

Accepted Demonstrations for InCoB/ISCB-Asia 2011 (as of Oct 11, 2011)		
Submission No.	Author(s)	Title
152	Sara Ballouz, Jason Liu, Richard George, Naresh P. Bains, Arthur Liu, Martin Oti, Bruno Gaeta, Diane Fatkin and Merridee Wouters	Gentrepid: a web server for candidate disease gene prediction
153	D.B.R.K. Gupta Udatha, Irene Kouskoumvekaki, Lisbeth Olsson and Gianni Panagiotou	Descriptor-based computational analysis reveals a novel classification scheme for feruloyl esterase enzyme families
181	Mohamed Mysara, Jonathan M Garibaldi and Mahmoud Elhefnawi	MysiRNA-Designer: a workflow for efficient siRNA design
183	Nadav Rappoport and Michal Linial	PANDORA concept graph – a source for functional insights from genomics and proteomics data
193	Nadav Rappoport, Nathan Linial and Michal Linial	ProtoNet: automatic organization of the 10 million protein sequences into an evolutionary driven family tree
200	Rajarajan Swaminathan, Indu Purushothaman, Sangeetha Kothandan and Madhan Mohan T	Potential "Antibiotics" from flowering plants - a unique database
208	Philippe Rocca-Serra, Eamonn Maguire and Susanna-Assunta Sansone	ISA community: supporting and enabling standards-compliant experimental curation
234	Paul Horton	fastapl and fastqpl, flexible tools for processing fasta and fastq format data
Accepted Posters for InCoB/ISCB-Asia 2011 (as of Oct 11, 2011)		
Submission No.	Author(s)	Title
Databases, Software Tools and Technology		
170	Jia Shiun Khoo and Mohd Firdaus-Raih	Assessing computational tools for RNA secondary structure prediction
175	Marie-Jean Meurs, René Witte, Gregory Butler, Justin Powlowski and Adrian Tsang	mycoMINE: a semantic text mining system for Lignocellulose research
209	Sebastián E Gutiérrez-Maldonado, Raul Araya-Secchi, Maria Jose Retamal, Ulrich G Volkman and Tomas Perez-Acle	Molecular ordering of dotriacontane supported on silica surfaces
185	Nanfeng Xu, Yipeng Du, Ming Lu and Tingting Li	hUbiquitome: a database of experimentally verified ubiquitination cascades in human
188	Pedro Ballester and John Mitchell	RF-score: a machine learning-based scoring function for molecular docking
222	Unitsa Sangket, Surakameth Mahasirimongkol, Wasun Chantratita, Pichaya Tandayya and Yuri S Aulchenko	ParallABEL: an R library for speedup of GWAS applying parallel computing
191	Anmol Kiran, John O'Mahony, Komal Sanjeev and Pavel Baranov	DARNED: the database of RNA editing
225	Nurul Nadzirin and Mohd. Firdaus Raih	Catalytic site comparison for functional assignment of crystallographic structures of hypothetical proteins
228	Anna Protasio, Isheng Jason Tsai and Matthew Berriman	A systematically improved high quality genome and transcriptome of the human blood fluke Schistosoma mansoni.
230	Maria Secrier and Reinhard Schneider	Understanding temporal patterns in cell cycle regulation through visualization
233	Hazrina Yusof Hamdani and Mohd Firdaus Mohd Raih	The unbroken network of hydrogen bond of RNA structures
108	Che-Lun Hung, Yaw-Ling Lin, Kuan-Ching Li and Guan-Jie Hua	CloudTSS: a TagSNP selection approach on cloud computing
117	Neeraja Krishnan, Prakhar Gaur, Rakshit Choudhury and Binay Panda	COPS: a sensitive and accurate tool for detecting copy number alterations in paired samples using short-read sequence data
119	Richard Newton and Lorenz Wernisch	Rwui, a web application to create user friendly web interfaces for R scripts
122	Priyanka Dhingra, Bharat Lakhani, Avinash Mishra, Satyanarayan Rao, Shashank Shekhar and B Jayaram	BHAGEERATH-H: a homology ab initio hybrid software suite for protein tertiary structure prediction
124	Naoyuki Asakawa, Seiichi Kibayashi, Ryoichi Kataoka, Junichi Goto and Noriaki Hirayama	AutoGPA : A novel 3D-QSAR method based on grid potential analysis and pharmacophore alignment
169	A Sri Devan and Mohd Firdaus Raih	Computational annotation of tertiary motifs in RNA crystallographic structures
199	Yuo-Hung Hsiao, Tse-Yi Wang and Kuang-Chi Chen	The study of disease comorbidity networks using Taiwan Medicare data
Disease Informatics		
202	Mahmoud M Elhefnawi, Suher Zada, Gehad Abdelrahman and Marwa Amer	A study of deregulated miRNA targets in hepatocellular carcinoma identifies novel insights into oncogenesis and drug targets
180	Han-Chu Hsu, Wei-Chung Shia and Fang-Rong Hsu	Genetic copy number variation in breast cancer
221	Allay Maududi, Mella Ferania, Chris Adhianto, Takenori Nitta, Yukio Hattori and Rini Puspitaningrum	D-loop mutation variation in Indonesian diabetes mellitus type 2
231	Muhammad Mamduh Ahmad Zabidi, Christopher Dawson, Siew Pey Gan, Pathmanathan Rajadurai, Vijaya Kumar Krishnan, Paul Lim, Selvaratnam Govindaraju, Lai Meng Looi, Alan Khoo, John Arrand, Paul Murray, Ching Ching Ng, Soo Hwang Teo and Lee Fah Yap	Four - Jointed Box 1 (FJX1) is a candidate oncogene in nasopharyngeal carcinoma
235	Yun Sunmin, Je-Gun Jung, Jihun Kim and Ju Han Kim.	The Network of disease-association with Etiological Factors on the Epigenomic Layer
236	Junhee Yoon, Jihun Kim and Ju Han Kim.	Drug response phenotype standardization and SNP-phenotype reliability score
126	Md Aminul Hoque, Fumio Ishizaki and Kohei Akazawa	Risk classification and nomogram development for the prostate cancer recurrence after radical prostatectomy
146	Yun Khoon Liew, Neela Vasanthakumari, Rukman Awang Hamat and Syafinaz Amin Nordin	Identifying Staphylococcus aureus infection diseases-specific proteins
150	Wilson Wen Bin Goh	A pipeline for MS data – an application towards liver cancer
Drug Design and Discovery		
182	Kejian Wang and Lun Yang	Deciphering the carditoxicity of blockbuster drugs by drug off-system – Vioox® and Avandia® as case study
217	Mahmoud Elhefnawi, Mohamed Omar and Mohamed Amin	Combination of ligand-based, structure-based and target-trained design for finding novel inhibitors of the Hepatitis c virus NS5B polymerase with acceptable ADMET profiles
218	Sukanta Mondal and Kenji Mizuguchi	A comparative analysis of the intrinsic dynamics of pantothenate synthetases
112	Sonika Malik, Suchi Sharma and Narayan Latha	Structure prediction and peptidomimetics based inhibitor design for CARD15/NOD2 using computational approaches: Implications in Crohn's disease
121	Prabu Manoharan and Nanda Ghoshal	Integrated ligand based drug designing program, investigating gamma secretase alternative site binding inhibitors and significances in Alzheimer's diseases management
136	Nik Nur Syazana Nik Mohamed Kamal, Theam Soon Lim and Yee Siew Choong	Binding affinity prediction of methadone in human cytochrome P450 3A4 variants
151	DBRK Gupta Udatha, Irene Kouskoumvekaki, Lisbeth Olsson and Gianni Panagiotou	Descriptor-based computational analysis reveals a novel classification scheme for feruloyl esterase enzyme families
155	Rajiv Das Kangabam, Yumnam Silla and Rajiv Kumar Singh	I+F14identification of 6-gingerol target proteins: a structural physico-chemical properties based approach
159	Shakhinur Islam Mondal, Simrika Thapa, Md Asrafal Alum, Abdullah Zubaer, Chinmoy Saha, Arzuba Akter and Md Salman Reza	Potential drug targets identification and homology modeling of a pertinent enzyme in Streptococcus pneumoniae serotype-2 prevailing in Bangladesh
161	Amit Kumar and Indira Ghosh	Selectivity studies of binding sites of human and plasmodial Ser/Thr Kinases
162	Ambuj Kumar, Prateek Tandon and Vidushi Kapoor	Application of angiostation protein in inhibition of TPA directed relapse of pancreatic ductal carcinoma
164	Wai Keat Yam and Habibah Wahab	The interaction of ribosome with erythromycin B: molecular dynamics study
167	Chun Wai Mai, Mallikarjuna Rao Pichika and Yew Beng Kang	Vanilloids as Toll-like receptor-4 antagonists: in vitro and in silico studies
Gene Expression Analysis		
173	Li-Chuan Weng, Huai-Kuang Tsai and Daryi Wang	Co-expression of neighboring genes in the zebrafish (Danio rerio) genome
174	Chuen-Yi Wang, Huai-Kuang Tsai, Li-Chuan Weng and Daryi Wang	Gain and loss of transcription factor binding Sites are common between yeast strains but few contribute to expression variation
210	Sandeep Singhal and Sandeep Singhal	Statistical issues in analysis of methylation arrays as compared to gene expression
8	Sawannee Sutheworapong and Kengo Kinoshita	A novel biclustering approach with iterative optimization targeting co-expressed gene clusters
144	Shashi Rekha Thummala, Rohan Misra and Akash Ranjan	Codon usage and gene expression patterns of biased genomes
Immunoinformatics		
224	Noor Asidah Mohamed and Abdul Manaf Ali	Structure prediction and evaluation of anti-MCF7 ScFv antibody
227	Christian Schönbach	Mouse models for human immune system diseases in context of strain-specific and cross-species differences

120	Zhiliang Chen, Marie J Kidd, Andrew M Collins and Bruno Gaeta	Genotyping human immunoglobulin heavy chain IGHV/IGHJ genes using maximum likelihood models
129	Monica Kurniawan, Thurston Hy Dang, Miles P Davenport and Vanessa Venturi	Bioinformatics investigation of the mechanisms generating T cell receptor diversity
133	Trevor Clancy and Eivind Hovig	Computational analysis of the tumor immune response with clinical predictive effects
158	Hui Yee Greenaway, Maire F Quigley, Vanessa Venturi, Pauline C Ng, Zachary S Ende, Tina McIntosh, Tedi E Asher, Jorge R Almeida, Samuel Levy, David A Price, Daniel C Douek and Miles P	Investigation of T cell receptor sharing using next generation sequencing
Proteins: Structure, Mutations and Interactions		
177	Jahanshah Ashkani and Jasper Rees	Computational modeling of protein interaction at the self-incompatibility locus of Rosaceae
206	Raul Araya, Carlos Lagos, Fernando Abarca, Agustin Martinez and Tomas Perez	Molecular dynamics Simulations of Cx26-Wt and deafness related mutants M34A, A40G and V37I
207	Fernando Abarca, Raul Araya-Secchi, Pilar Parada and Tomas Perez-Acle	De novo modelling and simulation of lipoprotein Licanantase of strain Licanantay: Acidithiobacillus thiooxidans DSM 17318
219	Jamaludin Sallim	A Swarm-based clustering algorithm for identifying functional modules and protein complexes in protein interaction networks
187	Mohd Fairus Mohd Yusof and Zeti Hussein	The function of cysteine in a protein structure is used as a basis for its classification
220	Sriganesh Srihari and Hon Wai Leong	Reusability of 'static' protein complex components during the yeast cell cycle
226	Ramesh Katam, Prashanth Suravajhala, Crayger Williams, Ranganath Gudimella, Sheikh Basha and Lekan Latinwo	Protein-protein interaction analysis of water stress responsive proteins to reveal essential functional orthologues in peanut
232	Se-Eun Bae, Sunghoon Jung, Ha-Yeon Kim and Hyeon S. Son	Protein Secondary Structure analysis using Discriminant Analysis
125	Richard Morgan, Yvette Luyten and Geoffrey Wilson	Rational engineering of DNA recognition: simple mutations that change Type II restriction enzyme specificity
127	Fatahiya Mohd Tap, Ameerah Ishak and Nurul Bahiyah Ahmad Khairudin	Molecular dynamics folding simulation of β -hairpins from protein G
132	Yumnam Silla, Elayanambi Sundaramoorthy and Shantanu Sengupta	S-Linked protein homocysteinylation: identifying structural physico-chemical properties of Hhmocysteinylated proteins
135	Gopal K Bhoi, Ashis Saha, Avinash Pradhan and Smrutirekha Parija	Comparative modeling and structure prediction on FSH and LH beta subunits from grass carp (Ctenopharyngodon idella)
139	Ninad Oak, Shimantika Sharma, Vijayaraghavan Sundararajan and Jayaraman Valadi	Machine learning methods to identify nuclear receptor ligand binding pockets
141	Aakanksha Pandey and Ambuj Kumar	Modeling and interaction analysis PDGF protein to find the key of regeneration in Danio rerio
143	Srajan Jain, Priyanka Jain, Rahul Tiwari, Isha Chaudhary and George Priya Doss C	Molecular dynamic simulation study of R164K mutation in 1DX0 prion protein and its influence on cation pi interaction
149	Hossein Fallahi	Comparing α -helices and β -sheets in thermophilic and mesophilic proteins
160	Rajiv Das Kangabam, Yumnam Silla, Priyanka Purkayastha and Rajiv Kumar Singh	Effect of missense mutation on PINK1 protein structure: a molecular modelling approach
Rnomics and NGS Analysis		
194	Shelly Mahlab, Tamir Tuller and Michal Linial	An outlook on healthy and diseased human proteomes via the tRNAs abundance
176	Gudimella Ranganath, Martti Tammi, Norzulaani Khalid and Jennifer Ann Harikrishna	Computational identification of functional siRNA in Musa acuminata
184	Costas Bouyioukos, Matthew J Moscou, Nicolas Champouret, Inmaculada Hernández-Pinzón, Eric R Ward and Brande B H Wulff	Transcriptome and genetic characterisation of Aegilops sharonensis – a wild diploid relative of wheat- by 454 GSFLX sequencing
118	Swetansu Pattnaik, Srividya Vaidyanathan, Pooja D and Binay Panda	Customization of SNV analysis pipeline for whole exome data using a combinatorial approach
128	Rajanikanta Mahapatra	Computational identification of sweet wormwood (Artemisia annua) miRNA and their mRNA targets
131	Binay Panda, Prakhar Gaur, Jyothish Soman and Ankur Narang	MUSIC (Mapping USING hybrid Computing) for next-generation sequencing data
138	Yoichi Takenaka, Tomoshige Ohno, Kayo Okuda, Shigeto Seno and Hideo Matsuda	Sequence determination and expression estimation of alleles from RNA-Seq data
166	Parawee Lekprasert, Michael Mayhew and Uwe Ohler	Energy features for miRNA target prediction under relaxed seed and no conservation requirements
168	Bernard Lee and Mohd Firdaus Raih	Computational discovery and validation analysis of small nucleolar RNAs in Leucosporidium antarcticum
Sequence Analysis and Evolution		
195	Zeti Hussein, Loke Kok Keong, Gor Mian Chee, Ismanizan Ismail, Zamri Zainal, Roohaida Othman, Syarul Nataqain Baharum, Maizom Hassan and Normah Mohd Noor	Functional inference of hypothetical proteins obtained from the roots of Polygonum minus Huds.
172	Mohd Syaifiq Rahim and Mohd Firdaus Raih	Molecular signature of extreme adaptation
196	Nurulhuda Abdul Manap, Roohaida Othman and Zeti Hussein	Sequence analysis of hypothetical proteins from Eucheuma denticulatum ESTs dataset
197	Yasuhiro Inoue and Yuki Sandaiji	Analysis of transmembrane protein sequences in Acropora digitifera genome
198	Yuki Sandaiji and Yasuhiro Inoue	Functional identification of transmembrane protein sequences in plant genomes
178	Zahra Jalali Sefid Dashti	Evolution of Iron regulatory proteins in Haematophagous insects
179	Pandurang Kolekar, Mohan Kale and Urmila Kulkarni-Kale	Whole proteome phylogeny of family Flaviviridae using alignment-free approach
75	Smarajit Das, Sanga Mitra, Satyabrata Sahoo, Rini Chakraborty, Chiranjit Saha, Shaoli Das, Suman Ghosal and Jayprokas Chakrabarti	Duplicated 3'-halves of tRNAs in Sulfolobales: viral genome integrations or more?
88	Yuslina Zakaria, Merridee Wouters, W. Bret Church and Bruno Gaeta	Inference of phylogenetic trees from protein structural information
134	Yoichi Takenaka, Shigeto Senoo and Hideo Matsuda	Perfect Hamming code with Burrow-Wheeler translation for genome mapping
140	Naresh Mvr, Raghunath Keshavachandran, Suravajhala Prashanth and P A Nazeem	EST mining and annotation of putative proteins in Zingiber officinale
142	Garima Khandelwal and B Jayaram	Energetic Finger Prints for Genomic Functional Units
145	Sridhar Jayavel and Gunasekaran Paramasamy	Analysis of genome sequences for Fur interacting sRNAs and coding genes possibly involving in iron metabolism
154	Hui San Ong, Rahmah Mohamed and Mohd Firdaus-Raih	Comparative genome sequence analysis reveals the extent of diversity and conservation of glycan associated proteins in Burkholderia spp
163	Anshu Chaudhary and Hridaya Shanker Singh	Phylogenetic utility of secondary structure & motif prediction in RNA molecules
165	Yogesh Paudel, Ole Madsen, Hendrik-Jan Megens, Mirte Bosse, Laurent Frantz and Martien A M Groenen	Analysis of structural variation in porcine genome
Systems Biology: Networks & Pathways		
171	Shweta Kolhi and A S Kolaskar	Categorization of bacterial metabolome
211	Rauf Malick, Nasir Touheed and Muhammad Azim	Meaningful data mining from directed TF network with multiple scoring metric measures
186	Sarahani Harun and Zeti Hussein	Analysis of bibliomic data towards the construction of PCOS interaction pathway
190	Vijaykumar Y Muley and Akash Ranjan	Comparative assessment of protein-protein functional linkage prediction methods: A case study of biological pathways
223	Daniele Santoni, Paola Paci and Filippo Castiglione	Do closely located genes have a higher likelihood to interact?
229	Kentaro Inoue, Shinichi Shimozone and Hiroyuki Kurata	Grid layout algorithm for biochemical networks using approximate pattern matching
137	Tri Hieu Nim, Marie-Véronique Clément, Jacob K White and Lisa Tucker-Kellogg	Parameter estimation web service tailored for data-rich biochemicalPathways
156	Ryo Araki, Yoichi Takenaka, Tomoshige Ohno, Yukito Watanabe, Shigeto Seno and Hideo Matsuda	Detect unique gene regulatory networks along dendrogram of cell differentiation