

2016 International Conference on Bioinformatics and Systems Biology (BSB 2016)

**Allahabad, India
4-6 March 2016**



**IEEE Catalog Number: CFP16F86-POD
ISBN: 978-1-5090-2262-5**

**Copyright © 2016 by the Institute of Electrical and Electronics Engineers, Inc
All Rights Reserved**

Copyright and Reprint Permissions: Abstracting is permitted with credit to the source. Libraries are permitted to photocopy beyond the limit of U.S. copyright law for private use of patrons those articles in this volume that carry a code at the bottom of the first page, provided the per-copy fee indicated in the code is paid through Copyright Clearance Center, 222 Rosewood Drive, Danvers, MA 01923.

For other copying, reprint or republication permission, write to IEEE Copyrights Manager, IEEE Service Center, 445 Hoes Lane, Piscataway, NJ 08854. All rights reserved.

******This publication is a representation of what appears in the IEEE Digital Libraries. Some format issues inherent in the e-media version may also appear in this print version.***

IEEE Catalog Number:	CFP16F86-POD
ISBN (Print-On-Demand):	978-1-5090-2262-5
ISBN (Online):	978-1-5090-2261-8

Additional Copies of This Publication Are Available From:

Curran Associates, Inc
57 Morehouse Lane
Red Hook, NY 12571 USA
Phone: (845) 758-0400
Fax: (845) 758-2633
E-mail: curran@proceedings.com
Web: www.proceedings.com

CURRAN ASSOCIATES INC.
proceedings
.com

BSB 2016

2016 International Conference on Bioinformatics and Systems Biology

March 04-06

Indian Institute of Information Technology, Allahabad, India

<https://wbsb.iita.ac.in/>

Table of Contents

S. No.	Title
01	Identification of Transcription Hubs that Control Lipid Metabolism and Carbon Concentrating Mechanism in Model Microalgae <i>Chlamydomonas reinhardtii</i> Using Regulatory Networks 1 Rahila Sardar, Kashif M. Shaikh, Pavan P. Jutur
02	Copy Number Variation Detection Workflow using Next Generation Sequencing Data 5 Prashanthi Dharanipragada, Nita Parekh
03	<i>In-silico</i> based designing of inhibitors against the virulence and filamentation of <i>Candida albicans</i>, a common human pathogen 10 Sonali Mishra, Krishna Misra
04	<i>In-silico</i> peptide based vaccine against Hepatitis C virus 14 Vikas Kaushik, Joginder Singh, Nidhi Sharma
05	Cross hybridization to <i>Arabidopsis thaliana</i> array reveals cold stress responsive genes in <i>Lepidium latifolium</i> 18 Atul Grover, Sadhana Singh, Basant Ballabh Bhatt, Mohammad Nasim, Pramod Katara
06	Modeling and Simulation Analysis of <i>Salmonella typhimurium</i> inside Human Epithelial Cells 22 Devender Arora, Vineet Singh, Ajeet Singh
07	Theoretical Model of Circular RNA Prediction and Classification 26 Rajnish Kumar, Tapobrata Lahiri, Gautam Kumar
08	Molecular modeling and dynamics study of nonsynonymous SNP in bread wheat HSP16.9B gene 31 Bharati Pandey, Saurabh Gupta, Atmakuri Ramakrishna Rao, Dev Mani Pandey, Ravish Chatrath
09	Extraction of associated quantitative traits by association mining 35 Kalpana Singh, Manish Kumar, Sekhar Verma
10	<i>In-silico</i> structure prediction and domain characterization of Inter alpha trypsin inhibitor heavy chain 4 39 Ankita Sharma, Pooja Kumari, Soundhara Rajan G, Rajesh Malhotra, Sagarika Biswas
11	Meta-analysis of potential miRNA in <i>Triticum aestivum</i> reveals their genome biased association with different metabolisms 44 Deepthi Nigam, Puneet Kumar Kadimi, Sanjeev Kumar, Dwijesh Chandra Mishra, Pankaj Pandey, Manoj Kumar Singh, Anil Rai, Subodh Kumar Sinha
12	Molecular interaction and simulation analysis for thyroid cancer pathway 49 Chandramani, Vaishali Mishra, Shilpa Chauhan, Manish Kumar Gupta
13	Identification of Conserved regulatory motif signatures in Human miRNA upstream regions 53 Pankaj Kumar Singh, Jayita Roy, Protip Basu, Vineet Vishal, Abhisek Ranjan Bera, Abhaydeep Pandey, Rahul Banik, Sayak Ganguli
14	Evolutionary divergence and comparative homology modeling analysis of LpxC enzyme from human pathogenic bacteria 56 Ayon Pal, Asim K Bothra, Uttam K Mandal, Subhasis Mukhopadhyay
15	Glycolysis as a determinant of genome and proteome composition of different extremophilic archaea species 61 Ayon Pal, Asim K Bothra, Subhasis Mukhopadhyay
16	Exploring the role of EZH2 (PRC2) as epigenetic target 66 Imlimaong Aier, Utkarsh Raj
17	Systems biology approach for gene set enrichment and topological analysis of Alzheimer's disease pathway 69 Ashwani kumar, Tiratha Raj Singh
18	Monitoring Deforestation using Acoustic Signals 74 Gajendra Sharma, Manish Kumar, Shekhar Verma
19	Stilbene analogues as inhibitors of breast cancer Stem cells through P-glycoprotein efflux; A 3D Quantitative Structure-Activity Relationship study 78 Anushree Tripathi, Krishna Misra
20	Improving extraction of protein – protein interaction datasets from KUPS using hashing approach 82 Gautam Kumar, Rajnish Kumar, Manoj Kumar Pal, Pragya Gupta, Rahul Gupta, Somya Mehra
21	Statistical discrimination of breast cancer microarray data 86 Gautam Kumar, Tapobarata Lahiri, Rajnish Kumar
22	Prediction of catalytic site of proteins based on amino acid triads approach using non parametric function 90 Shweta Srivastava, Gautam Kumar, Tapobarata Lahiri, Rajnish Kumar, Manoj Kumar Pal, Pragya Gupta, Rahul Gupta
23	<i>In silico</i> screening of <i>Prevotella intermedia</i> 17 identifies Lipopolysaccharide biosynthesis pathway genes as potential drug targets 94 Nithya Mathivanan, Kiruthika.G, Rahavi Subashree
24	QSAR Model Development for Solubility Prediction of Paclitaxel 98 Nupur S Munjal, Narendra Kumar, Manu Sharma, Chittaranjan Rout
25	Antimicrobial peptide Microcin C7 as an alternative drug candidate against Diphtheria toxin 102 Sumedha Ojha, Kanika Kundu, Subir Kundu
26	Estimating Percentage Epigenetic Modifications in human genome using NGS data 106 Aamna Lawrence, Rahul Shukla, Utkarsh Raj, Pritish Kumar Varadwaj
27	DrovePred: Server for DNA stem and BIME's Prediction using Particle Swarm Optimization 110 Aman Chandra Kaushik, Avinash Dhar, Shakti Sahi
28	3D structure prediction and molecular dynamics simulation studies of GPR139 115 Aman Chandra Kaushik, Shakti Sahi

S. No.	Title
29	Deciphering the structural community from the Deulajhari hot spring using the next-generation sequencing 119 Archana Singh, Mahendra Gaur, Enketeswara Subudhi
30	In silico Identification of Novel Virulent Protein of Phytophthora infestans related to Late Blight Disease 124 Rashmi Tripathi, Pawan Sharma, Pavan Chakraborty, Pritish Varadwaj
31	Structural and Functional annotation of human ALOX-5 129 Swechha Mishra, Sangeeta Singh
32	Count-based transcriptome analysis to identify differentially expressed genes for Breast Cancer 133 Rashmi Tripathi, Pawan Sharma, Pavan Chakraborty, Pritish Varadwaj
33	Who are the key players behind a disease state?: Outcomes of a new computational approach on cancer data 138 Jeethu V. Devasia, Priya Chandran
34	Noninvasive Arterial Blood Pressure Monitoring by active sensor based on the principle of pulse wave compensation 142 Antsiperov V, Mansurov G, Polupanov A, Basil Bonch-Bruevich
35	A new PVC/SPB detection method based on analytical spectra technique 146 Antsiperov VE, Bugaev AS, ZabrosaeV IV
36	Comprehensive Computational analysis of Chromosome 11 150 Abhivyakti Srivastava, Mottadi Shiva, Priyanka Kumari, Yasha Hasija
37	ShinyMDE: Shiny Tool for Microarray Meta-analysis for Differentially Expressed Gene Detection 154 H L Shashirekha, Agaz Hussain Wani
38	Discovery of cancer linked biomarker genes through common subcluster mining 159 Arnab Sadhu, Balaram Bhattacharyya
39	Identification of functional genetic variants in miRNA binding site in genes associated with lung cancer 164 Anju Gupta, Priyanka Kumari, Mottadi Shiva, Yasha Hasija
40	Predicting Conserved Domain and Structural Variations of Prenyl Transferase Sequence Variants in <i>Triticum urartu</i> 167 Mamta Sagar, Pramod Wasudev Ramteke
41	Identification of co-regulated genes of chick pea under abiotic stress 171 Dwijesh Chandra Mishra, Shikha Mittal, Indra Singh, Sanjeev Kumar, Anil Rai
42	Embryo and Endosperm Specific Comparative Transcriptome Analysis of <i>Triticum aestivum</i> in response to ABA and H2O2 Stress 175 Saurabh Gupta, Utkarsh Raj, Himansu Kumar, Pritish Kumar Varadwaj, Adhyana Gupta
43	Genome Analysis of <i>Rhizobium</i> Species using Codon Usage Bias Tools 179 Niyati Rai, D. C. Mishra, Sanjeev Kumar, Anil Rai, K. K. Chaturvedi, S.B. Lal, Anil Kumar, Mohammad Samir Farooqi, P. G. Majumdar, Sunil Archak
44	Genome-wide analysis and identification of abiotic stress responsive transcription factor family genes and miRNAs in bread wheat 183 Sarika Sahu, A. R. Rao, S. K. Muthusamy, K. C. Bansal, V. Chinnusamy
45	A bioinformatics study of miRNAs and their regulating targets in <i>Curcuma longa</i> (turmeric) 187 Noopur Singh, Swati Srivastava, Ashok Sharma
46	In silico interaction studies of first dual inhibitor against BACE-1/GSK-3β 190 Akhil Kumar, Gaurava Srivastava, Ashok Sharma
47	Glucose concentration varies logarithmically under both glycemic conditions in a computationally reconstructed human energy pool network (HEPNet) 194 Abhishek Sengupta, Priyanka Narad
48	A Method of Analysis of EEG Wave Trains in Early Stages of Parkinson's Disease 198 Olga S. Sushkova, Alexei A. Morozov, Alexandra V. Gabova
49	Identification of Human Proteins vulnerable to Multiple Organisms 202 S. Chatterjee, B.S. Sanjeev
50	A neural network based model of M and P LGN cells 206 Kuntal Ghosh
51	An account of Genomic Islands of zoonotic origin <i>Staphylococcus aureus</i> genomes – in silico approach 211 Relangi Tulasi Rao, Saghya Infant Shofia, Abhijit Manna, Kannan Jayakumar