PACBIO®

Attend our afternoon workshop

The Sequel™ System:
Covering all the Bases with SMRT® Sequencing

Wednesday, February 15
3:40 p.m. – 4:40 p.m.
Grand Ballroom

High-Quality Genomes, Transcriptomes & Epigenomes
Jonas Korlach, Ph.D., CSO, PacBio

***De Novo* Sequencing of the Naked Mole-Rat Genome**
Margaret Roy, M.S., Head of Genomics Sequencing, Calico Life Sciences LLC

High-Throughput HLA Class I Whole Gene and HLA Class II Long-Range Typing on PacBio® RS II and Sequel Platforms
Nezih Cereb, M.D., CEO & Co-founder, Histogenetics

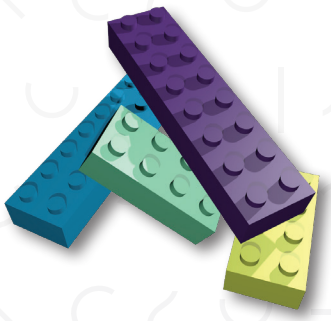
SMRT Sequencing Program Presentations

Tuesday, February 14

Concurrent Session: General Biology, Great Hall 2

7:30 – 7:50 PM
Jason Underwood, PacBio/University of Washington
"Long-read genome assembly and full-length transcript profiling of stem cells from great apes "

7:50 – 8:10 PM
Daniel Neafsey, Broad Institute of MIT and Harvard
"A community effort using multiple technologies to produce a dramatically improved genome assembly of the Zika virus mosquito vector"



Wednesday, February 15

Concurrent Session: Informatics, Great Hall 4 – 6

7:30 - 7:50 PM
Mark DePristo, Verily Life Sciences
"Mastering variant calling of SNPs and small indels with deep neural networks"

8:10 – 8:30 PM
Michael Schatz, Cold Spring Harbor Laboratory and Johns Hopkins University
"Personalized phased diploid genomes of the EN-Tex samples"

Concurrent Session: Transcriptome & Epigenomics, Great Hall 2

9:10 – 9:30
Theodore Davis, New England Biolabs
"APOBEC-Seq: An enzymatic method for methylome analysis at single-base resolution without bisulfite treatment"

Experience the PacBio 'Mini' Bar in Suite 317

Stop by our suite to discuss the latest Sequel® System data & workflows. At our 'mini' bar, create your very own minifigure doppelgänger.

Happy Hour: PacBio Suite 317 Tuesday at 5:15 p.m. & Wednesday at 6:15 p.m.

Beach Volleyball Anyone?

It's an annual tradition! Meet at the court near the Kids Area at the Diplomat Hotel at 7:30 a.m. on Tuesday and Wednesday morning. Drinks and snacks provided.

Poster Presentations featuring SMRT Sequencing

Great Hall 3

Odd-numbered posters are presented on Tuesday, 1:00 – 2:30 p.m.
Even-numbered posters are presented on Wednesday, 4:45 – 6:10 p.m.

105: Targeted SMRT Sequencing of difficult regions of the genome using a Cas9, non-amplification-based method
Tyson A. Clark, et al. PacBio

113: Improved library construction methods for the Pacific Biosciences sequencing platform using Swift custom Accel-NGS 2S linear ligation module for the PacBio® kit applied to challenging BAC clones for human genome reference improvement
Robert S. Fulton, et al. Washington University in Saint Louis

116: A whole genome SMRT Sequencing protocol that requires significantly less DNA input but maintains the ability to detect structural variants
Toumy Guettouche, et al. Roche Sequencing

210: Affordable long-read sequencing using the PacBio Sequel System
Yi Han, et al. Baylor College of Medicine

218: Detecting splice isoforms and fusion transcripts in single-cell transcriptomes using long-read sequencing
Iain C. Macaulay, et al. Earlham Institute

307: T-cell receptor profiling using PacBio sequencing of SMARTer libraries
Steve Oh, et al. PacBio

311: CRISPR-Cas9-Targeted SMRT Sequencing of medically relevant DNA repeat expansions
James C. Powell, et al. Icahn School of Medicine

404: Using the PacBio Sequel System to taxonomically and functionally classify metagenomic samples in a trial of patients undergoing fecal microbiota transplantation
Richard Hall, et al. PacBio

505: Personal diploid methylomes via analysis of phased heterozygous variants and single-molecule real-time sequencing
Yuta Suzuki, et al. The University of Tokyo

509: Generation of local reference genomes using PacBio and BioNano data, and analysis of the "dark matter" of structural variants in 1000 Swedish genomes
Ulf Gyllensten, et al. Uppsala University

515: SMRT Sequencing of barcoded amplicons with large short tandem repeat expansions
Shinichi Morishita, et al. The University of Tokyo

517: Single-molecule sequencing reveals the presence of distinct JC polyomavirus populations in patients with progressive multifocal leukoencephalopathy
Lars Paulin, et al. University of Helsinki

605: Clumpify: a new approach to read error correction
Brian Bushnell, Joint Genome Institute

703: Complex rearrangements and oncogene amplifications revealed by whole-genome long-read sequencing of a highly rearranged cancer cell line
Maria Nattestad, et al. Cold Spring Harbor Laboratory

709: Quantifying the impact of improved genome assemblies on functional genomics
Fritz J. Sedlazeck, et al. Johns Hopkins University

715: Structural variant detection with low-fold coverage PacBio sequencing
Aaron Wenger, et al. PacBio

804: Using the PacBio Iso-Seq method to search for novel colorectal cancer biomarkers
Meredith Ashby et al. PacBio

915: Comparison of somatic fusion calling from short-read versus long-read sequencing approaches reveals unexpected fusion diversity
Andrew V. Uzilov, et al. Icahn School of Medicine at Mount Sinai

1004: Analysis methods for amplification-free SMRT Sequencing and assessment on repeat expansions in Huntington's disease
Adam Ameur, et al. Uppsala University

1102: Profiling populations and diversity of gene pools with highly accurate single-molecule reads
Cheryl Heiner, et al. PacBio

1106: *De novo* PacBio long-read assembled avian genomes correct and add to genes important in neuroscience and conservation research
Jonas Korlach, et al. PacBio

1109: A method to improve read length of SMRT Sequencing
Justin Lenhart, et al. Swift Biosciences

1113: New advancements in next-generation sequencing approaches to address a variety of biological questions
Monika Mehta, et al. CCR Sequencing Facility

1213: Pacific Biosciences' standard blunt-end library preparation can produce a significant number of artefactual fusion DNA sequences
Xiaolin Wu, et al. Leidos Biomedical Research

1404: Whole-genome sequencing to determine origin of a recurrent multistate outbreak of *Salmonella Agona*
Maria Hoffmann, et al. U.S. Food and Drug Administration

1406: The use of 10x Genomics and Pacific Biosciences technologies to overcome heterozygous genome assembly challenges
Lisa Mathew, et al. Weill Cornell Medicine-Qatar

1016: Screening and characterization of causative structural variants for bipolar disorder in a significantly linked chromosomal region on Xq24-q27 in an extended pedigree from a genetic isolate
Jenny M. Ekholm, et al. PacBio

1105: A high-quality genome assembly of SMRT sequences reveals long-range haplotype structure in the diploid mosquito *Aedes aegypti*
Sarah Kingan, et al. PacBio

1107: A method for the identification of variants in Alzheimer's disease candidate genes and transcripts using hybridization capture combined with long-read sequencing
Steve Kujawa, et al. PacBio