grabham P, Mason CE, Beheshti A. 2020. Circulating miRNA Spaceflight Signature Reveals Targets for Countermeasure Development. *Cell Rep*. **8**;33(10):108448. doi: 10.1016/j.celrep.2020.108448. PMID: 33242410.
13. Tong L, Wu PY, Phan JH, Hassazadeh HR, Hones WD, Shi L, Fischer M, Mason CE, **Li S**, et al., 2020. Impact of RNA-seq data analysis algorithms on gene expression estimation and downstream prediction. *Sci Rep*. **10**(1):17925. PMID: PMC7578822.
14. Taghbalout A, Du M, Jillette N, Rosikiewicz W, Rath A, Heinen CD, **Li S**, Cheng AW. 2019. Enhanced CRISPR-based DNA demethylation by Casilio-ME-mediated RNA-guided coupling of methylcytosine oxidation and DNA repair pathways. *Nat Commun*. **20**;10(1):4296. PMID: PMC6754513.
15. Dominguez PM, Ghamlouch H, Rosikiewicz W, Kumar P, Béguelin W, Fontán L, Rivas MA, Pawlikowska P, Armand M, Mouly E, Torres-Martin M, Doane AS, Calvo Fernandez MT, Durant M, Della-Valle V, Teater M, Cimmino L, Droin N, Tadros S, Motanagh S, Shih AH, Rubin MA, Tam W, Aifantis I, Levine RL, Elemento O, Inghirami G, Green MR, Figueroa ME, Bernard OA\*, Aoufouchi S\*, **Li S\***, Shaknovich R\*, Melnick AM\*. 2018. TET2 Deficiency Causes Germinal Center Hyperplasia, Impairs Plasma Cell Differentiation, and Promotes B-cell Lymphomagenesis. *Cancer Discov*. **8**(12):1632-1653. PMID: PMC6279514.
16. Rutherford SC, Fachel AA, **Li S**, Sawh S, Muley A, Ishii J, Saxena A, Dominguez PM, Caldas Lopes E, Agirre X, Chambwe N, Correa F, Jiang Y, Richards KL, Betel D, Shaknovich R. 2018. Extracellular vesicles in DLBCL provide abundant clues to aberrant transcriptional programming and genomic alterations. *Blood*. **132**(7):e13-e23. PMID: PMC6265635.
17. Zuo WL, Shenoy SA, **Li S**, O'Beirne SL, Strulovici-Barel Y, Leopold PL, Wang G, Staudt MR, Walters MS, Mason C, Kaner RJ, Mezey JG, Crystal RG. 2018. Ontogeny and Biology of Human Small Airway Epithelial Club Cells. *Am J Respir Crit Care*. **1**;198(11):1375-1388. PMID: PMC6290945.
18. Hassan C, Afshinnekoo E, **Li S**, Wu S, Mason CE. 2017. Genetic and epigenetic heterogeneity and the impact on cancer relapse. *Exp Hematol*. **54**:26-30. Review. PMID: PMC5651672.
19. Kleppe M, Spitzer MH, **Li S**, Hill CE, Dong L, Papalexi E, De Groote S, Bowman RL, Keller M, Koppikar P, Rapaport FT, Teruya-Feldstein J, Gandara J, Mason CE, Nolan GP, Levine

RL. 2017. Jak1 Integrates Cytokine Sensing to Regulate Hematopoietic Stem Cell Function and Stress Hematopoiesis. *Cell Stem Cell*. 21(4):489-501. PMID: PMC5847260.

20. **Li S**<sup>†</sup>, Garrett-Bakelman FE<sup>†</sup>, Chung SS, Sanders MA, Hricik T, Rapaport F, Patel J, Dillon R, Vijay P, Brown AL, Perl AE, Cannon J, Bullinger L, Luger S, Becker M, Lewis ID, To LB, Delwel R, Löwenberg B, Döhner H, Döhner K, Guzman ML, Hassane DC, Roboz GJ, Grimwade D, Valk PJ, D'Andrea RJ, Carroll M, Park CY, Neuberg D, Levine R, Melnick AM, Mason CE. 2016. Distinct evolution and dynamics of epigenetic and genetic heterogeneity in acute myeloid leukemia. *Nat Med*. 22(7):792-9. PMID: PMC4938719.
21. Teng M, Love MI, Davis CA, Djebali S, Dobin A, Graveley BR, **Li S**, Mason CE, Olson S, Pervouchine D, Sloan CA, Wei X, Zhan L, Irizarry RA. 2016. A benchmark for RNA-seq quantification pipelines. *Genome Biol*. 17:74. PMID: PMC4842274.
22. **Li S**<sup>†</sup>, Łabaj PP<sup>†</sup>, Zumbo P<sup>†</sup>, Sykacek P, Shi W, Shi L, Phan J, Wu PY, Wang M, Wang C, Thierry-Mieg D, Thierry-Mieg J, Kreil DP, Mason CE. 2014. Detecting and correcting systematic variation in large-scale RNA sequencing data. *Nat Biotechnol*. 32(9):888-95. PMID: PMC4160374.  
*Publication 20-22 were highlighted as the cover of Nature Biotechnology 2014 September issue.*
23. **Li S**<sup>†</sup>, Tighe SW<sup>†</sup>, Nicolet CM, Grove D, Levy S, Farmerie W, Viale A, Wright C, Schweitzer PA, Gao Y, Kim D, Boland J, Hicks B, Kim R, Chhangawala S, Jafari N, Raghavachari N, Gandara J, Garcia-Reyero N, Hendrickson C, Roberson D, Rosenfeld J, Smith T, Underwood JG, Wang M, Zumbo P, Baldwin DA, Grills GS, Mason CE. 2014. Multi-platform assessment of transcriptome profiling using RNA-seq in the ABRF next-generation sequencing study. *Nat Biotechnol*. 32(9):915-925. PMID: PMC4167418.
24. Su Z<sup>†</sup>, Łabaj P<sup>†</sup>, **Li S**<sup>†</sup>, et al., 2014. A comprehensive assessment of RNA-seq accuracy, reproducibility and information content by the Sequencing Quality Control Consortium. *Nat Biotechnol*. 32(9):903-14. PMID: PMC4321899.
25. **Li S**, Garrett-Bakelman F, Perl AE, Luger SM, Zhang C, To BL, Lewis ID, Brown AL, D'Andrea RJ, Ross ME, Levine R, Carroll M, Melnick A, Mason CE. 2014. Dynamic evolution of clonal epialleles revealed by methclone. *Genome Biol*. 15(9):472. PMID: PMC4242486.
26. Munro SA, Lund SP, Pine PS, Binder H, Clevert DA, Conesa A, Dopazo J, Fasold M, Hochreiter S, Hong H, Jafari N, Kreil DP, Łabaj PP, **Li S**, Liao Y, Lin SM, Meehan J, Mason CE, Santoyo-Lopez J, Setterquist RA, Shi L, Shi W, Smyth GK, Stralis-Pavese N, Su Z, Tong W, Wang C, Wang J, Xu J, Ye Z, Yang Y, Yu Y, Salit M. 2014. Assessing technical performance in differential gene expression experiments with external spike-in RNA control ratio mixtures. *Nat Commun*. 5:5125. PMID: 25254650.
27. Ricarte-Filho JC<sup>†</sup>, **Li S**<sup>†</sup>, Garcia-Rendueles ME, Montero-Conde C, Voza F, Knauf JA, Heguy A, Viale A, Bogdanova T, Thomas GA, Mason CE, Fagin JA. 2013. Identification of kinase fusion oncogenes in post-Chernobyl radiation-induced thyroid cancers. *J Clin Invest*. 123(11):4935-44. PMID: PMC3809792.
28. **Li S**, Garrett-Bakelman FE, Akalin A, Zumbo P, Levine R, To BL, Lewis ID, Brown AL, D'Andrea RJ, Melnick A, Mason CE. 2013. An optimized algorithm for detecting and

annotating regional differential methylation. *BMC Bioinformatics*. 14 Suppl 5:S10. PMID: PMC3622633.

29. Pipes L<sup>†</sup>, Li S<sup>†</sup>, Bozinoski M<sup>†</sup>, Palermo R, Peng X, Blood P, Kelly S, Weiss JM, Thierry-Mieg J, Thierry-Mieg D, Zumbo P, Chen R, Schroth GP, Mason CE, Katze MG. 2013. The non-human primate reference transcriptome resource (NHPRT) for comparative functional genomics. *Nucleic Acids Res*. 41(Database issue):D906-14. PMID: PMC3531109.
30. Meyer JA, Wang J, Hogan LE, Yang JJ, Dandekar S, Patel JP, Tang Z, Zumbo P, Li S, Zavadil J, Levine RL, Cardozo T, Hunger SP, Raetz EA, Evans WE, Morrison DJ, Mason CE, Carroll WL. 2013. Relapse-specific mutations in NT5C2 in childhood acute lymphoblastic leukemia. *Nat Genet*. 45(3):290-4. PMID: PMC3681285
31. Engström PG, Steijger T, Sipos B, Grant GR, Kahles A; RGASP Consortium, Alioto T, Behr J, Bertone P, Bohnert R, Campagna D, Davis CA, Dobin A, Engström PG, Gingeras TR, Goldman N, Grant GR, Guigó R, Harrow J, Hubbard TJ, Jean G, Kahles A, Kosarev P, Li S, et al.,. 2013. Systematic evaluation of spliced alignment programs for RNA-seq data. *Nat Methods*. 10(12):1185-91. PMID: PMC4018468.
32. Abdel-Wahab O, Gao J, Adli M, Dey A, Trimarchi T, Chung YR, Kuscu C, Hricik T, Ndiaye-Lobry D, Lafave LM, Koche R, Shih AH, Guryanova OA, Kim E, Li S, Pandey S, Shin JY, Telis L, Liu J, Bhatt PK, Monette S, Zhao X, Mason CE, Park CY, Bernstein BE, Aifantis I, Levine RL. 2013. Deletion of Asx1 results in myelodysplasia and severe developmental defects in vivo. *J Exp Med*. 210(12):2641-59. PMID: PMC3832937.
33. Akalin A, Kormaksson M, Li S, Garrett-Bakelman FE, Figueroa ME, Melnick A, Mason CE. 2012. methylKit: a comprehensive R package for the analysis of genome-wide DNA methylation profiles. *Genome Biol*. 13(10):R87. PMID: PMC3491415.
34. Zuo WL<sup>†</sup>, Li S<sup>†</sup>, Huang JH, Yang DL, Zhang G, Chen SL, Ruan YC, Ye KN, Cheng CH, Zhou WL. 2011. Sodium coupled bicarbonate influx regulates intracellular and apical pH in cultured rat caput epididymal epithelium. *PLoS One*. 6(8):e22283. PMID: PMC3159570.
35. Zuo WL, Du JY, Huang JH, Li S, Zhang G, Chen SL, Ruan YC, Cheng CH, Zhou WL. 2011. Tyrosine phosphorylation modulates store-operated calcium entry in cultured rat epididymal basal cells. *J Cell Physiol*. 226(4):1069-73. PMID: 20857412.
36. Zuo WL, Huang JH, Shan JJ, Li S, Wong PY, Zhou WL. Functional studies of acid transporter in cultured rat epididymal cell. 2010. *Fertil Steril*. 93(8):2744-9. PMID: 20362281
37. Du JY, Zuo WL, Ruan YC, Yang ZH, Chen MH, Chen SL, Li S, Wu ZL, Xiang H, Zhou WL. 2009. Stimulating effects of dopamine on chloride transport across the rat caudal epididymal epithelium in culture. *Biol Reprod*. 80(1):13-23. PMID: 18784353.

## Review and Opinions

1. Somarelli JA, Gardner H, Cannataro VL, Gunady EF, Boddy AM, Johnson NA, Fisk JN, Gaffney SG, Chuang JH, Li S, Ciccarelli FD, Panchenko AR, Megquier K, Kumar S, Dornburg A, DeGregori J, Townsend JP. 2020. Molecular Biology and Evolution of Cancer: From Discovery to Action. *Mol Biol Evol*. 1;37(2):320-326. PMID: PMC6993850.

2. **Li S**, Mason CE, Melnick A. Genetic and epigenetic heterogeneity in acute myeloid leukemia. 2016. *Curr Opin Genet Dev.* 36:100-6. Review. PMID: PMC4903929.
3. Vijay P, McIntyre AB, Mason CE, Greenfield JP, **Li S**. 2016. Clinical Genomics: Challenges and Opportunities. *Crit Rev Eukaryot Gene Expr.* 26(2):97-113. Review. PMID: PMC5470591.
4. **Li S** and Mason CE. 2014. The pivotal regulatory landscape of RNA modifications. *Annual Review of Genomics and Human Genetics.* 15:127-150. PubMed PMID: 24898039.

## **Software**

1. **methykit**: A comprehensive R package for the analysis of genome-wide DNA methylation and epigenetic sequencing profiles. (<http://code.google.com/p/methykit/>)
2. **edmr**: A R package for comprehensive DMR analysis based on bimodal normal distribution model and cost function for regional methylation analysis optimization. (<https://github.com/ShengLi/edmr>)
3. **methclone**: A C++ program for epigenetic clonal shift analysis using bisulfite conversion sequencing data. (<https://code.google.com/p/methclone/>)
4. **R-make**: A distributed analysis pipeline that processes RNA sequencing reads. (<http://physiology.med.cornell.edu/faculty/mason/lab/r-make/index.html>)
5. **Epihet**: A Bioconductor R package to assess intra-tumor epigenetic heterogeneity burden. (<http://bioconductor.org/packages/devel/bioc/html/epihet.html>)
6. **SCI**: A python package to detect 3D genome sub-compartments from HiC data. (<https://github.com/TheJacksonLaboratory/sci> and <https://github.com/TheJacksonLaboratory/sci-DNN>)
7. **ChIA-PIPE**: A ENCODE ChIA-PET data pipeline for comprehensive analysis and visualization. ([https://github.com/TheJacksonLaboratory/chia\\_pipe](https://github.com/TheJacksonLaboratory/chia_pipe))
8. **CUP-AI-Dx**: a deep-learning tool to infer a tumor's primary tissue of origin from its transcriptional signature for cancer of unknown primary. (<https://github.com/TheJacksonLaboratory/CUP-AI-Dx>)

## **Invited & Selected Talks**

### **International**

1. "Somatic mutations drive specific, but reversible epigenetic heterogeneity states in AML" (2020), American Association for Cancer Research Annual Meeting, San Diego, CA, USA.
2. "Computationally decoding the blueprints of tumor cells for immune escape" (2019), Xi'an Jiaotong University, Xi'an, China.
3. "Beyond the genome – decoding the cancer epigenome dynamics" (2018), Assisted Reproduction Technologies – long term perspectives, Krakow, Poland.
4. "CompartmentExplorer: an accurate method for genomic compartments prediction from 3D genome data" (2018), International Society for Computational Biology, Chicago, IL, USA.

5. "Disordered epigenetic regulation in acute myeloid leukemia" (2017), The American Society of Hematology Annual Meeting, Atlanta, GA, USA.
6. "Epigenome evolution in relapsed acute myeloid leukemia" (2016), American Association for Cancer Research Annual Meeting, New Orleans, LA, USA.
7. "Epigenome dynamics of cancer evolution" (2016), Ludwig Institute for Cancer Research, Oxford University, Oxford, UK.
8. "Leukemia epigenetic dynamics revealed through a novel algorithm and NGS technology" (2016), Institute of Genetics and Molecular Medicine, University of Edinburgh, Edinburgh, UK.
9. "Genetic and epigenetic tumor evolution in gliomatosis cerebri" (2015), Society for Neuro-Oncology Annual Meeting, San Antonio, TX, USA.
10. "Establishing clinical-grade RNA sequencing" (2015) Bio-IT World Conference & Expo, Boston, MA, USA.
11. "Detecting and correcting systematic variation in largescale RNA sequencing data" (2014), The 16th MAQC/SEQC Project Meeting by Fudan University and United States Food and Drug Administration, Shanghai, China.
12. "edmr: an optimized algorithm for detecting and annotating regional differential methylation" (2013), The 3th Annual Research in Computational Molecular Biology (RECOMB) satellite workshop on massively parallel sequencing, Beijing, China.
13. "RNA Sequencing data analysis framework by BAGET" (2011), Sequence Mapping and Assembly Assessment Project RGASP3 / DNGASP, Barcelona, Spain.

## **National**

1. "Epigenetic evolution and heterogeneity in acute myeloid leukemia" (2020), The Jackson Laboratory 29<sup>th</sup> Annual Short Course on Experimental Models of Human Cancer, Bar Harbor, ME, USA.
2. "Somatic mutations drive specific, but reversible epigenetic heterogeneity states in AML", (2020), Pennsylvania State University, Hershey, PA, USA.
3. "Beyond the double helix: a tumor epigenome odyssey" (2020), Northwestern University, Chicago, IL, USA.
4. "Beyond the double helix: a tumor epigenome odyssey" (2019), City University of New York, New York, NY, USA.
5. "Beyond the double helix: a tumor epigenome odyssey" (2019), Society for Molecular Biology & Evolution Satellite Workshop on the Molecular Biology and Evolution of Cancer. Yale University, New Haven, CT, USA.
6. "Cancer DNA methylome heterogeneity and evolution" (2019), Weill Cornell Medicine, New York, NY, USA.
7. "Mining the big data from 1D epigenome to 3D genome" (2019), The Jackson Laboratory Annual Scientific Symposium, Bar Harbor, ME, USA.
8. "Beyond the genome – deciphering the cancer DNA methylome dynamics" (2017), Workshop on 3D Genome Mapping Technology, Farmington, CT, USA.

9. "Genetic fuel for epigenetic heterogeneity in acute myeloid leukemia" (2017), The Jackson Laboratory Monthly Scientific Director's Forum, Farmington, CT, USA.
10. "Epigenetics of leukemic cells" (2017). Beth Israel Deaconess Medical Center/The Jackson Laboratory Immunotherapy Symposium, Boston, MA, USA.
11. "Epigenome dynamics of blood cancer" (2017), The Jackson Laboratory 26<sup>th</sup> Annual Short Course on Experimental Models of Human Cancer, Bar Harbor, ME, USA.
12. "Beyond the genome – decode the leukemia epigenome dynamics via a novel algorithm and high-throughput sequencing technology" (2017), NGS Tech & Applications Conference, Philadelphia, PA, USA.
13. "Deciphering the heterogeneous epigenome of acute myeloid leukemia" (2016), The New York Academy of Sciences, Epigenetics in Cancer: Translational Medicine Approaches, New York, NY, USA.
14. "Cancer epigenome dynamics revealed through a novel algorithm and next generation sequencing technology" (2016), Illumina, San Diego, CA, USA.
15. "Epigenome dynamics of cancer evolution" (2016), University of Florida, Gainesville, FL, USA.
16. "Cancer epigenome dynamics revealed through a novel algorithm and next generation sequencing technology" (2016), AbbVie, Chicago, IL, USA.
17. "Epigenome dynamics of cancer evolution" (2016), State University of New York Upstate, Syracuse, NY, USA.
18. "Cancer dynamics revealed through novel algorithms and next generation sequencing technology" (2016), Indiana University - Purdue University Indianapolis, Indianapolis, IN, USA.
19. "Epigenetic evolution in relapsed acute myeloid leukemia" (2015), NGS Data Analysis & Informatics Conference, San Diego, CA, USA.
20. "NGS normalization software comparison" (2015), Next Generation Sequencing (NGS) USA congress, Boston, MA, USA.
21. "The ABRF NGS study: A multi-platform assessment of transcriptome profiling by RNA-Seq" (2014), Genome Webinar Seminar Panelist.
22. "Epigenetic basis of acute myeloid leukemia relapse" (2014), Annual Conference of the Association of Biomolecular Resource Facilities, Albuquerque, NM, USA.
23. "Multi-platform and cross-methodological reproducibility of transcriptome profiling by RNA-seq" (2013), Northeast Regional Life Sciences Core Directors Conference of Association of Biomolecular Resource Facilities, New York, NY, USA.

## **Professional Experience**

### **1. *Ad Hoc* Reviewer for Scientific Journals**

*Cancer Discovery*

*Blood*

*Genome Biology*

*Science Advances*

*Nature Communications*

*Bioinformatics*



*BMC Biology*  
*Cancer Informatics*  
*BMC Genomics*  
*Genetics & Epigenetics*  
*Bioinformatics Research and Applications*

2. **Ad Hoc Reviewer for Grant Application**

*Worldwide Cancer Research*

3. **Conference Organizer**

The Jackson Laboratory Scientific Symposium, Bar Harbor, ME (2017-2020)

The Jackson Laboratory Faculty Retreat, Portland, ME (2017, 2020)

The Jackson Laboratory Cancer Center Annual Retreat (2020)

The Jackson Laboratory Computational Community Retreat (2020)

4. **Professional Associations:**

American Association of Cancer Research

International Society for Computational Biology

5. **Internship:**

Data Analyst, Future Talent Program, Merck & Co., Inc. Boston, MA (2011)

**Teaching**

- 2014 – 2017, 2019, 2021 *Guest lecturer*, “Epigenome dynamics of cancer evolution” in the course of Clinical and Research Genomics. Tri-Institutional MD/PhD program, New York, NY.
- 2016 *Guest lecturer*, “RNA-sequencing methods, standards and RNA modifications” in the course of Clinical and Research Genomics. Tri-Institutional MD/PhD program, New York, NY.
- 2014 *Instructor*, “DNA methylation bisulfite sequencing data analysis”. ICB Epigenomics Data Analysis, Weill Cornell Medical College, New York, NY.
- 2014 *Instructor*, “Basics of next-gen sequencing”. ICB Epigenomics Data Analysis, Weill Cornell Medical College, New York, NY.
- 2013 – 2014 *Teaching assistant*, “Clinical and Research Genomics”. Tri-Institutional MD/PhD program, New York, NY.
- 2013 *Teaching assistant*, “Epigenomics approaches in disease”. ICB Epigenomics Data Analysis, Weill Cornell Medical College, New York, NY.