

# GENETICS & GENOMICS

## MAY 8<sup>th</sup> ~ 9<sup>th</sup> 2019

| Date  | Time             | Track                                                                       | Presentation Title                                                                                                                                             | Speaker                                                                                                                                                                                 |
|-------|------------------|-----------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 8-May | 06:00 - 07:00 AM | The Epigenome in Health and Disease                                         | Novel DNA Methylation in Mammals                                                                                                                               | Tao Wu, PhD<br>Assistant Professor, CPRIT Scholar for Cancer Research, Department of Molecular and Human Genetics, Dan L Duncan Comprehensive Cancer Center, Baylor College of Medicine |
| 8-May | 06:00 - 09:00 AM | Progression in Genome Editing Including Single Base Editing and Application | Upgrading the CRISPR Toolbox - New Strategies Sharpen the CRISPR-Cas9 Scissors Utilizing Visualization and Chromatic Accessibility                             | Michelle Ding, M.S.<br>R&D Scientist, MilliporeSigma<br>Yanfang Jiang, PhD<br>Senior R&D Scientist, MilliporeSigma                                                                      |
| 8-May | 07:30 - 08:30 AM | Interpreting Genome Sequence Information from Telomere to Telomere          | Keynote Presentation: Interpreting the Zero \$ Genome via Base Editing, Organoids & in Situ Omics                                                              | George M. Church, PhD<br>Professor of Genetics, Director of the Center for Computational Genetics, Harvard Medical School                                                               |
| 8-May | 09:00 - 10:00 AM | Progress in Genome Editing Including Single Base Editing and Application    | Circular Synthesized CRISPR/Cas gRNAs for Functional Interrogations in Single and Multiplex Formats                                                            | Manuel Kaulich, PhD<br>CSO, Vivlion                                                                                                                                                     |
| 8-May | 09:00 - 10:00 AM | Interpreting Genome Sequence Information from Telomere to Telomere          | Development of an Arrayed Whole Human Genome KO Library for Functional Genomics Screening, Using an Optimized Multi-sgRNA Approach                             | Kevin Holden, PhD<br>Head of Science, Synthego                                                                                                                                          |
| 8-May | 10:30 - 11:30 AM | Progression in Genome Editing Including Single Base Editing and Application | Discovering Cellular Mechanisms and Biomarkers in Anti-PD1 Non-Responders Using Ingenuity Pathway Analysis Software and OmicSoft OncoLand Datasets from QIAGEN | Devendra Mistry, PhD<br>Senior Field Application Scientist, QIAGEN Advanced Genomics                                                                                                    |
| 8-May | 10:30 - 11:30 AM | Interpreting Genome Sequence Information from Telomere to Telomere          | Using Networks to Understand Cancer Risk                                                                                                                       | John Quackenbush, PhD<br>Professor of Computational Biology and Bioinformatics, Chair of the Department of Biostatistics, Harvard University, Dana-Farber Cancer Institute              |

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| 8-May | 12:00<br>-<br>01:00<br>PM | Interpreting Genome Sequence Information from Telomere to Telomere        | Next-Generation Transcriptome and miRNome Sequencing: Intelligent Approaches to Insightful Outcomes            | Jonathan Shaffer, PhD, MBA<br>Director, R&D, NGS Assay Technologies, QIAGEN                                                                                             |
| 8-May | 01:30<br>-<br>02:30<br>PM | Interpreting Genome Sequence Information from Telomere to Telomere        | Highly Accurate Long Sequence Reads for Comprehensive Genomic Analysis                                         | Jonas Korlach, PhD<br>Chief Scientific Officer, Pacific Biosciences                                                                                                     |
| 9-May | 06:00<br>-<br>07:00<br>AM | Interpreting Genome Sequence Information from Telomere to Telomere        | AI-Driven Literature Curation for Determining Genomic Variant Pathogenicity                                    | Mark Kiel, MD, PhD<br>Co-Founder and Chief Science Officer, Genomenon                                                                                                   |
| 9-May | 07:30<br>-<br>08:30<br>AM | The Epigenome in Health and Disease                                       | Keynote Presentation: Big Data and Health                                                                      | Michael Snyder, PhD<br>Professor and Chair, Genetics, Director, Stanford Center for Genomics and Personalized Medicine, Stanford University School of Medicine          |
| 9-May | 09:00<br>-<br>10:00<br>AM | Interpreting Genome Sequence Information from Telomere to Telomere        | Completing the Human Genome: The Progress and Challenge of Satellite DNA Assembly                              | Karen Miga, PhD<br>Assistant Research Scientist; UCSC Genomics Institute, University of California, Santa Cruz                                                          |
| 9-May | 09:00<br>-<br>10:00<br>AM | Polygenic Risk Scores: PheWas and GWAS and Utility of Biobank Information | Polygenic Risk Scores: PheWas and GWAS and Utility of Biobank Information                                      | Guillaume Paré, MD, MSc, FRCPC<br>Associate Professor, Director, Genetic and Molecular Epidemiology Laboratory, McMaster Genome Institute                               |
| 9-May | 10:30<br>-<br>11:30<br>AM | Interpreting Genome Sequence Information from Telomere to Telomere        | Background and Troubleshooting for RT-PCR                                                                      | Gillian Browne, PhD<br>Global Market Development Scientist, Gene Editing and Novel Modalities, MilliporeSigma                                                           |
| 9-May | 10:30<br>-<br>11:30<br>AM | Chromosomal Instability, Somatic Cell Recombination and Genomic Stability | Somatic Gene Recombination in the Brain                                                                        | Jerold Chun, MD, PhD<br>Professor and Senior Vice President, Sanford Burnham Prebys Medical Discovery Institute                                                         |
| 9-May | 12:00<br>-<br>01:00<br>PM | Interpreting Genome Sequence Information from Telomere to Telomere        | A Metagenomic Assay to Interrogate the Role of Virome and Microbiome in Cancer                                 | Erle Robertson, PhD<br>Harry P. Schenck Endowed Chair Professor, Vice-Chair, Department of Otorhinolaryngology, Perelman School of Medicine, University of Pennsylvania |
| 9-May | 01:30<br>-<br>02:30<br>PM | Interpreting Genome Sequence Information from Telomere to Telomere        | The NIH Rare Disease Undiagnosed Diseases Network; Lessons Learnt and Challenges Faced in the First Four Years | Liz Worthey, PhD<br>Faculty Investigator, HudsonAlpha Institute for Biotechnology                                                                                       |