

SYMPOSIUM Oakland Center, Lake Huron Room, March 7, 2019

Morning Session: Functional Genomics

9:00 am	Khrystyna Schubelka9:20Oakland UniversityamGenetic basis of the	Sophia Chaudhry9:40 amWayne State Universityam	Valerie Irizarry University of Michigan Crosstalk between tumor
	twinning phenomenon in humans	novel risk factors in hereditary ovarian cancer patients	cells and it's microenvironment during pancreatic cancer
10:20 am	Reagan Miller10:40Oakland UniversityamAnalyzing the Role ofEndothelial CellActivation in AML	Dominic Mier Oakland University11:00 amCRISPR Generated Knockout of a Novel Splicing Factor Involved in the Splicing of U12 Type Introns11:00 am	Justin Kulchycki Oakland University A Molecular Switch for Cell Type-Specific B4galnt2 Expression in Mice

Welcome Note 12:00 Dr. Ora Hirsch Pescovitz President, Oakland University

Keynote Lecture 12:10 Dr. Stephen J O'Brien,

Professor, NOVA Southeastern University "Promises-promises. Has the genome science revolution fulfilled a few?"

Lunch

1:00-2:00

Afternoon Session: Computational Genomics

2:00 pm	Alexandra Weber University of Michigan	2:20 pm	Anton Mahama Oakland University	2:40 pm	Wilfried Guiblet Penn State University
	Identifying structural variation in the human genome using whole genome sequencing data		Domain-level analysis of low complexity regions: an Archaea example		Non-B DNA Structures Affect Replication Speed, Sequencing Errors, and Mutation Rates
3:20 pm	Kirill Grigorev Cornell University	3:40 pm	Ashley Superson Oakland University	4:00 pm	Sarah Medley Oakland University
	Comparative circadian transcriptomics: novel and conserved features of the mammalian pineal gland		Using a taxon sampling pipeline to explore robustness of the Tree of Life		A bioinformatics approach to identify new candidate immunogenic regions in Plasmodium
4:20 pm	Edmundo Torres- Gonzales Penn State University	4:40 pm	Walter W. Wolfsberger Oakland University	5:00 pm	Israel Rivera The University of Georgia
	Insights from Ancestry studies in Puerto Rico		Visualisation tools for population genetics analyses, based on study of Puerto Rican horse breeds		Evolution of intracellular survival in Bordetellae

Q&A

Rochester Royal Park Hotel 6:00-7:00

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