

Sep 26 (Day 1)



InCoB2010 – The 9<sup>th</sup> International Conference on Bioinformatics

Waseda International Conference Center, Tokyo, September 26-28, 2010

Ibuka Masaru Auditorium



09:00-17:00	<b>Registration</b>
09:45-10:00	<b>Opening Address and Greetings</b> InCoB Co-chairs, APBioNet President, representatives of JSBi, IMMS, and CBI
10:00-12:00	<b>Synthetic Biology (Chair: Mitsuhiro Itaya, Keio University)</b>
	<b>InCoB2010 Keynote 1</b>
10:00-11:00	<b>Building a synthetic cell</b> Clyde A. Hutchison III - J. Craig Venter Institute (San Diego), USA
11:00-11:30	<b>Coffee Break</b>
11:30-12:00	<b>Construction of a genetic AND gate under a new standard for assembly of genetic parts</b> Shotaro Ayukawa, Akio Kobayashi, Yusaku Nakashima, Hidemasa Takagi, Shogo Hamada, Masahiko Uchiyama, Katsuyuki Yugi, Satoshi Murata, Yasubumi Sakakibara, Masami Hagiya, Masayuki Yamamura and Daisuke Kiga (BMC Genomics)
12:00-13:30	<b>Lunch Break</b>
12:15-13:15	<b>APBioNet Annual Meeting and Elections (Conference Room 1)</b>
13:30-15:30	<b>Evolution and Sequence Analysis I (Chair: Hideo Matsuda, Osaka University)</b>
13:30-14:00	<b>Gradual transition from mosaic to global DNA methylation patterns during deuterostome evolution</b> Kohji Okamura, Kazuaki Matsumoto and Kenta Nakai (BMC Bioinformatics)
14:00-14:30	<b>DODO: an efficient orthologous genes assignment tool based on domain architectures</b> Ting-wen Chen, Timothy Wu, Wailap Ng and Wen-chang Lin (BMC Bioinformatics)
14:30-15:00	<b>In vitro homology search array comprehensively reveals highly conserved genes and their functional characteristics in non-genome sequenced species</b> Atsushi Ogura, Masaaki Yoshida, Mutsumi Fukuzaki and Jun Sese (BMC Genomics)
15:00-15:30	<b>Evolutionary patterns of amino acid substitutions in 12 <i>Drosophila</i> genomes: data mining in phylogenetic context</b> Lev Yampolsky and Michael Bouzinier (BMC Genomics)
15:30-16:00	<b>Coffee Break and Poster Viewing</b>
16:00-18:00	<b>RNomics and Next-Generation Sequencing (Chair: Yasubumi Sakakibara, Keio University)</b>
16:00-16:30	<b>Robust and accurate prediction of noncoding RNAs from aligned sequences</b> Yutaka Saito, Kengo Sato and Yasubumi Sakakibara (BMC Bioinformatics)
16:30-17:00	<b>RNA editing of nuclear transcripts in <i>Arabidopsis thaliana</i></b> Yijun Meng, Dijun Chen, Chuanzao Mao, YongFeng Jin, Ping Wu and Ming Chen (BMC Genomics)
17:00-17:30	<b>Discovery and characterization of medaka miRNA genes by next generation sequencing platform</b> Sung-Chou Li, Wen-Ching Chan, Meng-Ru Ho, Ling-Yueh Hu, Chun-Hung Lai, Chun-Nan Hsu, Pung-Pung Hwang and Wen-chang Lin (BMC Genomics)
17:30-18:00	<b>DiScRIBinATE: A rapid method for accurate taxonomic classification of metagenomic sequences</b> Tarini Ghosh, Monzoorul Haque and Sharmila Mande (BMC Bioinformatics)
Conference Room 1	
9:45-12:15	
12:15-13:15	<b>APBioNet Annual Meeting and Elections</b>
13:30-15:25	<b>Prediction of Subcellular Protein Locations and Protein-Protein Interactions (Chair: Kenta Nakai, Human Genome Center)</b>
13:30-14:00	<b>PathLocdb: a comprehensive database for subcellular localization of metabolic pathway and its application for multiple localization analysis</b> Min Zhao and Hong Qu (BMC Genomics)
14:00-14:30	<b>Network analysis of human protein location</b> Gaurav Kumar and Shoba Ranganathan (BMC Bioinformatics)
14:30-14:55	<b>Prediction of subcellular locations of proteins: where to proceed?</b> Kenichiro Imai and Kenta Nakai (Late-breaking abstract)
14:55-15:25	<b>Integrating diverse biological and computational sources for reliable protein-protein interactions</b> Min Wu, Xiaoli Li, Hon Nian Chua, Chee Keong Kwoh and See Kiong Ng (BMC Bioinformatics)
15:25-16:00	<b>Coffee Break and Poster Viewing (Conference Room 3)</b>
16:00-18:00	<b>Structure-based Drug Discovery and Design (Co-Chairs: Hiroshi Wako, Waseda University and Shoba Ranganathan, Macquarie University)</b>
16:00-16:30	<b>Identification of a better HDAC class II inhibitor through binding energy calculations and descriptor</b> Tambunan Usman Sumo Friend and Evi Kristin Wulandari (BMC Bioinformatics)
16:30-17:00	<b>IKK<math>\beta</math> inhibitor identification: a novel multi-filter driven scaffold</b> Shanthi Nagarajan, Hyunah Choo, Yong Seo Cho, Kwang-Seok Oh, Byung Ho Lee and Ae Nim Pae (BMC Bioinformatics)
17:00-17:30	<b>Probing anti-cancerous potency of the prospective herbal drug withaferin A: a case study on two mammalian 20S proteasomes</b> Abhinav Grover, Ashutosh Shandilya, Virendra Bisaria and Durai Sundar (BMC Genomics)
17:30-18:00	<b>TSCC: two-stage combinative clustering for virtual screening using protein-ligand interactions and physical-chemical features</b> Daniel Cliniciu, Yen-Fu Chen, Cheng-Neng Ko, Chi-Chun Lo and Jinn-Moon Yang (BMC Genomics)

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continued



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Conference Room 2



9:45-13:30

13:30-15:20

**Biological Databases and Software Tools I** (Chair: Tetsuro Toyoda, Bioinformatics And Systems Engineering division (BASE), RIKEN)

13:30-13:50	<b>PheMaDB: A web-based database management system for storage, retrieval, visualization, and analysis of OmniLog phenotypic microarray data</b> Wenling Chang, <b>Keri Sarver</b> , Brandon Higgs, Timothy Read, Nichole Nolan, Kimberly Bishop-Lilly and Shanmuga
13:50-14:10	<b>BioCichlid: central dogma-based 3D visualization system of time-course microarray data on a hierarchical biological network</b> Ryosuke Ishiwata, Masaki Morioka, <b>Soichi Ogishima</b> and Hiroshi Tanaka
14:10-14:30	<b>ApiLoc: an orthology-linked database of subcellular protein localisations</b> Ben Woodcroft, Robert Radloff, Kristie-Lee Scanlon, Maria Doyle, Christopher Tonkin, Lee Yeoh, Terry Speed and Stuart
14:30-14:50	<b>A comprehensive and an update database on human and animal vaccines</b> <b>Rajarajan Swaminathan</b> , Yogambal Muthu and Madhan Mohan Thangavelu
14:50-15:20	<b>GenoCon: an international rational-genome-design contest on a freemium semantic-web platform associating business and educational communities in synthetic biology</b> <b>Tetsuro Toyoda</b> , Bioinformatics And Systems Engineering division (BASE), RIKEN (GenoCon sponsored talk)
15:20-15:35	<b>SPLP: life science integrated DB project: development of web and active workflow</b> <b>Kazuhiko Fukui</b> , Toshiyuki Tashiro, Yukimitsu Yabuki, Tamotsu Noguchi, Kiyoshi Asai - Computational Biology Research Center, AIST, Japan

15:35-16:00

**Coffee Break and Poster Viewing** (Conference Room 3)

16:00-17:50

**Disease Informatics I** (Chair: Hiroshi Tanaka, Tokyo Medical and Dental University)

16:00-16:30	<b>The interplay between evolution, regulation and tissue specificity in the human hereditary disease</b> <b>Shivashankar Nagaraj</b> , Aaron Ingham and Antonio Reverter (BMC Genomics)
16:30-17:00	<b>Gerontome: a web-based database server for aging-related genes and analysis pipelines</b> Jekeun Kwon, <b>Byungwook Lee</b> and Haeyoung Chung (BMC Genomics)
17:00-17:10	<b>Using a gene-set based analysis of expression profiles to guide pathway analysis of GWAS: A study in Alzheimer's disease</b> <b>Suling Lin</b> , Ian Campbell, Geoff MacIntyre, James Bailey, Adam Kowalczyk, Erik Thompson, Melissa Southey, John Hopper and Izhak Haviv (poster selected for short talk)
17:10-17:20	<b>Biomarkers of survival after melanoma</b> <b>Sarah-Jane Schramm</b> and Graham J Mann (poster selected for short talk)
17:20-17:50	<b>Algorithms and semantic infrastructure for mutation impact extraction and grounding</b> Jonas Bergman Laurila, Nona Naderi, Rene Witte, <b>Alexandre Kouznetsov</b> , Christopher Baker and Alexandre Riazanov (BMC Genomics)
17:50-18:20	<b>PCR-based molecular characterization and in-silico analysis of food-borne trematode parasites <i>Paragonimus westermani</i>, <i>Fasciolopsis buski</i> and <i>Fasciola gigantica</i> from Northeast India using ITS2 rDNA</b> <b>Pramod K. Prasad</b> , Veena Tandon and Anupam Chatterjee (Bioinformatics)

Conference Room 3



9:15-18:00

**Mounting of All Posters (No. 1 - 49) (9:15-13:30) and Viewing (13:30-18:00)**

1	Hsu C-T <i>et al.</i>	Explore the possible synergistic effects on survival in breast cancer patients (#91)
2	Mittal V <i>et al.</i>	Identification of potential apicoplast associated therapeutic targets in human & animal pathogen <i>Toxoplasma gondii</i> ME49- A subtractive genomics approach (#110)
3	Yamaguchi Y. <i>et al.</i>	Clinical trial map to explore clinical trials registry, ClinicalTrials.gov (#127)
4	Akanuma H. <i>et al.</i>	Bayesian network analysis of chemical toxicities for health risk assessments (#128)
5	Tiwari A <i>et al.</i>	Dual estimation of hormone secretion profiles from salivary hormone measurements (#135)
6	Sawai H <i>et al.</i>	A knowledge based prioritization for risk genes for bipolar disorder (#137)
7	Hsiao C-C <i>et al.</i>	Pathway integration reveals molecular interaction preferences of diseases (#147)
8	Kwon J-S <i>et al.</i>	Gene-set-based genome-wide association analysis of bone density (#148)
9	Waki K and Masuya H	The search system for experimental mice using disease and ontology information (#163)
10	Tsai Y-S <i>et al.</i>	Combination of clinical factors with histological grading improves molecular classification of breast cancers (#192) CANCELLED
11	Toh SH <i>et al.</i>	Discriminative microarray analysis in paired samples reveals global reprogramming of the transcriptional profile in lung adenocarcinoma (#192)
12	Ohtsuka S <i>et al.</i>	The connectin-like protein gene of amphioxus striated muscle (#131)
13	Bao Y <i>et al.</i>	Amphioxus striated muscle has beta-actinin and tropomodulin (#134)
14	Katam R <i>et al.</i>	Leaf proteome analysis of water deficit stress responses in peanut (#120)
15	Inoue K and Kurata H	A novel spectral clustering of protein interaction networks (#122)
16	Ku J <i>et al.</i>	Hidden bottleneck proteins in yeast protein-protein interaction networks (#140)
17	Patil A <i>et al.</i>	HitPredict: A database of high confidence protein-protein interactions (#141)
18	Wu J-W <i>et al.</i>	Predicting protein-protein interactions using a hybrid approach (#168)
19	Chien T-Y <i>et al.</i>	Prediction of DNA-binding profiles by protein-DNA complexes (#169)
20	Hsueh C-H <i>et al.</i>	Predicting DNA-binding proteins using disorder information (#170)
21	Kikuchi M <i>et al.</i>	A global structure and evolutionary constraint of functional modules in the protein interaction network (#173)
22	Gupta A <i>et al.</i>	Training a Network of Hypothetical Proteins: Problems and Challenges (#62)

18:45-20:45

**Welcome Party at Okuma Garden Hall**

Sep. 27 (Day 2)



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9:00-17:00 Registration

9:15-10:45 Systems Biology: Biological Networks and Signaling Pathways (Chair: Durai Sundar, Indian Institute of Technology (IIT) Delhi)

9:15-09:45	<b>Analysis and verification of the HMGB1 signaling pathway</b> Haijun Gong, Paolo Zuliani, Anvesh Komuravelli, James Faeder and Edmund Clarke (BMC Bioinformatics)
9:45-10:15	<b>Inhibition of the NEMO/IKK<math>\beta</math> association complex formation, a novel mechanism associated with the NF-<math>\kappa</math>B activation suppression by <i>Withania somnifera</i>'s key metabolite withaferin A</b> Abhinav Grover, Ashutosh Shandilya, Ankita Punetha, Virendra Bisaria and Durai Sundar (BMC Genomics)
10:15-10:45	<b>Modularity of <i>Escherichia coli</i> sRNA regulation revealed by sRNA-targets and protein network analysis</b> Timothy H. Wu, Ian Yi-Feng Chang, Li-chieh Julie Chu, Hsuan-Cheng Huang and Wailap Victor Ng (BMC Bioinformatics)

10:45-11:45 Coffee Break and Poster Session (Conference Room 3) At least one author must be present at the poster.

11:45-12:45 InCoB2010 Keynote 2 (Chair: Kenta Nakai, Human Genome Center)

	<b>Systems drug discovery and software platform for healthcare research and services</b> Hiroaki Kitano - The Systems Biology Institute, Japan
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12:45-14:15 Lunch break (lunch boxes will be distributed at the entrance of conference rooms 1 and 2, starting at 12:55)

14:15-16:15 Disease Informatics II (Chair: Yasushi Okazaki, Saitama Medical University)

14:15-14:45	<b>A quantitatively-modeled homozygosity mapping algorithm, qHomozygosityMapping, utilizing whole genome single nucleotide polymorphism genotyping data</b> Huqun, Shun-ichiro Fukuyama, Hiroyuki Morino, Hiroshi Miyazawa, Tomoaki Tanaka, Tomoko Suzuki, Masakazu Kohda, Hideshi Kawakami, Yasushi Okazaki, Kuniaki Seyama and Koichi Hagiwara (BMC Bioinformatics)
14:45-15:15	<b>iCOD: an integrated clinical omics database based on the systems-pathology view of disease</b> Kazuro Shimokawa, Kaoru Mogushi, Satoshi Shoji, Atsuko Hiraishi, Hiroshi Mizushima and Hiroshi Tanaka (BMC Genomics)
15:15-15:45	<b>dbDEMC: a database of differentially expressed miRNAs in human cancers</b> Zhen Yang, Fei Ren, Changning Liu, Shunmin He, Gang Sun, Qian Gao, Lei Yao, Yangde Zhang, Ruoyu Miao, Yi Zhao, Yang Zhong, Haitao Zhao and Ying Cao (BMC Genomics)
15:45-16:15	<b>T3SEdb: Data warehousing of virulence effectors secreted by the bacterial type III secretion system</b> Daniel Ming Ming Tay, Kunde Ramamoorthy Govindarajan, Asif M Khan, Terenze Yao Rui Ong, Hanif M Samad, Wei Wei Soh, Minyan Tong, Fan Zhang and Tin Wee Tan (BMC Bioinformatics)

16:15-16:45 Coffee Break and Poster Removal

16:45-17:45 InCoB2010 Keynote 3 (Chair: Christian Schönbach, Kyushu Institute of Technology)

	<b>Technology innovation in pathogen identification in the asian-African research network for infectious diseases</b> Yoshiyuki Nagai, Kazuhisa Okada, Yoshihide Hayashizaki and Toshihiro Horii - RIKEN Center of Research Network for Infectious Diseases (CRNID), Japan
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17:45-17:55 Best Paper and Poster Awards

17:55-18:05 Preview of InCoB2011 (Co-chairs of InCoB2011)

Conference Room 1	三井情報株式会社 MITSUBISHI KNOWLEDGE INDUSTRY	三菱スペース・ソフトウェア株式会社 MITSUBISHI SPACE SOFTWARE CO., LTD.	
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9:15-10:45 Biological Databases and Software Tools II (Co-Chairs: TBA and Tin Wee Tan, National University of Singapore)

9:15-9:30	<b>An improved tool of pairwise alignment of RNA tertiary structures</b> Kun-Tze Chen, Chih-Wei Wang and Chin Lung Lu
9:30-9:45	<b>OpenHTS: an integrated tool for the analysis of hormone concentration time-series data</b> Abhishek Tiwari, Peter Hunter and John Ingram
9:45-10:00	<b>OGtree2: A tool for reconstructing genome trees of prokaryotes using overlapping genes</b> Chung-Han Yang, Chih-Hsien Cheng, Hsien-Tai Chiu and Chin Lung Lu
10:00-10:15	<b>Genomics Fox Tool (GFT): an interface for comparative and functional analysis of microbial genomes</b> Gopal Ramesh Kumar and Kandavel Palanikannan.
10:15-10:45	<b>ProViDE: A software tool for accurate estimation of viral diversity in metagenomic samples</b> Tarini Shankar Ghosh, Monzoorul Haque M, Dinakar Komanduri and Sharmila S Mande (Bioinformatics)

10:45-11:45 Coffee Break and Poster Session (Conference Room 3) At least one author must be present at the poster.

23	Ghatani S <i>et al.</i>	Molecular phylogenetic analysis of pouched amphistome parasites (Trematoda: Digenea: Gastrothylacidae) using ribosomal ITS2 sequence and secondary structures (#87)
24	Kim S and Kim W	KBOL: Korea Barcode of Life Database and Species Identification System (#119)
25	Hong, S <i>et al.</i>	Shape-based retrieval of CNV regions in read coverage data (#139)
26	Murakami K <i>et al.</i>	Motif Distribution Viewer: a Web-based tool for finding localized promoter motifs (#152)
27	Kurochkin I <i>et al.</i>	Defining long non-protein coding RNAs associated with neuronal differentiation (#156)
28	Schönbach C.	Prediction and analysis of splicing regulatory signals (#165)
29	Ishikawa M <i>et al.</i>	A method for isoform-level gene expression analysis using RNA-Seq data (#188)
30	Wako H <i>et al.</i>	ProMode-Elastic: database of elastic-network-model based normal mode analysis (#132)
31	Yura K and Nagai Y	Correlation between binding mode of ATP and its usage in proteins (#136)
32	Yamanaka M	A new classification method of protein secondary structure (#149)
33	Singh M <i>et al.</i>	Inhibitory activity of coumarins on HIV-1 PR: a virtual screening and molecular docking study (#32) CANCELLED
34	Choubey J <i>et al.</i>	Comparative docking study of nitrogen containing bisphosphonate with human farnesyl pyrophosphate synthase for treatment of osteoporosis (#64)
35	Kumar S <i>et al.</i>	Modeling of the envelope protein (E) of tick-borne encephalitis virus and their screening of potent drugs using molecular docking approach (#83)

12:45-14:05 Lunch break (lunch boxes will be distributed at the entrance of conference room 1, starting at 12:55)

Sep. 27 (Day 2) continued		 <b>InCoB2010 – The 9th International Conference on Bioinformatics</b> Waseda International Conference Center, Tokyo, September 26-28, 2010	
13:05-13:50		 <b>Computational Biology Research Center</b>	 <b>Luncheon Session</b>
13:05-13:20	<b>Software for next-gen sequencer analysis</b> <b>Kiyoshi Asai</b> - Computational Biology Research Center, AIST, Japan		
13:20-13:40	<b>An exhaustive structural classification at atomic resolution reveals that geometric similarities of protein-protein interfaces are confined within homologous families</b> <b>Akira R. Kinjo</b> - Protein Data Bank Japan and Institute for Protein Research, Osaka University, Japan		
<b>Conference Room 1</b>			
14:05-16:15		<b>Sequence Analysis II</b> (Chair: Kei Yura, Ochanomizu University)	
14:05-14:35	<b>UPS 2.0: unique probe selector for probe design and oligonucleotide microarrays in</b> Shu-Hwa Chen, Chen- Zen Lo, Sheng-Yao Sue, Bao-Han Kuo, Chao A Hsiung and <b>Chung-Yen Lin</b> (BMC Genomics)		
14:35-15:05	<b>NGSQC: cross-platform quality analysis pipeline for deep sequencing data</b> <b>Manhong Dai</b> , Robert Thompson, Christopher Maher, Rafael Contreras, Mark Kaplan, David Markovitz, Gil Omenn and <b>Fan Meng</b> (BMC Genomics)		
15:05-15:15	<b>Alternative splicing pattern recognition in NGS transcriptome data of <i>C. elegans</i> developmental stages</b> <b>Sungmin Kim</b> and Won Kim (poster selected for short talk)		
15:15-15:45	<b>Sequence-dependent histone variant positioning signatures</b> <b>Ngoc Tu Le</b> , Tu Bao Ho and Bich Hai Ho (BMC Genomics)		
15:45-16:15	<b>Clustering ortholog groups in transcript level</b> Yizhen Jia, <b>Thomas Wong</b> , You-Qiang Song, David Smith and Siu-Ming Yiu (BMC Genomics)		
<b>Conference Room 2</b>		    	
9:00-10:45		<b>Systems Biology: Gene Regulatory and Biochemical Networks</b> (Chair: Tatsuya Akutsu, Kyoto University)	
9:00-09:30	<b>Qualitative reasoning of dynamic gene regulatory interactions from gene expression data</b> <b>Yu Chen</b> , Byungkyu Park and Kyungsook Han (BMC Genomics)		
9:30-10:00	<b>Functional Data Analysis for Identifying nonlinear models of gene regulatory networks</b> <b>Georg Summer</b> and Theodore Perkins (BMC Genomics)		
10:00-10:30	<b>Sensitivity analysis of dynamic biological systems with time-delays</b> <b>Wu-Hsiung Wu</b> , Feng-Sheng Wang and Maw-Shang Chang (BMC Bioinformatics)		
10:30-10:45	<b>An integrative strategy for optimizing large-scale biochemical systems</b> Kazuhiro Maeda, Yuya Fukano, Daichi Nitta, Shunsuke Yamamichi and <b>Hiroyuki Kurata</b> (poster selected for short talk)		
10:45-11:45		<b>Coffee Break and Poster Session</b> (Conference Room 3) At least one author must be present at the poster.	
12:45-14:15		<b>Lunch break</b> (Lunch boxes will be distributed at the entrance of conference room 1, starting at 12:55.)	
14:15-16:15		<b>Proteome Analysis: Mutations to Interactions</b> (Chair: Akira Kinjo, Osaka University)	
14:15-14:45	<b>Mining the influenza A proteome for adaptive mutations linked to human transmissibility</b> Olivo Miotto, AT Heiny, Randy Albrecht, Adolfo Garcia-Sastre, Tin Wee Tan, J Thomas August and <b>Vladimir Brusic</b> (IMMS invited talk)		
14:45-15:15	<b>Intrinsically disordered domains deviate significantly from random sequences in innate immune and generic mammalian proteins</b> Shunsuke Teraguchi, Ashwini Patil and <b>Daron Standley</b> (BMC Bioinformatics)		
15:15-15:45	<b>Predicting RNA-binding residues from evolutionary information and sequence conservation</b> <b>Yu-Feng Huang</b> , Li-Yuan Chiu, Chun-Chin Huang and Chien-Kang Huang (BMC Genomics)		
15:45-16:15	<b>Exploring hierarchical and overlapping modular structure in the yeast protein interaction network</b> <b>Changning Liu</b> , Jing Li and Yi Zhao (BMC Genomics)		
16:15-16:45		<b>Coffee Break and Poster Removal</b>	
<b>Conference Room 3</b>		   	
9:15-16:15		<b>Poster Viewing</b>	
10:45-11:45		<b>Poster Session (all posters; no. 1-49)</b> (Chair: Igor Kurochkin, Bioinformatics Institute, A*STAR) At least one author must be present at the poster.	
36	Mallick M <i>et al.</i>	Docking analysis of trypanothione reductase inhibition in <i>Leishmania donovani</i> (#125)	
37	Yagi Y <i>et al.</i>	Computational study of HIV-1 protease using fragment molecular orbital Method (#129)	
38	Kumar S <i>et al.</i>	1,3-DHA, a drug molecule for <i>S. aureus</i> infection by targeting HtsA receptor (#133)	
39	Matsuda K <i>et al.</i>	Analysis of structural aspect of chemical compounds using InChI formats (#153)	
40	Kagawa H <i>et al.</i>	Structure deviation analysis of proteins complexed with various ATP analogs (#154)	
41	Tomita T <i>et al.</i>	Qualitative Inference rules for analyses of biological object interactions (#157)	
42	Verwoerd W	Interactive extraction of subnets: the Netsplitter software implementation (#7)	
43	Bhattacharjee B <i>et al.</i>	Mapping of natural appetite regulating compounds in the appetite regulatory receptor network – an systems biology approach (#109)	
44	Minamide H <i>et al.</i>	Exploring huge parameter space of a large-scale model of biochemical networks (#121)	
45	Tabata S <i>et al.</i>	Development of elementary mode-based algorithms for designing a metabolic system (#124)	
46	Chaturachai S <i>et al.</i>	<i>De novo</i> pathway design platform for exploring biosynthetic capacity in genome scale model of microorganisms as cell factories (#130)	
47	Konishi T <i>et al.</i>	Principal component analysis for designed experiments (#138)	
48	Ito S <i>et al.</i>	Possible behaviors analysis of gene regulatory networks by linear temporal logic (#142)	
49	Miyachika H. <i>et al.</i>	An MCMC algorithm for gene regulatory network prediction with Bayesian network (#158)	
16:15-16:45		<b>Poster Removal</b>	
19:30-21:30		<b>Conference Dinner at Gonpachi</b> in Shibuya	

Sep 28 (Day 3)		 <b>InCoB2010 – The 9<sup>th</sup> International Conference on Bioinformatics</b> Waseda International Conference Center, Tokyo, September 26-28, 2010	
Conference Room 1		 <b>Workshop on Synthetic Biology, Molecular Robotics and Translational Bioinformatics</b>	
		   	
09:15-09:20	<b>Opening Address by Workshop Chair</b> <b>Akihiko Konagaya</b> - Tokyo Institute of Technology		
09:20-10:15	<b>Translational Bioinformatics</b> (Chair: Yutaka Natsumeda, Yokohama City University)		
	<b>InCoB2010–CBI-invited Talk</b> <b>False positives in personalized genomics</b> <b>Dennis P. Wall</b> - Harvard Medical School, USA		
10:15-10:35	<b>Coffee Break</b>		
10:35-12:05	<b>Technical Session</b> (Chair: Akihiko Konagaya, Tokyo Institute of Technology)		
10:35-11:05	<b>StrokeMed: an integrated literature database for stroke and the differentiation of stroke syndrome</b> <b>Young Joo Kim</b> and <b>Young Kyu Park</b> (CBI-invited talk)		
11:05-11:35	<b>On experiences of i2b2 (informatics for integrating biology and the bedside) database with Japanese clinical patients' data</b> <b>Takako Takai-Igarashi</b> , Ryo Akasaka, Kenji Suzuki, Takahisa Furukawa, Makiko Yoshida, Keisuke, Inoue Tomohisa Maruyama, Toshimasa Maejima, Masahiro Bando, Masakazu Takasaki, Miki Sakota, Maki Eguchi, Akihiko Konagaya, Hiroya Matsuura, Toyotaro Suzumura and Hiroshi Tanaka (Bioinformatics)		
11:35-12:05	<b>Semantic visualization of high-dimensional biomedical data</b> <b>Marjan Trutschl</b> , Urska Cvek, Evan Boswell, Phillip Kilgore, Charles McCarthy, John Wessler, Rona Scott, Robert Rhoads and John Clifford (CBI-invited talk)		
12:05-13:30	<b>Lunch Break</b> (Lunch boxes will be distributed at the entrance of conference room 2, starting at 12:05.)		
12:15-13:15	<b>EpiVax Inc. Luncheon Session</b> (Conference Room 2)		
13:30-14:40	<b>Computational Biology in Peta-Scale and Grid Dimensions</b> (Chair: Tin Wee Tan National University of Singapore)		
13:30-14:25	<b>InCoB2010–CBI-Invited Talk</b> <b>Peta-scale computing in network biology</b> <b>Chun-Hsi Huang</b> - University of Connecticut, USA		
14:25-14:45	<b>A metadata management system for composing bioinformatics workflows</b> Takuya Ishibashi, Yoshiyuki Kido, Takanori Fukumoto, Shigeto Seno, Yoichi Takenaka and <b>Hideo Matsuda</b> (Late-breaking abstract)		
14:45-14:50	<b>Break</b>		
14:50-16:30	<b>Molecular Modelling and Protein-Protein Interactions</b> (Chair: Yukio Tada, University of Tokyo)		
14:50-15:20	<b>Molecular modeling study of glucokinase (GK) and its activators</b> <b>Yuno Lee</b> , Songmi Kim, Shalini John and <b>Keun Woo Lee</b> (CBI-invited talk)		
15:20-15:30	<b>In silico prediction of PPI network with structure-based all-to-all docking</b> <b>Masahito Ohue</b> , Yuri Matsuzaki, Yusuke Matsuzaki, Toshiyuki Sato and Yutaka Akiyama (poster selected for short talk)		
15:30-16:00	<b>Improving protein secondary structure prediction based on short subsequences with local structure similarity</b> <b>Hsin-Nan Lin</b> , Ting-Yi Sung, Shinn-Ying Ho and WenLian Hsu (BMC Genomics)		
16:00-16:30	<b>A dynamic programming re-ranking approach to enhance PPI interactor extraction</b> <b>Po-Ting Lai</b> and Richard Tzong-Han Tsai (IPSI Transactions on Bioinformatics)		
16:30-16:50	<b>Coffee Break</b>		
16:50-18:30	<b>Synthetic Biology and Molecular Robotics</b> (Chair: Tsuguchika Kaminuma, CBI Society)		
16:50-17:20	<b>Extending robotics to the molecular scale</b> <b>Satoshi Murata</b> - Tohoku University, Japan (CBI-invited talk)		
17:20-17:50	<b>Biophysical approach to cell-sized molecular robots</b> <b>Masahiro Takinoue</b> - The University of Tokyo, Japan (CBI-invited talk)		
17:50-18:20	<b>Traceable and sharable database of biological experiments in synthetic biology</b> <b>Ibuki Kawamata</b> , Daisuke Kiga, Masanori Arita, Fumiaki Tanaka and Masami Hagiya - University of Tokyo, Japan (CBI-invited talk)		
18:20-18:30	<b>Material fabrication with BioBrick standardized genetic parts</b> <b>Takefumi Moriya</b> , Shohei Kitano, Yumiko Kinoshita, Yusuke Kaneta, Mitsuhiko Odera, Shoya Hirose, Eriko Uchikoshi, Taichi Nakamura, Thiprampai Thamamongood, Ali Motazedian, Misaki Kaneko, Toshitaka Matsubara, Kazuaki Amikura, Shotaro Ayukawa, Masami Hagiya, Masayuki Yamamura and Daisuke Kiga (poster selected for short talk)		
18:30-18:40	<b>Closing Remarks</b> <b>Akihiko Konagaya</b> (Workshop Chair), <b>Kenta Nakai</b> (InCoB Co-chair) and <b>Tin Wee Tan</b> (APBioNet Secretary)		
Notes:			

Sep 28 (Day 3)  
continued



InCoB2010 – The 9<sup>th</sup> International Conference on Bioinformatics  
Waseda International Conference Center, Tokyo, September 26-28, 2010

Conference Room 2	 <b>3<sup>rd</sup> Conference of Basic and Clinical Immunogenomics and Immunomics (BCII)</b>     
09:15-09:20	<b>Opening Address by BCII Conference Chair</b> <b>Vladimir Brusic</b> - Cancer Vaccine Center, Dana-Farber Cancer Institute, Boston, USA
09:20-12:05	<b>New Software Algorithms for Immune System/Infectious Disease Modelling</b> (Chair: Vladimir Brusic, Dana-Farber Cancer Institute, USA)
	<b>InCoB2010 – 3<sup>rd</sup> BCII InvitedTalk</b>
09:20-10:15	<b>HLA targeting of viruses</b> <b>Nebojsa Jovic</b> - Microsoft Research, eScience Group, USA
10:15-10:35	<b>Coffee Break</b>
10:35-11:05	<b>Model refinement through high-performance computing: an agent-based HIV example</b> <b>Dimitri Perrin, Heather J. Ruskin and Martin Crane</b> (Immunome Research)
11:05-11:35	<b>Hierarchical kernel mixture models for the Prediction of AIDS disease progression using HIV structural gp120 profiles</b> <b>Paul D Yoo, Yung Shwen H, Jason Ng, Michael Charlestone, Nitin K Saksena, Pengyi Yang, Albert Y Zomaya</b> (BMC)
11:35-12:05	<b>Modeling the competition between lung metastases and the immune system using agents</b> <b>Marzio Pennisi, Francesco Pappalardo, Arianna Palladini, Giordano Nicoletti, Patrizia Nanni, Pier-Luigi Lollini and Santo Motta</b> (BMC Bioinformatics)
12:05-13:30	<b>Lunch Break</b>
12:15-13:15	 <b>EpiVax Inc. Luncheon Session</b>
	<b>Putting immunoinformatics to work to develop better vaccines and protein therapeutics</b> <b>Anne S. De Groot</b> (talk will be delivered by Leslie Cousens) EpiVax, Inc., USA
13:30-14:55	<b>Next Generation Vaccine Design</b> (Chair: Cao Zhiwei, Tongji University)
	<b>InCoB2010 – 3<sup>rd</sup> BCII Invited Talk</b>
13:30-14:25	<b>Challenges in intelligent vaccine design; the swine flu story</b> <b>Nikolai Petrovsky</b> - Flinders Medical Centre and Flinders University, Australia
14:25-14:55	<b>Bioinformatics analysis of <i>Brucella</i> vaccines and vaccine targets using VIOLIN</b> <b>Yongqun He and Zuoshuang Xiang</b> (Immunome Research)
15:00-16:00	<b>Structural Immunoinformatics</b> (Chair: Christian Schönbach, Kyushu Institute of Technology)
15:00-15:30	<b>Stacking and energetic contribution of aromatic islands at the binding interface of antibody proteins</b> <b>Di Wu, Jing Sun, Tianlei Xu, Shuning Wang, Guoqing Li, Yixue Li and Zhiwei Cao</b> (Immunome Research)
15:30-16:00	<b>pDOCK: a new technique for rapid and accurate docking of peptide ligands to major histocompatibility</b> <b>Javed Khan and Shoba Ranganathan</b> (Immunome Research)
16:00-16:30	<b>Coffee Break</b>
16:30-18:00	<b>Immunoinformatics Applications</b> (Chair: Joo Chuan Tong, Institute for InfoComm Research, A*STAR )
16:30-16:30	<b>Clustering-based identification of clonally-related immunoglobulin gene sequence sets</b> <b>Zhiliang Chen, Andrew M Collins, Yan Wang and Bruno A. Gaeta</b> (Immunome Research)
17:00-17:30	<b>SVM-based prediction of linear B-cell epitopes using Bayes feature extraction</b> <b>Lawrence Wee, Diane Simarmata, Yiu-Wing Kam, Lisa FP Ng and Joo Chuan Tong</b> (BMC Genomics)
17:30-18:00	<b>TAP Hunter: a SVM-based system for predicting TAP ligands using local description of amino acid</b> <b>Tze Hau Lam, Hiroshi Mamitsuka, Ee Chee Ren and Joo Chuan Tong</b> (Immunome Research)
18:00-18:10	<b>Closing Remarks</b>
	<b>Vladimir Brusic</b> (BCII Chair), <b>Christian Schönbach</b> (InCoB2010 Co-chair), <b>Nikolai Petrovsky</b> (IIMMS General Secretary, Immunome Research, Editor-in-Chief) and <b>Shoba Ranganathan</b> (APBioNet President)

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