

W GENOME SCIENCES

December Newsletter



Notes from the Chair

The Department of Genome Sciences began 2021, like much of the rest of the world, focused largely on COVID-19. After managing the department's transition to pandemic operations, our Chair, Stan Fields, took a long-planned and somewhat delayed start to his sabbatical in mid-December, 2020. I therefore write to you as Interim Chair, with just a few weeks left now before Stan's return.

From a scientific standpoint, members of the department were actively working to combat the virus. These efforts included substantial work by the Seattle Flu Study, which includes Genome Sciences PIs

Trevor Bedford, Debbie Nickerson, Jay Shendure, and Lea Starita, to provide at-home testing for Seattle residents as well as campus-based testing for UW students, faculty and staff, as well as extensive sequencing of SARS-CoV-2 genomes in collaboration with the State of Washington. Several Genome Sciences affiliate faculty at the Hutch, have conducted groundbreaking work in terms of deep mutational scanning (Jesse Bloom) and genomic epidemiology (Trevor Bedford) of SARS-CoV-2.

The pandemic also affected the department's day-to-day operations. By late March, anyone who wanted to was allowed to come back to Foege to do research, though masking rules remain in place and most meetings continue to be carried out by Zoom. Starting fall quarter, all courses have been carried out in person. In practice, however, on any given day a reasonably large proportion of department members still work from home. One step we took to address the challenge of decreased social interaction was to have an in-person retreat in September at the Sleeping Lady Resort in Leavenworth — with masking, social distancing, and many outdoor activities. Remote participants attended the scientific talks, including a fantastic keynote presentation from Beronda Montgomery, author of *Lessons from Plants*. You can see from the photo above how happy people were to reconnect with one another.

Perhaps our biggest success for the past year has been the recruitment of two outstanding new core faculty members and assisting in the recruitment of a new affiliate faculty member at the Hutch. Lea Starita (she/her) had been a Research Assistant Professor of Genome Sciences since 2017. She develops and applies advanced genomic technologies for interpreting genetic variants of unknown significance. She also serves as the co-director of The Brotman Baty Institute's Advanced Technology Lab and is a key member of the Seattle Flu Study. Lea began as an Assistant Professor on August 1, and has already landed a major grant, along with Doug Fowler, for the NIH's new Impact of Genomic Variation on Function project. Philip Abitua (he/him), a developmental biologist studying annual killifish and how they've evolved to survive in extreme environments, began as Assistant Professor on September 1. In addition to deep knowledge of early vertebrate development, Phil will bring cutting edge techniques into the department, such as single-cell analysis with live imaging of whole embryos. Finally, we are pleased that Nasa Sinnott-Armstrong (they/them) will be joining the Fred Hutch as an Assistant Member and Genome Sciences as an Affiliate Assistant Professor next year. Nasa's research focuses on gene-environment interactions and how social factors contribute globally to the genetic risk of cardiometabolic diseases. Nasa is particularly interested in education and plans to develop coursework bridging genetics and other disciplines, including environmental science, sociology, and engineering.

In addition, the department continues to make great scientific progress, as outlined below in the description of research highlights and list of faculty and trainee awardees. The department brought in >\$68 million in research funding, which is the highest amount for the past decade and includes 101 awards to 24 different faculty members. The department also received funding from the Curci Foundation, which is designed to increase our ability to recruit talented PhD students from other countries. In addition, we successfully applied to become part of the ARCS Foundation fellowship program, which provides resources to help with recruiting top applicants to our graduate program and

providing them community once they are here. The department has hosted a number of ARCS Scholars via the MSTP and MCB programs, so we are glad to be joining.

In recognition of the importance of diversity, equity, and inclusion (DEI) in all aspects of our program, the department convened a new DEI committee in September, 2020, composed of faculty, students, postdocs and staff. The committee has already accomplished a lot: formulating a department mission statement; significantly expanding the department's DEI web pages; creating the Genome Sciences Anonymous Incident Reporting system for tracking and responding to incidents of bias, bullying and harassment; instituting a weekly "Genome Sciences Community Lunches and Life Stories" aimed at building our community and promoting inclusivity; running a series of anti-racism training sessions for our training faculty; hosting quarterly departmental town hall meetings to discuss issues related to DEI; organizing a series of approximately monthly DEI symposia that provide interactive discussion on topics such as intersectionality, microaggressions, and ageism; and updating the department's application page to provide extensive advice on how best to prepare an application to graduate school. The committee is hard at work on a series of other initiatives in this area.

We were disappointed to have to postpone our 20-year anniversary symposium celebration due to the pandemic. The new date is tentatively set for November, 2022. More details will be forthcoming in the spring.

The department is grateful to all of you for your continuing support, and we look forward to another year of scientific and educational progress in 2022.

Happy New Year and best wishes for 2022.

Bill Noble
Interim Chair

New Faculty



Genome Sciences is pleased to announce that **Dr. Lea Starita** has accepted our offer to be an assistant professor. Lea develops and applies advanced genomic technologies for interpreting genetic variants of unknown significance. She also serves as the co-director of The Brotman Baty Institute's Advanced Technology Lab and is a key member of the Seattle Flu Study.



Genome Sciences is pleased to announce that **Dr. Philip Abitua** has accepted our offer to be an assistant professor. Phil is a developmental biologist studying annual killifish and how they've evolved to survive in extreme environments. In addition to deep knowledge of early

vertebrate development, Phil brings cutting edge techniques into the department, such as single-cell analysis with live imaging of whole embryos.

News & Honors



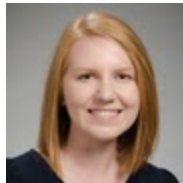
NIH Awards \$16 million as Part of ‘Impact of Genome Variation on Function’ Consortium



Dr. Trevor Bedford and Dr. Erick Matsen have been selected as HHMI Investigators. Dr. Trevor Bredford has also been named a MacArthur Genius.



Dr. Jean-Benoît Lalanne has been awarded a Damon Runyon Fellowship.



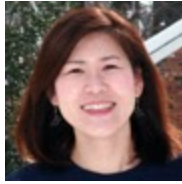
Dr. Renee Geck, Miranda Mudge, and Ryan Carlson have been awarded NRSA fellowships



Dr. Kelley Harris has been awarded the SMBE Early Career Faculty Award.



Robin Aguilar has been awarded an HHMI Gilliam Graduate Fellowship.



Soyeon Showman has been awarded The Bonita and David Brewer Fellowship.

Research Updates

Beliveau Lab: [PaintSHOP enables the interactive design of transcriptome- and genome-scale oligonucleotide FISH experiments](#)

Berg Lab: [Detecting New Allies: Modifier Screen Identifies a Genetic Interaction Between Imaginal disc growth factor 3 and comover, a Rho-kinase Substrate, During Dorsal Appendage Tube Formation in Drosophila](#)

Berger Lab: [Discovery of synthetic lethal and tumor suppressor paralog pairs in the human genome](#)

Bloom Lab: [Complete Mapping of Mutations to the SARS-CoV-2 Spike Receptor-Binding Domain that Escape Antibody Recognition](#)

Bradley Lab: [Pharmacologic modulation of RNA splicing enhances anti-tumor immunity](#)

Brewer-Raghuraman Lab: [Phenotypic and Genotypic Consequences of CRISPR/Cas9 Editing of the Replication Origins in the rDNA of Saccharomyces cerevisiae](#)

Dunham Lab and Fowler Lab: [Massively parallel characterization of CYP2C9 variant enzyme activity and abundance](#)

Eichler Lab: [The structure, function and evolution of a complete human chromosome 8](#)

Feder Lab: [Understanding patterns of HIV multi-drug resistance through models of temporal and spatial drug heterogeneity](#)

Fields Lab: [Expanding the binding specificity for RNA recognition by a PUF domain](#)

Harris Lab: [A modified fluctuation assay reveals a natural mutator phenotype that drives mutation spectrum variation within Saccharomyces cerevisiae](#)

Jarvik Lab: [Variant Classification Concordance using the ACMG-AMP Variant Interpretation Guidelines across Nine Genomic Implementation Research Studies](#)

King Lab: [Genetics of schizophrenia in the South African Xhosa](#)

Manoil Lab: [Ranking essential bacterial processes by speed of mutant death](#)

Matsen Lab: [Combining genotypes and T cell receptor distributions to infer genetic loci determining V\(D\)J recombination probabilities](#)

Monnat Lab: [Unsupervised discovery of dynamic cell phenotypic states from transmitted light movies](#)

Nickerson Lab: [Germline SAMD9L truncation variants trigger global translational repression](#)

Noble Lab: [Single-cell landscape of nuclear configuration and gene expression during stem cell differentiation and X inactivation](#)

Queitsch Lab: [Synthetic promoter designs enabled by a comprehensive analysis of plant core promoters](#)

Shendure Lab: [A human cell atlas of fetal chromatin accessibility](#)

Starita Lab and Fowler Lab: [Closing the gap: Systematic integration of multiplexed functional data resolves variants of uncertain significance in BRCA1, TP53, and PTEN](#)

Swanson Lab: [Recurrent Duplication and Diversification of Acrosomal Fertilization Proteins in Abalone](#)

Valdmanis Lab: [Characterizing nucleotide variation and expansion dynamics in human-specific variable number tandem repeats](#)

Villen Lab: [Identification of phosphosites that alter protein thermal stability](#)

