

Accepted Papers for BMC Genomics (BMC G), BMC Bioinformatics (BMC B) and Immunome Research (IR) InCoB/ISCB-Asia 2011 Supplement Issues (as of Oct 11, 2011)

Submission No.	Journal Supplement	Authors	Title
Databases and Software Tools			
2	BMC G	Zhen Yang, Ying Yu, Lei Yao, Guangui Li, Lin Wang, Yiyao Hu, Haibin Wei, Li Wang, Riadh Hammami, Roxanne Razavi, Yang Zhong and Xufang Liang	DetoxiProt: an integrated database for detoxification proteins
14	BMC G	Langho Lee, Kai Wang, Gang Li, Zhi Xie, Yuli Wang, Jiangchun Xu, Shaoxian Sun, David Pocalyko, Jong Bhak, Chulhong Kim, Kee-Ho Lee, Ye Jin Jang, Young Il Yeom, Hyang-Sook Yoo and Seungwoo Hwang	Liverome: a curated database of liver cancer-related gene signatures with self-contained context information
109	BMC G	Monzoorul Haque Mohammed, Tarini Shankar Ghosh, Rachamalla Maheedhar Reddy, Nitin Kumar Singh, CvsK Reddy and Sharmila Mande	INDUS - a composition based approach for rapid and accurate taxonomic classification of metagenomic sequences
46	BMC G	Mingoo Kim, Hyunjung Shin, Tae Su Chung, Je-Gun Joung and Ju Han Kim	Extracting regulatory modules from gene expression data by sequential pattern mining
67	BMC G	Jamshaid Ali, Paila Uma Devi and Akash Ranjan	ApicoAlign: an alignment and sequence search tool for apicomplexan proteins
35	BMC B	Mohd Firdaus-Raih, Anne-Marie Harrison, Peter Willett and Peter Artymiuk	Novel base triples in RNA structures revealed by graph theoretical searching methods
110	BMC B	Alfredo Benso, Stefano Di Carlo, Gianfranco Politano, Alessandro Savino and Hafeez Hafeezurrehman	Building gene expression profile classifiers with a simple and efficient reject option in R
98	BMC B	Chang Liu, Dong Liang, Ting Gao, Xiaohui Pang, Jingyuan Song, Hui Yao, Jianping Han, Zhihua Liu, Xiaojun Guan, Kun Jiang, Huan Li and Shilin Chen	PTIGS-IdIt, an integrated web server for species identification by DNA sequences of the psbA-trnH intergenic region
Disease Informatics			
22	BMC G	Wei-Chung Shia, Fang-Rong Hsu, Tien-Hsiung Ku, Yu-Ming Tsao, Chien-Hsun Hsia, Yung-Ming Chang, Ching-Hui Huang, Yeh-Ching Chung, Shih-Lan Hsu and Kae-Woei Liang	Genetic copy number variants in myocardial infarction patients with hyperlipidemia
114	BMC G	Swee Heng Toh, Philip Prathipati, Efthimos Motakis, Pavan Surya Yanamandra, Chee Keong Kwoh and Vladimir Kuznetsov	A robust tool for discriminative analysis and feature selection in paired samples impacts the identification of the genes essential for reprogramming lung tissue to adenocarcinoma
42	BMC G	Chia-Lang Hsu, Yen-Hua Huang, Chien-Ting Hsu and Ueng-Cheng Yang	Prioritizing disease candidate genes by a gene interconnectedness-based approach
73	BMC G	Keng-Hsuan Huang, Kun-Tze Chen and Chin Lung Lu	Sorting permutations by cut-circularize linearize-and-paste operations
59	BMC B	Sheng-An Lee, Theresa Tsun-Hui Tsao, Ko-Chun Yang, Han Lin, Yu-Lun Kuo, Chien-Hsiang Hsu, Wen-Kuei Lee, Kuo-Chuan Huang and Cheng-Yan Kao	Construction and analysis of the protein-protein interaction networks for schizophrenia, bipolar disorder, and major depression
58	BMC B	Smitha Sunil Kumaran Nair, N V Subba Reddy and Hareesha K S	Exploiting heterogeneous features to improve in-silico prediction of peptide status – amyloidogenic or non-amyloidogenic
Immunomics			
94	IR	Jing Sun, Tianlei Xu, Shuning Wang, Guoqing Li, Di Wu and Zhiwei Cao	Does difference exist between epitope and non-epitope residues?
87	IR	Pandurang Kolekar, Mohan Kale and Urmila Kulkarni-Kale	Genotyping of mumps viruses based on SH gene: development of a server using alignment-free and alignment-based methods
123	IR	Lars Olsen, Guang Lan Zhang, Ellis Reinherz and Vladimir Brusic	FLAVIdB: a data mining system for knowledge discovery in flaviviruses with direct applications in immunology and vaccinology
39	IR	Marsia Gustiananda	Immunoinformatics analysis of H5N1 proteome for designing an epitope-derived vaccine and predicting the prevalence of pre-existing cellular-mediated immunity toward bird flu virus in Indonesian population
Sequence Analysis and Evolution			
12	BMC G	Kohji Okamura, Riu Yamashita, Noriko Takimoto, Koki Nishitsuji, Yutaka Suzuki, Takehiro Kusakabe and Kenta Nakai	Profiling ascidian promoters as the primordial type of vertebrate promoter
13	BMC G	Yoichi Takenaka, Shigeto Seno and Hideo Matsuda	Perfect Hamming code with a hash table for faster genome mapping
55	BMC G	Danny Poo, Shaojiang Cai and James Mah	UASIS: universal automatic SNP identification system
56	BMC G	Zhao Min and Hong Qu	High similarity of phylogenetic profiles of rate-limiting enzymes with inhibitory relation in human, rat, mouse, budding yeast and E. coli
106	BMC G	Lawrence Jk Wee, Lisa Fp Ng, Joo Chuan Tong and Esmond Ps Er	In silico prediction of the granzyme B degradome
6	BMC B	Michael Fernandez, Yutaro Kumagai, Daron Standley, Akinori Sarai, Kenji Mizuguchi and Shandar Ahmad	Prediction of dinucleotide-specific RNA-binding Sites in proteins
40	BMC B	David Deluca, Derin Keskin, Guang Lan Zhang, Ellis Reinherz and Vladimir Brusic	Scanning influenza sequences for PB1-F2 encoding RNA segments
70	BMC B	Sungwook Choi and Kyungsook Han	Prediction of RNA-binding amino acids from protein and RNA sequences
Proteome Analysis: Structures, Mutations and Interactions			
15	BMC G	Ashwini Patil, Kenta Nakai and Kengo Kinoshita	Assessing the utility of gene co-expression stability in combination with correlation in the analysis of protein-protein interaction networks
57	BMC G	Hufeng Zhou and Limsoon Wong	Comparative analysis and assessment of M. tuberculosis H37Rv Protein-protein interaction datasets
78	BMC G	Akira Kinjo, Yutaro Kumagai, Huy Dinh, Osamu Takeuchi and Daron Standley	Functional characterization of protein domains common to animal viruses and their hosts
107	BMC G	Thi Hyunh, Javed Khan and Shoba Ranganathan	A multi-species comparative structural bioinformatics analysis of inherited mutations in beta-D-Mannosidase reveals a genotype-phenotype correlation
64	BMC B	Tzong Yi Lee, Shu-An Chen, Tsung-Cheng Lu, Neil Arvin Bretaña and Tzu-Hsiu Cheng	Investigation and identification of protein γ-glutamyl carboxylation sites

111	BMC B	Sy Bing Choi, Normi M Yahaya and Habibah A Wahab	Revealing the functionality of hypothetical protein KPN00728 from <i>Klebsiella pneumoniae</i> MGH78578: molecular dynamics simulation approaches
31	BMC B	Sorayya Malek, Sharifah Mumtazah Syed Ahmad, Sarinder Kks, Pozi Millow and Aishah Salleh	Assessments of predictive models for chlorophyll-a concentration at tropical water bodies
Rnomics and Next Generation Sequencing			
30	BMC G	Monzoorul Haque Mohammed, Tarini Shankar Ghosh, Sudha Chadaram and Sharmila Mande	i-rDNA: alignment-free algorithm for rapid in silico detection of ribosomal gene fragments from metagenomic sequence data sets
53	BMC G	Seong Siang Ong and Ratnam Wickneswari	Expression profile of small RNAs in <i>Acacia mangium</i> secondary xylem tissue with contrasting lignin content - a potential regulatory sequence in monolignol biosynthetic pathway
66	BMC G	Gagan Garg and Shoba Ranganathan	In silico secretome analysis approach for next generation sequencing transcriptomic data
79	BMC G	Atsushi Ogura, Mengjie Lin, Yuya Shigenobu, Atushi Fujiwara, Kazuho Ikeo and Satoshi Nagai	Effective gene collection from the metatranscriptome of marine microorganisms
25	BMC G	Ting-Wen Chen, Timothy H Wu, Wailap V Ng and Wen-Chang Lin	Interrogation of alternative splicing events in duplicated genes during evolution
82	BMC G	Suparna Mitra, Mario Stärk and Daniel Huson	Analysis of 16S rRNA environmental sequences using MEGAN
113	BMC G	Arsen Batagov, Vladimir Kuznetsov and Igor Kurochkin	Identification of nucleotide patterns enriched in secreted RNAs as putative cis-acting elements targeting them to exosome nano-vesicles
26	BMC B	Mi Hyeon Kim, Hwa Jeong Seo, Je-Gun Joung and Ju Han Kim	Comprehensive evaluation of matrix factorization methods for the analysis of DNA microarray gene expression data
85	BMC B	Tarini Shankar Ghosh, Monzoorul Haque Mohammed, Hannah Rajasingh, Sudha Chadaram and Sharmila Mande	HabiSign: a novel approach for comparison of metagenomes and rapid identification of habitat-specific sequences
Structure-based Drug Design and Discovery			
92	BMC B	Abhinav Grover, Vibhuti Agrawal, Ashutosh Shandilya, Virendra Bisaria and D Sundar	Non-nucleosidic inhibition of Herpes simplex virus DNA polymerase: mechanistic insights into the anti-herpetic mode of action of herbal drug withaferin-A
1	BMC B	Usman Sumo Friend Tambunan, Bramantya Nindyapati and Atri Aditya Parikesit	In silico Modification of suberoylanilide hydroxamic acid (SAHA) as potential inhibitor for class II histone deacetylase (HDAC) <i>Homo sapiens</i>
19	BMC B	Lim See Ven, Mohd Basyaruddin Abdul Rahman and Bimo Tejo	Structure-based and ligand-based virtual screening of novel methyltransferase inhibitors of the Dengue virus
68	BMC B	Varun Khanna and Shoba Ranganathan	In silico approach to screen compounds active against parasitic nematodes of major socio-economic importance
Systems Biology: Bioimaging, Biological Networks and Signaling Pathways			
27	BMC B	Tiehua Du, Weechoo Puah and Martin Wasser	Cell cycle phase classification in 3D in vivo microscopy of <i>Drosophila</i> embryogenesis
36	BMC B	Merlin Veronika, Roy Welsch, Alvin Ng, Paul Matsudaira and Jagath Rajapakse	Correlation of cell membrane dynamics and cell motility
20	BMC B	Chengcheng Liu, Mingxi Yao and Christopher Hogue	Near-membrane ensemble elongation in the proline-rich LRP6 intracellular domain may explain the mysterious initiation of the Wnt signaling pathway
102	BMC B	Christopher Poirel, Clifford Owens and T M Murali	Network-based functional enrichment
49	BMC B	Donny Soh, Difeng Dong, Yike Guo and Limsoon Wong	Finding consistent disease subnetworks across datasets
16	BMC B	Chien-Hsiang Hsu, Tse-Yi Wang, Cheng-Yan Kao and Kuang-Chi Chen	A quantitative analysis of monochromaticity in genetic interaction networks
81	BMC B	Jagath Rajapakse and Piyushkumar Mundra	Stability of building gene regulatory networks with sparse autoregressive models