08:30-09:00 Registrations

Independence B

conferenceseries.com 09:00-09:30 **Opening Ceremony**

Keynote Forum

09:30-10:10 **Title: Resistance to endocrine therapy in breast cancer: A systems biology approach**
Robert Clarke, Georgetown University Medical Center, USA

10:10-10:50 **Title: InfoMaps: Anticipatory linked context sensitive access to broadly heterogeneous data**
Georges Grinstein, University of Massachusetts Lowell and Weave Visual Analytics, USA

Networking & Refreshment Break: 10:50-11:10 @ Foyer

Major Sessions:
Structural Bioinformatics | Systems Biology | Evolutionary Bioinformatics

Session Chair: Hugo Geerts, In Silico Biosciences, USA
Session Co-chair: Gregory J Tawa, National Institutes of Health, USA

11:10-11:40 **Title: From big data to smart data in CNS disorders, developing predictive models by combining systems biology with quantitative systems pharmacology**
Hugo Geerts, In Silico Biosciences, University of Pennsylvania, USA

11:40-12:10 **Title: Beyond molecular structure: Biomarker discovery and drug repurposing using gene coexpression modules**
Gregory J Tawa, National Institutes of Health, USA

12:10-12:40 **Title: Evolution-informed biomarker discovery for precision oncology**
Li Liu, Arizona State University, USA

Lunch Break: 12:40-13:30 @ Benjamin's

13:30-14:00 **Title: Exploring tumor biology via integrated analysis of tumor transcriptome datasets with MiSTIC**
Sylvie Mader, Université de Montréal, Canada

14:00-14:30 **Title: Application of multi scale modeling of vascular tumor growth**
Matthias Reuss, University of Stuttgart, Germany

14:30-15:00 **Title: An integrative model to improve anemia treatment in non-small cell lung carcinoma patients**
Ursula Klingmueller, German Cancer Research Center, Germany

15:00-15:30 **Title: Interactions of a novel class of beta-lactam antibiotics with their targets penicillin-binding proteins from different sources studied by covalent docking approach**
Anna Marabotti, University of Salerno, Italy

Networking & Refreshment Break: 15:30-15:50 @ Foyer

15:50-16:20 **Title: Quantitative analyses of protein-protein in living cells using Fluorescence Correlation Spectroscopy and Fluorescence Cross Correlation Spectroscopy**
Heinz Peter Nasheuer, National University of Ireland Galway, Ireland

16:20-16:50 **Title: Comparative metagenomic analysis of soil microbial communities across three hexavalent chromium contamination levels isolated from chromite mine area**
Sukanta K Pradhan, Orissa University of Agriculture and Technology, India

Panel Discussion

Day 2 **August 23, 2016**

Independence B

Keynote Forum

09:05-09:45 **Michael Christman,** Coriell Institute for Medical Research, USA

09:45-10:25 **Title: Identification of early drivers of *HBV* associated Hepatocarcinogenesis**
Mark A Feitelson, Temple University, USA

Networking & Refreshment Break: 10:25-10:45 @ Foyer

Sessions:
Computational Systems Biology | Bioinformatics Technologies in Medicine | Stitching Bioinformatics Approach to Pharmacy

Session Chair: Heinrich Roder, Biodesix, Inc., USA
Session Co-chair: Ravi Radhakrishnan, University of Pennsylvania, USA

Session Introduction

10:45-11:15	**Title: Bridging the gap: From hypothesis-independent tests to understanding of biological mechanisms** **Heinrich Roder,** Biodesix, Inc., USA
11:15-11:45	**Title: *In silico* oncology: Computational horizons in cancer systems biology and multiscale cancer modeling** **Ravi Radhakrishnan,** University of Pennsylvania, USA
11:45-12:15	**Title: Explore cancer genomic databases to support immuno-oncology drug discovery** **Junping Jing,** GlaxoSmithKline R&D, USA
12:15-12:45	**Title: Inhibitor design for blocking the protein-carbohydrate interactions** **Shijun Zhong,** Dalian University of Technology, China

Lunch Break: 12:45-13:30 @ Benjamin's

13:30-14:00	**Title: High-throughput investigation of protein-DNA substrate coevolution in meganuclease family enzymes** **Thomas A McMurrough,** Western Univeristy, Canada
14:00-14:20	***Video Presentation:* A novel data-driven identification and activity scoring of functional modules – The case of a cell differentiation process - and a minimal graphical language (bStyle) to model and simulate biological processes** **Corrado Priami,** The Microsoft Research - University of Trento COSBI, Italy

Posters Session: 14:20-15:00

