

Abiri, Najmeh Stacked Denoising Autoencoder Imputation: An Approach to Impute Missing Values	39
Abou EL-Wafa, Wael Hardware implementation for parallel Multiple sequence alignment based on Smith-Waterman algorithm	40
Ahlbrandt, Janko The semantic gap in medical data – basic requirements for smart analysis of big medical data	41
Ambler, Jon GenGraph toolkit, simple generation and manipulation of graph genomes.	42
Barjatya, Aditi Redefining Biological Health Data into Actionable Intelligence	43
Bastkowski, Sarah Genetic and Phenotypic Determinants of Flavonoid Absorption and Metabolism	44
Benjak, Andrej Phylogeny of <i>Mycobacterium leprae</i> using whole genome sequencing	45
Birol, Inanc ntCard: Cardinality estimation of genomics data through a streaming algorithm	46
Butkiewicz, Mariusz Predicting the translational consequences of reading-frame changes induced by stop-lost and frame-shift variants	47
Chacon, Diego Analysis of chromosomal instability in 123 breast cancer samples through integrative proteogenomics	48
Dangi, Vijay An Interdisciplinary Approach to Study Northern Indian Subcontinent Jatland Population	49

Dasgupta, Abhishek		
Metagenomics Approach for determining the bacterial diversity of Digboi, India (the birthplace of Asia's oldest refinery)	50	
D'Aurizio, Romina		
Enhancing copy number variants detection from whole-exome and target sequencing data using EXCAVATOR2	51	
David-Rus, Diana		
Data mining and statistical methods for smFRET data analyses	52	
Elhefnawi, Mahmoud		
Copy number variation detection application on top of Apache Spark	53	
Elsheikh, Samar		
Summary Association Statistics Obtained from Genome-Wide Association Studies, a New Era of Whole Genome Studies	54	
Gao, Xu		
Relationship of tobacco smoking and smoking-related DNA methylation with epigenetic age acceleration	55	
Grosse-Holz, Friederike		
Mapping the protease repertoire of the agroinfiltrated apoplast	56	
Grossman, Robert		
An Overview of the NCI Genomic Data Commons Data Harmonization Process and Some Lesson Learned	57	
Heyer, Robert		
Deciphering the functioning of microbial communities by metaproteomics	58	
Kiani, Narsis A.		
Perturbation Multi - Omic Signature of Multiple Sclerosis: Connecting Proteins, Disease, and Small Compounds	59	
Kumar, Abhishek	Presenter: Paramasivam, Nagarajan	
Big Data meets Familial Cancer	60	

Kusnezowa, Anna		
In silico approach for the design of metagenomic libraries for functional analysis		61
Leuenberger, Pascal		
Cell-wide analysis of protein thermal unfolding across species unravels the determinants of proteome stability		62
M. Labib, Rania		
CYP2B6rs2279343 is associated with improved survival of Pediatric Rhabdomyosarcoma treated with Cyclophosphamide		63
Mahmoud, Alkhansa		
Insulin levels correlated to age in normal health women		64
Marabita, Francesco	Presenter: Horemuz, Michal	
A pilot study of the simultaneous analysis of sensor and molecular data from an athlete		65
Petelczyc, Monika		
When prevention failed and after diagnosis the proper medical treatment should be proposed: the nonlinear methods in cardiological risk assessment		66
Petrosyan, Armen		
Energy- information evaluation of chemical reactions by modeling arithmetic graphs		67
Pireddu, Luca		
Scalable genomics: from raw data to aligned reads on Apache Yarn		68
Ramoul, Abir		
Co-occurrence of blaNDM-1 with blaOXA-23 or blaOXA-58 in clinical multidrug-resistant Acinetobacter baumannii isolates, Algeria.		69
Raposo, Alexandre		
Ascl1 coordinately regulates gene expression and the chromatin landscape during neurogenesis		70

Restrepo, Nicole	
Exploring the heritability of Age-related Macular Degeneration endophenotypes in the Ohio Amish	71
Sidhu, Rishi	
Application of Technology and Mathematics to Biology: A case study in integrating Metabolomic Data and Gene Expression data for improved Metabolic Pathway Modeling	72
Sudhesan, Anjana	
Association of CRP +1846C/T (rs1205) gene polymorphism with psoriasis risk in South Indian Tamils	74
Taus, Thomas	
Inferring selection coefficients and dominance parameters from Pool-seq time series E&R data	76
Thiesen, Hans-Juergen	
The combined analysis of CNA and RNA expression analysis leads to gene sets that distinguish high grade and low grade clear cell renal cell carcinoma (ccRCC)	77
Tiwary, Basant K.	Presenter: Roy, Sujata
Analysis of Gene Network and Application of Barabasi-Albert model to find out the core genes involved in Glaucoma	78
Tomic, Branko	
Synergy of large scale data in thrombophilia etiopathology elucidation -web based platform approach	79
van Dam, Jesse	
RDF2Graph a tool to recover, understand and validate the ontology of an RDF resource	80

van Nimwegen, Erik	Presenter: Pachkov, Mikhail	
Completely automated gene regulatory network inference from RNA-Seq and ChIP-Seq data		81
Weidemann, Andreas		
Data and Model Management for Distributed Systems Biology Projects		82
Wicik, Zofia		
Specific sequence variants in DNA repair genes are associated with successful aging in Polish Caucasians: the POLGENOM project		83
Zhulin, Igor		
Establishing the precise evolutionary history of a gene improves prediction of disease-causing missense mutations		84