Lea M. Starita, Ph.D.

Current Positions
Assistant Professor, Genome Sciences, University of Washington
Co-director, Advanced Technology Lab, Brotman Baty Institute for Precision Medicine

Contact Information

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Education

June 1999	Rutgers College, New Brunswick NJ B.A with Highest Honors in Molecular Biology and Biochemistry
December 2005	Harvard University, Cambridge MA Ph.D. in Biological and Biomedical Sciences Thesis Title: Substrates for the BRCA1/BARD1 Ubiquitin Ligase Thesis Advisor: Jeffrey D. Parvin, M.D., Ph.D

Post Graduate Training

2006 - 2012	Postdoctoral Fellow with Dr. Stanley Fields, Genome Sciences, University of Washington

Faculty Positions

2017 – 2021	Research Assistant Professor, Genome Sciences, University of Washington
2017 – present	Co-director, Advanced Technology Lab, Brotman Baty Institute for Precision Medicine
2021 – present	Assistant Professor, Genome Sciences, University of Washington

Honors and Awards

1999	Phi Beta Kappa, Rutgers University
2002	Massachusetts Department of Public Health, Breast Cancer Research Fellowship
2002 – 2005	U.S. Department of Defense, Breast Cancer Research Pre-doctoral Fellowship
2006 – 2007	University of Washington, Genome Sciences, Training Grant National Institutes of Health, Ruth L. Kirschstein National Research Service Award

Board Certification
N/A

Current Licenses to Practice
N/A

Diversity, Equity and Inclusion Activities

2019	Mentored Serina Young through the UW Genome Sciences Research Experience for Undergraduates (REU) program
2020 – present	Established the BBI Precision Medicine Scholars program by procuring funding for each of the Seattle REU programs at UW, SCRI and FH to fund an extra position each summer for these students.
2021 – present	Established and organized BBI Precision Medicine Event for the REU programs at UW, SCRI and FH to students to network with each other and faculty from the three institutes

2021	Mentored BBI Precision Medicine Scholar Amira Ellison through the UW Genome Sciences REU program
2021	Attended the Lavender Rights DEI training program

Professional Organizations

2018 – present	Seattle Flu Study, Investigator
2019 – present	Atlas of Variant Effect (AVE) Alliance, Founding Member and member of Executive Committee
2021 – present	Atlas of Variant Effect (AVE) Alliance, Founding co-chair of the Clinical Variant Interpretation Work Stream
2021 – present	Atlas of Variant Effect (AVE) Alliance, member of the Outreach, Diversity and Inclusion Committee
2021 – present	NHGRI GREGoR Consortium, co-chair of FONT, the functional genomics organizing committee
2021 – present	NHGRI GREGoR Consortium, variant to function subcommittee member
2021 – present	NHGRI IGVF Consortium, steering committee member
2021 – present	NHGRI IGVF Consortium, co-chair of the Catalog working group
2021 – present	UW Center for Environmental Forensic Science, executive committee

Teaching and Training Responsibilities

Graduate Students Trained

2018 – present	Florence Chardon (UW Genome Sciences; joint with Jay Shendure)
2019 – present	Shawn Fayer (UW Genome Sciences; joint with Doug Fowler)
2021 – 2022	Moez Dawood (CMAP Intern, Baylor College of Medicine)

Rotation Students

Fall 2021	Malvika Tejura (UW Genome Sciences)
Fall 2021	Elliott Swanson (UW Genome Sciences)
Winter 2022	Ben Mallory (UW Genome Sciences)

Graduate Students Committees

2018 – present	Eliah Overbey	UW Genome Sciences	Advisor: D. Hawkins
2019 – present	Nick Popp	UW MSTP, Genome Sciences	Advisor: D. Fowler
2020 – present	Austin Gabel	UW MSTP, Genome Sciences	Advisor: R. Bradley
2020 – present	Rachel Wellington	UW MCB	Advisor: S. Doulatov
2020 – present	Sayeh Gorjifard	UW Genome Sciences	Advisor: C. Queitsch
2021 – present	Chase Suiter	UW Genome Sciences	Advisor: J. Shendure
2021 – present	Moez Dawood	Baylor College of Medicine	Advisor: R. Gibbs
2021 – present	Cassia Wagner	UW MSTP, Genome Sciences	Advisor: T. Bedford

Postdocs Trained

2021 – present	Riddhiman Garge PhD, co-advised with Jay Shendure

Classroom Teaching

2017 & 2021	Guest lecture for Genome Sciences 372
2019 – 2021	Guest lecture for Genome Sciences 552 Technology for Genome Analysis
2021	Guest lecture for Genome Sciences 373

Editorial Responsibilities

N/A

Special International Responsibilities

Workshops & Courses

2018 – 2019	Multiplex assays for measuring variant effects, Lecture and workshop Clinical Genomics and NGS Course, Bertinoro, IT

International Conference Organization

2019 – present	CRISPR and Beyond: Perturbations at Scale to Understand Genomes Wellcome Genome Center, Hinxton, UK
2019 – present	Mutational Scanning Symposia and Workshop, Seattle, WA and Toronto, ON

Commercial Scientific Advisory Board and Consulting Roles

2019 – present	Nostos Genomics, Berlin, DE
2021	MediSix Therapeutics, Singapore

Documentary

2020	Took part in BBC documentary *54 Days* on the early days of Covid-19

Special National Responsibilities

2018	Grant review for the Mark Foundation
2021	Interviewed by CNN to discuss SARS-CoV-2 variants of concern
2021	Took part in Bloomberg documentary – *Why America is not ready for the next pandemic*
2021	Briefed Senator Patty Murray on the state of genomic surveillance and pandemic preparedness

Special Local Responsibilities

2019 – present	Member, Graduate Admissions Committee (UW Genome Sciences)
2019	Member, Seminar Series Committee (UW Genome Sciences)
2019	Briefed Washington State lawmakers on the scientific and economic impact of CRISPR technology, Olympia and Bellevue, March and June
2019	Organized the Brotman Baty Single Cell Symposium, Seattle, WA
2020	Lecture, Discovery Lunch Series, Washington Technology Alliance
2020	GeekWire interview in support of the BBI Mutational Scanning Symposium
2020	Panelist, Policy Matters Summit – Gene Editing and Biotechnology, Washington Technology Alliance
2020 – present	Laboratory testing for Seattle Coronavirus Assessment Network
2020 – present	Laboratory testing for UW's Husky Coronavirus Testing Program
2021	Interviewed by KOMO-TV to discuss SARS-CoV-2 variants of concern
2021	Interviewed by KIRO-TV to discuss SARS-CoV-2 variants of concern
2021	Interviewed by Seattle Times to SARS-CoV-2 variants of concern

Research Funding

Active Support

Brotman Baty Institute 9/29/2017 – 12/31/2022
The mission of the Brotman Baty Advanced Technology Lab is to bring advanced genomic technologies developed in Genome Sciences and elsewhere into production.
Role: Co-Director of the BBI Advanced Technology Lab

R01CA228083 | NIH/NCI | $477,448 (Starita) 12/1/2018 – 11/30/2023
Multiplexed functional analysis of BRCA1 and BARD1 missense variants in DNA repair
Role: Co-Investigator (PI: Parvin)

RM1HG010461 | NIH/NHGRI | $678,745 (Starita) 5/8/2019 – 2/28/2024
Center for the Multiplexed Assessment of Phenotype
Role: Co-Investigator (MPI: Fields, Fowler)

Seattle Flu Study | Gates Ventures | $10,749,844 (Starita) 11/1/2018 – 7/31/2022
The Seattle Flu Study is a large-scale pandemic monitoring and intervention program
Role: Co-PI

U01CA242954 | NIH/NCI | $30,606 (Starita) 9/1/2019 – 8/31/2022
Integrating germline variation data for estimating heritable cancer risk
Role: Co-Investigator (PI: Cline)

U01HG011744 | NIH | $639,222 (Starita) 4/1/2021 – 8/31/2026
University of Washington Mendelian Genomics Research Center
Role: Co-Investigator (MPI: Nickerson, Eichler, Bamshad)

U01HG011744 | NIH | $5,082,099 9/1/2022 – 5/31/2026
Center for Actionable Variant Analysis
Role: Contact PI (MPI: Starita, Fowler)

P425F204348 | US Department of Education (DOED) | $15,035 3/13/2020 – 9/30/2022
CARES Act Higher Education Emergency Relief Fund
PI: Hall

Completed Support
T32HG000035 | NIH NHGRI 9/26/2005 – 7/15/2007
Interdisciplinary Training in Genomic Sciences
Role: Trainee

F32GM080126 | NIH NIGMS | $99,000 (Starita) 7/16/2007 – 7/15/2009
Proteome-Wide Analysis of E3 Ubiquitin Ligase-Substrate Relationships
Role: PI

U01HG011744 | CDC | $749,911(total contract) 5/15/2021 – 2/15/2022
Viral genome sequencing and open source software development to support genetic epidemiology in Washington State
Role: Contact PI (MPI: Starita, Nickerson, Bedford)

Bibliography

A. Peer Reviewed Publications

1. Carr-Schmid A, Valente L, Loik VI, Williams T, **Starita LM**, Kinzy TG. Mutations in elongation factor 1beta, a guanine nucleotide exchange factor, enhance translational fidelity. Mol Cell Biol. 1999 Aug;19(8):5257-66. doi: 10.1128/MCB.19.8.5257. PMID: 10409717; PMCID: PMC84369.

2. Schlegel BP, **Starita LM**, Parvin JD. Overexpression of a protein fragment of RNA helicase A causes inhibition of endogenous BRCA1 function and defects in ploidy and cytokinesis in mammary epithelial cells. Oncogene. 2003 Feb 20;22(7):983-91. doi: 10.1038/sj.onc.1206195. PMID: 12592385.

3. **Starita LM**, Machida Y, Sankaran S, Elias JE, Griffin K, Schlegel BP, Gygi SP, Parvin JD. BRCA1-dependent ubiquitination of gamma-tubulin regulates centrosome number. Mol Cell Biol. 2004 Oct;24(19):8457-66. doi: 10.1128/MCB.24.19.8457-8466.2004. PMID: 15367667; PMCID: PMC516733.

4. Sankaran S, **Starita LM**, Groen AC, Ko MJ, Parvin JD. Centrosomal microtubule nucleation activity is inhibited by BRCA1-dependent ubiquitination. Mol Cell Biol. 2005 Oct;25(19):8656-68. doi: 10.1128/MCB.25.19.8656-8668.2005. PMID: 16166645; PMCID: PMC1265743.

5. **Starita LM***, Horwitz AA*, Keogh MC, Ishioka C, Parvin JD, Chiba N. BRCA1/BARD1 ubiquitinate phosphorylated RNA polymerase II. J Biol Chem. 2005 Jul 1;280(26):24498-505. doi: 10.1074/jbc.M414020200. Epub 2005 May 10. PMID: 15886201.

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6. Simons AM, Horwitz AA, **Starita LM**, Griffin K, Williams RS, Glover JN, Parvin JD. BRCA1 DNA-binding activity is stimulated by BARD1. Cancer Res. 2006 Feb 15;66(4):2012-8. doi: 10.1158/0008-5472.CAN-05-3296. PMID: 16489000.

7. Sankaran S, **Starita LM**, Simons AM, Parvin JD. Identification of domains of BRCA1 critical for the ubiquitin-dependent inhibition of centrosome function. Cancer Res. 2006 Apr 15;66(8):4100-7. doi: 10.1158/0008-5472.CAN-05-4430. PMID: 16618730.

8. Ozturk SB, Vishnu MR, Olarewaju O, **Starita LM**, Masison DC, Kinzy TG. Unique classes of mutations in the Saccharomyces cerevisiae G-protein translation elongation factor 1A suppress the requirement for guanine nucleotide exchange. Genetics. 2006 Oct;174(2):651-63. doi: 10.1534/genetics.106.059899. Epub 2006 Sep 1. PMID: 16951075; PMCID: PMC1602096.

9. Pujana MA,* Han JD,* **Starita LM**,* Stevens KN, Tewari M, Ahn JS, Rennert G, Moreno V, Kirchhoff T, Gold B, Assmann V, Elshamy WM, Rual JF, Levine D, Rozek LS, Gelman RS, Gunsalus KC, Greenberg RA, Sobhian B, Bertin N, Venkatesan K, Ayivi-Guedehoussou N, Solé X, Hernández P, Lázaro C, Nathanson KL, Weber BL, Cusick ME, Hill DE, Offit K, Livingston DM, Gruber SB, Parvin JD, Vidal M. Network modeling links breast cancer susceptibility and centrosome dysfunction. Nat Genet. 2007 Nov;39(11):1338-49. doi: 10.1038/ng.2007.2. Epub 2007 Oct 7. PMID: 17922014.
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10. **Starita LM**,* Lo RS,* Eng JK, von Haller PD, Fields S. Sites of ubiquitin attachment in Saccharomyces cerevisiae. Proteomics. 2012 Jan;12(2):236-40. doi: 10.1002/pmic.201100166. Epub 2011 Dec 20. PMID: 22106047; PMCID: PMC3337332.
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11. **Starita LM**,* Pruneda JN,* Lo RS, Fowler DM, Kim HJ, Hiatt JB, Shendure J, Brzovic PS, Fields S, Klevit RE. Activity-enhancing mutations in an E3 ubiquitin ligase identified by high-throughput mutagenesis. Proc Natl Acad Sci U S A. 2013 Apr 2;110(14):E1263-72. doi: 10.1073/pnas.1303309110. Epub 2013 Mar 18. PMID: 23509263; PMCID: PMC3619334.
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12. Swaney DL, Beltrao P, **Starita LM**, Guo A, Rush J, Fields S, Krogan NJ, Villén J. Global analysis of phosphorylation and ubiquitylation cross-talk in protein degradation. Nat Methods. 2013 Jul;10(7):676-82. doi: 10.1038/nmeth.2519. Epub 2013 Jun 9. PMID: 23749301; PMCID: PMC3868471.

13. Kitzman JO,* **Starita LM**,* Lo RS, Fields S, Shendure J. Massively parallel single-amino-acid mutagenesis. Nat Methods. 2015 Mar;12(3):203-6, 4 p following 206. doi: 10.1038/nmeth.3223. Epub 2015 Jan 5. PMID: 25559584; PMCID: PMC4344410.
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14. **Starita LM**, Young DL, Islam M, Kitzman JO, Gullingsrud J, Hause RJ, Fowler DM, Parvin JD, Shendure J, Fields S. Massively Parallel Functional Analysis of BRCA1 RING Domain Variants. Genetics. 2015 Jun;200(2):413-22. doi: 10.1534/genetics.115.175802. Epub 2015 Mar 30. Erratum in: Genetics. 2017 Dec;207 (4):1713. PMID: 25823446; PMCID: PMC4492368.

15. Lee C, Banerjee T, Gillespie J, Ceravolo A, Parvinsmith MR, **Starita LM**, Fields S, Toland AE, Parvin JD. Functional Analysis of BARD1 Missense Variants in Homology-Directed Repair of DNA Double Strand Breaks. Hum Mutat. **2015** Dec;36(12):1205-14. doi: 10.1002/humu.22902. Epub 2015 Sep 22. PMID: 26350354; PMCID: PMC6005381.

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17. Matreyek KA,* **Starita LM**,* Stephany JJ, Martin B, Chiasson MA, Gray VE, Kircher M, Khechaduri A, Dines JN, Hause RJ, Bhatia S, Evans WE, Relling MV, Yang W, Shendure J, Fowler DM. Multiplex assessment of protein variant abundance by massively parallel sequencing. Nat Genet. 2018 Jun;50(6):874-882. doi: 10.1038/s41588-018-0122-z. Epub 2018 May 21. PMID: 29785012; PMCID: PMC5980760.
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18. Findlay GM, Daza RM, Martin B, Zhang MD, Leith AP, Gasperini M, Janizek JD, Huang X, **Starita LM**,* Shendure J*. Accurate classification of BRCA1 variants with saturation genome editing. Nature. 2018 Oct;562(7726):217-222. doi: 10.1038/s41586-018-0461-z. Epub 2018 Sep 12. PMID: 30209399; PMCID: PMC6181777.
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19. **Starita LM**,* Islam MM,* Banerjee T, Adamovich AI, Gullingsrud J, Fields S, Shendure J, Parvin JD. A Multiplex Homology-Directed DNA Repair Assay Reveals the Impact of More Than 1,000 BRCA1 Missense Substitution Variants on Protein Function. Am J Hum Genet. 2018 Oct 4;103(4):498-508. doi: 10.1016/j.ajhg.2018.07.016. Epub 2018 Sep 12. PMID: 30219179; PMCID: PMC6174279.
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the Life Course During the 2018/19 Influenza Season. Clin Infect Dis. 2021 Sep 7;73(5):802-807. doi: 10.1093/cid/ciab131. PMID: 33590002; PMCID: PMC7929037.

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*co-corresponding authors

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B. Book Chapters

1. **Starita LM**, Fields S. Deep Mutational Scanning: Library Construction, Functional Selection, and High-Throughput Sequencing. Cold Spring Harb Protoc. 2015 Aug 3;2015(8):777-80. doi: 10.1101/pdb.prot085225. PMID: 26240405.

2. **Starita LM**, Fields S. Deep Mutational Scanning: Calculating Enrichment Scores for Protein Variants from DNA Sequencing Output Files. Cold Spring Harb Protoc. 2015 Aug 3;2015(8):781-3. doi: 10.1101/pdb.prot085233. PMID: 26240406.

C. Review Articles and Perspectives

1. **Starita LM**, Parvin JD. The multiple nuclear functions of BRCA1: transcription, ubiquitination and DNA repair. Curr Opin Cell Biol. 2003 Jun;15(3):345-50. doi: 10.1016/s0955-0674(03)00042-5. PMID: 12787778.

2. **Starita LM**, Parvin JD. Substrates of the BRCA1-dependent ubiquitin ligase. Cancer Biol Ther. 2006 Feb;5(2):137-41. doi: 10.4161/cbt.5.2.2479. Epub 2006 Feb 4. PMID: 16479151.

3. Gasperini M, **Starita LM**, Shendure J. The power of multiplexed functional analysis of genetic variants. Nat Protoc. 2016 Oct;11(10):1782-7. doi: 10.1038/nprot.2016.135. Epub 2016 Sep 1. PMID: 27583640; PMCID: PMC6690347.

4. Manolio TA, Fowler DM, **Starita LM**, Haendel MA, MacArthur DG, Biesecker LG, Worthey E, Chisholm RL, Green ED, Jacob HJ, McLeod HL, Roden D, Rodriguez LL, Williams MS, Cooper GM, Cox NJ, Herman GE, Kingsmore S, Lo C, Lutz C, MacRae CA, Nussbaum RL, Ordovas JM, Ramos EM, Robinson PN, Rubinstein WS, Seidman C, Stranger BE, Wang H, Westerfield M, Bult C. Bedside Back to Bench: Building Bridges between Basic and Clinical Genomic Research. Cell. 2017 Mar 23;169(1):6-12. doi: 10.1016/j.cell.2017.03.005. PMID: 28340351; PMCID: PMC5511379.

5. **Starita LM**, Ahituv N, Dunham MJ, Kitzman JO, Roth FP, Seelig G, Shendure J, Fowler DM. Variant Interpretation: Functional Assays to the Rescue. Am J Hum Genet. 2017 Sep 7;101(3):315-325. doi: 10.1016/j.ajhg.2017.07.014. PMID: 28886340; PMCID: PMC5590843.

6. Gelman H, Dines JN, Berg J, Berger AH, Brnich S, Hisama FM, James RG, Rubin AF, Shendure J, Shirts B, Fowler DM, **Starita LM**; Brotman Baty Institute Mutational Scanning Working Group. Recommendations for the collection and use of multiplexed functional data for clinical variant interpretation. Genome Med. 2019 Dec 20;11(1):85. doi: 10.1186/s13073-019-0698-7. PMID: 31862013; PMCID: PMC6925490.

7. Brnich SE, Abou Tayoun AN, Couch FJ, Cutting GR, Greenblatt MS, Heinen CD, Kanavy DM, Luo X, McNulty SM, **Starita LM**, Tavtigian SV, Wright MW, Harrison SM, Biesecker LG, Berg JS; Clinical Genome Resource Sequence Variant Interpretation Working Group. Recommendations for application of the functional evidence PS3/BS3 criterion using the ACMG/AMP sequence variant interpretation framework. Genome Med. 2019 Dec 31;12(1):3. doi: 10.1186/s13073-019-0690-2. PMID: 31892348; PMCID: PMC6938631.

8. Boeckh M, Chu HY, Englund JA, Lockwood CM, Nickerson DA, Shendure J, **Starita L**. The Seattle Flu Study: when regulations hinder pandemic surveillance. Nat Med. 2022 Jan;28(1):7-8. doi: 10.1038/s41591-021-01587-0. PMID: 34937879.

D. Preprints

1. Bedford T, Logue JK, Han PD, Wolf CR, Frazar CD, Pelle C, Ryke E,… **Starita LM**… et al. "Viral Genome Sequencing Places White House COVID-19 Outbreak into Phylogenetic Context." Epidemiology. medRxiv. 2020 https://doi.org/10.1101/2020.10.31.20223925.

2. Kline EC, Panpradist N, Hull IT, Wang Q, Oreskovic AK, Han PD, **Starita LM**, Lutz BR. Multiplex Target-Redundant RT-LAMP for Robust Detection of SARS-CoV-2 Using Fluorescent Universal Displacement Probes. medRxiv [Preprint]. 2021 Aug 23:2021.08.13.21261995. doi: 10.1101/2021.08.13.21261995. PMID: 34462755; PMCID: PMC8404892.

3. Gulati GK, Panpradist N, Stewart SWA, Beck IA, Boyce C, Oreskovic AK, García-Morales C, Avila-Ríos S, Han PD, Reyes-Terán G, **Starita LM**, Frenkel LM, Lutz BR, Lai JJ. Inexpensive workflow for simultaneous monitoring of HIV viral load and detection of SARS-CoV-2 infection. medRxiv [Preprint]. 2021 Aug 24:2021.08.18.21256786. doi: 10.1101/2021.08.18.21256786. PMID: 34462759; PMCID: PMC8404901.

4. Paredes MI, Lunn SM, Famulare M, Frisbie LA, Painter I, Burstein R, Roychoudhury P, Xie H, Mohamed Bakhash SA, Perez R, Lukes M, Ellis S, Sathees S, Mathias PC, Greninger A, **Starita LM**, Frazar CD, Ryke E, Zhong W, Gamboa L, Threlkeld M, Lee J, Nickerson DA, Bates DL,

Hartman ME, Haugen E, Nguyen TN, Richards JD, Rodriguez JL, Stamatoyannopoulos JA, Thorland E, Melly G, Dykema PE, MacKellar DC, Gray HK, Singh A, Peterson JM, Russell D, Torres LM, Lindquist S, Bedford T, Allen KJ, Oltean HN. Associations between SARS-CoV-2 variants and risk of COVID-19 hospitalization among confirmed cases in Washington State: a retrospective cohort study. medRxiv [Preprint]. 2021 Oct 27:2021.09.29.21264272. doi: 10.1101/2021.09.29.21264272. PMID: 34729567; PMCID: PMC8562551.

E. Clinical Trials

None

Invited Talks

National | International

Quantifying the functional impact of all possible missense mutations in BRCA1. GSA Yeast Meeting, Seattle WA, USA 2014

Massively parallel experimental analysis of missense mutations in *BRCA1* for interpreting clinical variants of uncertain significance. Plenary session, ASHG, Baltimore MD, September 2015

Massively parallel experimental analysis of missense mutations in *BRCA1,* Technology. Biology. Big Data. Cell Symposium, Berkeley CA, USA, October 2016

Massively parallel experimental analysis of missense mutations in *BRCA1* for interpreting clinical variants of uncertain significance*,* HGVS annual scientific meeting, Vancouver Canada, October 2016

Massively parallel experimental analysis of missense mutations in *BRCA1* for interpreting clinical variants of uncertain significance. NHGRI Genomic Medicine IX, Silver Spring MD USA April 2016

Massively parallel experimental analysis of missense mutations in *BRCA1* for interpreting clinical variants of uncertain significance. BRCA Symposium, Montreal Canada, May 2016

Multiplex assays for measuring variant effects. Spring Mutations, UCSF, QBI, San Francisco CA, March 2017

Multiplex assays for measuring variant effects. Keynote speaker, Australian Genomics Health Alliance, Adelaide Australia, November 2017

Multiplex assays for measuring variant effects. 8th Barossa Meeting, Barossa Valley Australia, November 2017

Multiplex assays for measuring variant effects. TOPMed2, NHLBI, Washington D.C., November 2017

Multiplex assays for measuring variant effects. Lecture and workshop Clinical Genomics and NGS Course, Bertinoro Italy, May 2018

Saturation genome editing for measuring the effect of SNV on BRCA1 function. ENIGMA consortium, Edinburgh United Kingdom, June 2018

The Future of Variant Interpretation, ENIGMA/BCAC/CIMBA consortium, Edinburgh United Kingdom, June 2018

Saturation genome editing for measuring the effect of SNV on BRCA1 function. ASHG, San Diego CA, September 2018

Multiplex assays for measuring variant effects. Leveraging Genomic Diversity, Keystone Symposium, Kampala Uganda, November 2018

Understanding the functional effects of coding variation, State of the Art Presentation, NHGRI 20/20 Strategic Planning Meeting, Silver Spring MD, January 2019

Multiplexed functional assays to assess BRCA1 variants, AACR, Atlanta GA, March 2019

Multiplex assays for measuring variant effects. Lecture and workshop Clinical Genomics and NGS Course, Bertinoro Italy, May 2019

Understanding the functional effects of coding variation at scale, European Society for Human Genetics, Gothenburg Sweden, June 2019

Multiplexed functional assays to assess BRCA1 variants, Coffee-Holden Prostate Cancer Academy, Los Angeles CA, June 2019

Understanding the functional effects of coding variation at scale, ENCODE User Meeting, Seattle WA, June 2019

Multiplexed functional assays to assess BRCA1 variants, Benzon Symposium, Copenhagen Denmark, September 2019

The Seattle Flu Study and early SARS-CoV-2 testing, keynote session, The Allied Genetics Conference, Virtual, April 2020

Understanding the functional effects of coding variation at scale, CRISPR and Beyond, Wellcome Genome Center, virtual, September 2020

The Seattle Flu Study, a pandemic surveillance platform, Association for Molecular Pathology, virtual, November 2020

Progress and Promise of MAVE for Clinical Variant Interpretation, Mutational Scanning Symposium 2021, virtual, April 2021

Understanding the functional effects of coding variation at scale, BRCA 2021, virtual, May 2021

Understanding the functional effects of coding variation at scale, Forum on Neuroscience and Nervous System Disorders, virtual, October 2021

Saturation Genome Editing of PALB2 Reveals Functionally Abnormal Missense Variants, ENIGMA consortium, virtual, October 2021

Regional
Understanding the functional effects of coding variation at scale, Klenk Symposium, Cologne Germany, September 2019

Understanding the functional effects of coding variation at scale, St. Jude Biomedical Symposium, Memphis TN, October 2019

Technology Development for Public Health, Keynote address, Lehigh Valley Molecular and Cellular Biology Society, virtual, April 2021

Local
Multiplex assays for measuring variant effects. HudsonAlpha, Huntsville AL, May 2018

Understanding the functional effects of coding variation at scale, Invited lecture, NCI Frederick MD, March 2019

Understanding the functional effects of coding variation at scale, Center for Genome Regulation, Barcelona Spain, February 2020

The Seattle Flu Study, a pandemic surveillance platform, OHSU Genome Sciences Seminar Series, virtual, November 2020

The Seattle Flu Study, a pandemic surveillance platform, UC Riverside Institute for Integrative Genome Biology (IIGB) virtual seminar program, virtual, November 2020

Technology Development for Public Health, Department of Molecular and Systems Biology Geisel School of Medicine, Dartmouth University, virtual, March 2021

The Seattle Flu Study, a pandemic surveillance platform, Keynote address, Biomedical Sciences Graduate Program Retreat, Ohio State University, virtual, October 2021.

Other Employment

2012-2015	Research Scientist with Dr. Stanley Fields, Genome Sciences, University of Washington
2015-2017	Research Scientist with Dr. Jay Shendure, Genome Sciences, University of Washington