



PacBio Applications Workshop

Monday November 12th, 2:00 PM – 5:30 PM
Auditorium B, Génopode Building
University of Lausanne, Dorigny

Agenda

- 2:00 – 2:10 Welcome and Core Facility Overview
Keith Harshman, Ph.D., Genomic Technologies Facility, Center for Integrative Genomics
- 2:10 – 2:30 Single Molecule Real Time Sequencing – Current Performance and Future Outlook
Ralph Vogelsang, Ph.D., Pacific Biosciences
- 2:30 – 3:00 Using Pacbio Data for the Oak Genome Assembly
Sandra P. Calderon Copete, Vital-IT / Swiss Institute of Bioinformatics
- 3:00 – 3:30 Using PacBio Sequencing to Elucidate the Functions of DNA Adenine Methylation in *Caulobacter crescentus*
Diego Gonzalez, Department of Fundamental Microbiology, UNIL
- 3:30 – 4:00 Break with Coffee and Cake
- 4:00 – 4:30 Methylome Analysis of Different Neisseria Pathogens
Christoph D. Schmid, PhD, Swiss Tropical and Public Health Institute, Basel
- 4:30 – 5:00 Gap Closure and Sequencing Bias Analysis Using Pacbio Sequencing Data
Laurent Falquet, PhD, Vital-IT / Swiss Institute of Bioinformatics
- 5:00 – 5:30 New and Upcoming Applications of PacBio SMRT Sequencing Technology
Gerrit Kuhn, Ph.D., Pacific Biosciences

Organizers

Keith Harshman, University of Lausanne, Genomic Technologies Facility
Phone: 0041-21-692-3906 Email: keith.harshman@unil.ch
Ralph Vogelsang, Pacific Biosciences
Phone: 0049 176 76588857 E-mail: rvogelsang@pacificbiosciences.com