

GIW 2006
The Seventeenth International Conference on Genome Informatics
Pacifico Yokohama, Japan
December 18–20, 2006

Scope

GIW is the longest running international bioinformatics conference, which provides unique opportunities that bridge theory and experiments, academia and industry, and East and West. Its scope includes all work that is ultimately devoted to the computational understanding of biological systems on a molecular basis.

Sponsored and Organized by

Bioinformatics Center (Kyoto University)
Human Genome Center (University of Tokyo)
Japanese Society for Bioinformatics (JSBi)

Steering Committee

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Registration

Registration should be done at: <http://giw.ims.u-tokyo.ac.jp/giw2006/registration.html> until December 3, 2006. Registration fee includes a copy of Genome Informatics Vol. 17, No. 2 and coffee breaks. We offer registration fee discount for JSBi and ISCB members.

		until Dec. 3, 2006	after Dec. 3, 2006
Standard Registration	Standard	JPY17,000.-	JPY22,000.-
	ISCB Member	JPY16,000.-	JPY21,000.-
	JSBi Member	JPY8,000.-	JPY13,000.-
	JSBi & ISCB Member	JPY7,000.-	JPY12,000.-
Student Registration	Standard	JPY12,000.-	JPY17,000.-
	ISCB Member	JPY11,000.-	JPY16,000.-
	JSBi Member	JPY5,000.-	JPY10,000.-
	JSBi & ISCB Member	JPY4,000.-	JPY9,000.-

(Banquet on December 19 evening : JPY6,000.-)

Secretary and Local Arrangements

Human Genome Center, Institute of Medical Science, University of Tokyo
4-6-1 Shirokanedai, Minato-ku, Tokyo 108-8639, Japan
Tel: +81-3-5449-5615 / Fax: +81-3-5449-5442
E-mail: giw2006@ims.u-tokyo.ac.jp
URL: <http://giw.ims.u-tokyo.ac.jp/giw2006/index.html>

Location

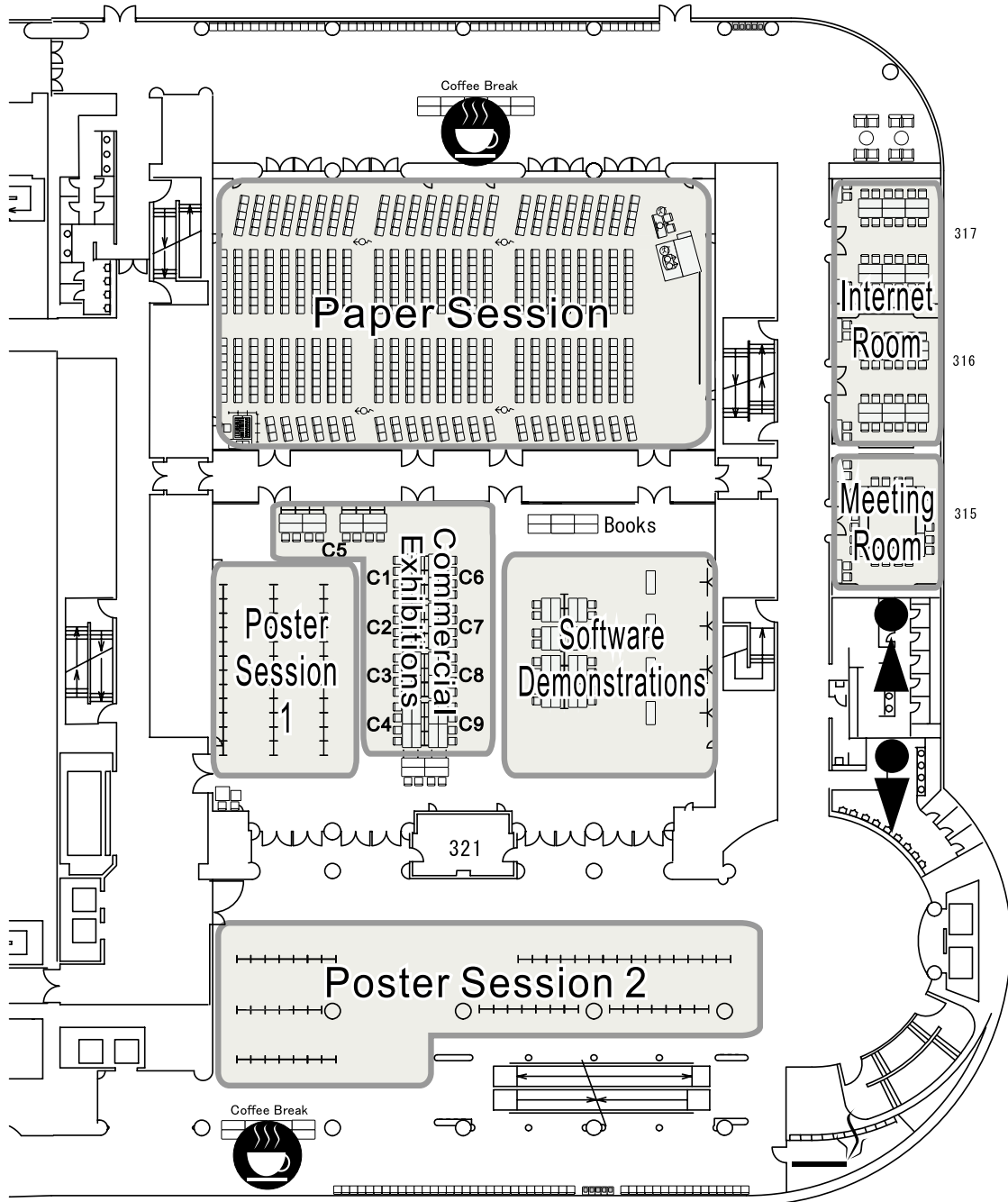
The conference will take place at PACIFICO YOKOHAMA. Please get off at Minato Mirai Station on the Minato Mirai Line (connecting from the Tokyu Toyoko Line). It takes about 3 minutes' walk from the Minato Mirai Station to Pacifico Yokohama.
Address: 1-1-1, Minato Mirai, Nishi-ku, Yokohama 220-0012, Japan
Tel: +81-45-221-2155
URL: http://www.pacifico.co.jp/index_e.html

Conference Center

2F

Registration Desk
Entrance

3F



GIW 2006 Advanced Program

Registration

December 18, 2006: 08:30 - 17:30

December 19, 2006: 08:30 - 18:00

December 20, 2006: 08:30 - 15:30

Monday, December 18, 2006

Opening Address

09:00 - 09:10 Yasubumi Sakakibara(Keio U.) and Temple F. Smith(Boston U.)

Paper Session 1

Chair: Byoung-Tak Zhang (Seoul National U.)

09:10 - 09:35 Hybrid Gibbs-Sampling Algorithm for Challenging Motif Discovery: GibbsDST, *Kazuhito Shida*

09:35 - 10:00 Computational Annotation of Transcription Factor Binding Sites in *D. Melanogaster* Developmental Genes, *Vipin Narang, Wing-Kin Sung, Ankush Mittal*

10:00 - 10:25 A Gram Distribution Kernel Applied to Glycan Classification and Motif Extraction, *Tetsuji Kuboyama, Kouichi Hirata, Kiyoko F. Aoki-Kinoshita, Hisashi Kashima, Hiroshi Yasuda*

10:25: - 11:00 Break

Keynote Address

Chair: Yasubumi Sakakibara (Keio U.)

11:00 - 12:00 RNAs Everywhere: Genome-Wide Annotation of Structured RNAs, *Ivo L Hofacker* (University of Vienna)

12:00 - 13:30 Lunch

Posters and Software Demonstrations Session 1

13:30 - 14:30 (Odd Number)

Paper Session 2

Chair: Masanori Arita (U.Tokyo)

14:30 - 14:55 Discovering Signal Transduction Networks Using Signaling Domain-Domain Interactions, *Thanh Phuong Nguyen, Tu Bao Ho*

14:55 - 15:20 Finding Conserved and Non-Conserved Reactions Using a Metabolic Pathway Alignment Algorithm, *José C. Clemente, Kenji Satou, Gabriel Valiente*

15:20 - 15:45 A Function-Centric Approach to the Biological Interpretation of Microarray Time-Series, *Pablo Minguez, Fátima Al-Shahrour, Joaquín Dopazo*

15:45: - 16:15 Break

Paper Session 3

Chair: Katsuhisa Horimoto (CBRC)

16:15 - 16:40 RaPiDS: An Algorithm for Rapid Expression Profile Database Search, *Paul B. Horton, Larisa Kiseleva, Wataru Fujibuchi*

16:40 - 17:05 Development of an Approach for *Ab Initio* Estimation of Compound-Induced Liver Injury Based on Global Gene Transcriptional Profiles, *Xudong Dai, Yudong D. He, Hongyue Dai, Pek Y. Lum, Christopher J. Roberts, Jeffrey F. Waring, Roger G. Ulrich*

17:05 - 17:30 The Distribution and Deposition Algorithm for Multiple Oligo Nucleotide Arrays, *Kang Ning, Hon Wai Leong*

17:30 - 17:55 Detection and Restoration of Hybridization Problems in Affymetrix GeneChip Data by Parametric Scanning, *Tomokazu Konishi*

Tuesday, December 19, 2006

- Paper Session 4** Chair: Kenji Satou (JAIST)
- 09:00 - 09:25 Gene Ontology Annotation by Density and Gravitation Models, *Wen-Juan Hou, Kevin Hsin-Yih Lin, Hsin-Hsi Chen*
- 09:25 - 09:50 Text Mining and Protein Annotations: the Construction and Use of Protein Description Sentences, *Martin Krallinger, Rainer Malik, Alfonso Valencia*
- 09:50 - 10:15 Assessing Clustering Results with Reference Taxonomies, *Gabriel Valiente*
- 10:15 - 10:45 Break

- Paper Session 5** Chair: Tetsuo Shibuya (U.Tokyo)
- 10:45 - 11:10 Pairwise Alignment with Rearrangements, *Le Sy Vinh, Andrés Varón, Ward C. Wheeler*
- 11:10 - 11:35 Techniques for Multi-Genome Synteny Analysis to Overcome Assembly Limitations, *Arjun Bhutkar, Susan Russo, Temple F. Smith, William M. Gelbart*
- 11:35 - 12:00 A Markov Chain Model for Haplotype Assembly from SNP Fragments, *Rui-Sheng Wang, Ling-Yun Wu, Xiang-Sun Zhang, Luonan Chen*
- 12:00 - 13:30 Lunch

- Keynote Address** Chair: Temple F. Smith (Boston U.)
- 13:30 - 14:30 The New Phase of Transcriptome Analysis, *Yoshihide Hayashizaki (RIKEN,GSC)*

- Paper Session 6** Chair: Hiroyuki Toh (Kyushu U.)
- 14:30 - 14:55 MetaClustering: Discovery of The Different Sample Clusterings in Gene Expression Data, *David Venet, Hugues Bersini, Hitoshi Iba*
- 14:55 - 15:20 Biomarkers for Epithelial Ovarian Cancers, *Pritha Mahata*
- 15:20 - 15:45 PepSOM: An Algorithm for Peptide Identification by Tandem Mass Spectrometry Based on SOM, *Kang Ning, Hoong Kee Ng, Hon Wai Leong*
- 15:45: - 16:00 Break

JSBi Annual Meeting

16:00 - 16:30

Posters and Software Demonstrations Session 2

16:30 - 18:00 (Even Number)

Banquet

18:30 - 20:30 Ballroom "Pacific" at Inter Continental The Grand Yokohama

Wednesday, December 20, 2006

- Paper Session 7** Chair: Gabriel Valiente (Tech.U.Catalonia)
- 09:00 - 09:25 DAPID: A 3D-Domain Annotated Protein-Protein Interaction Database, *Yung-Chiang Chen, Heng-Chu Chen, Jinn-Moon Yang*
- 09:25 - 09:50 A Method to Detect Important Residues Using Protein Binding Site Comparison, *Keunwan Park, Dongsup Kim*
- 09:50 - 10:15 Modeling and Estimation of Dynamic EGFR Pathway by Data Assimilation Approach Using Time Series Proteomic Data, *Shinya Tasaki, Masao Nagasaki, Masaaki Oyama, Hiroko Hata, Kazuko Ueno, Ryo Yoshida, Tomoyuki Higuchi, Sumio Sugano, Satoru Miyano*
- 10:15 - 10:40 A Large-Scale Computational Approach to Drug Repositioning, *Yvonne Y. Li, Jianghong An, Steven J.M. Jones*

Posters and Software Demonstrations Session 3

- 10:40 - 12:00 (Even and Odd Number)
- 12:00 - 13:30 Lunch

- Keynote Address** Chair: Hiroshi Mamitsuka (Kyoto U.)
- 13:30 - 14:30 Increasing Confidence of Protein-Protein Interactomes, *Limsoon Wong* (National University of Singapore)

- Paper Session 8** Chair: Tatsuya Akutsu(Kyoto U.)
- 14:30 - 14:55 A Generalized Threading Model Using Integer Programming that Allows for Secondary Structure Element Deletion, *Kyle Ellrott, Jun-tao Guo, Victor Olman, Ying Xu*
- 14:55 - 15:20 Protein Topology Classification Using Two-Stage Support Vector Machines, *Jayavardhana Gubbi, Alistair Shilton, Michael Parker, Marimuthu Palaniswami*
- 15:20 - 15:45 Robotic Path Planning and Protein Complex Modeling Considering Low Frequency Intra-Molecular Loop and Domain Motions, *Carlos A. Del Carpio, Pei Qiang, Eiichiro Ichiishi, Hideyuki Tsuboi, Michihisa Koyama, Nozomu Hatakeyama, Akira Endou, Hiromitsu Takaba, Momoji Kubo, Akira Miyamoto*

Closing and Award Ceremony

- 15:45 - 16:00

Commercial Exhibitions

- C1: Ryoka Systems Inc.
- C2: NABE International Corporation
- C3: Mathematical Systems, Inc.
- C4: Pathway Solutions Inc.
- C5: SGI Japan, Ltd.
- C6: Active Motif, Inc.
- C7: SCRUM Inc.
- C8: HITACHI, LTD
- C9: BIOBASE GmbH

Software Demonstrations

- S01 Mass Spectral Database for Metabolome Analysis, *Hisayuki Horai, Kazuhiro Suwa, Masanori Arita, Yoshito Nihei, Takaaki Nishioka*
- S02 CADLIVE: Integration for Large-Scale Network Data, *Yuki Shimokawa, Kazuhiro Maeda, Kentaro Inoue, Hiroyuki Kurata*
- S03 RIKEN Natural Products Depository (RIKEN NPDepo), *Hideaki Konno, Takeshi Tomiki, Tomio Saito, Masashi Ueki, Takeo Asaoka, Ryuichiro Suzuki, Masakazu Uramoto, Hideaki Kakeya, Hiroyuki Osada*
- S04 PreSPI: Prediction System for Protein Interaction, *Woo-Hyuk Jang, Choon-Oh Lee, Dong-Soo Han*
- S05 Construction of *Candida Albicans* Protein Network from Yeast Protein Interactions in System Biology, *Chung-Yen Lin, Chieh-Hwa Lin, Chi-Shiang Cho, Fan-Kai Lin, Shu-Hwa Chen, Chao A. Hsiung*
- S06 ExPlain: Causal Analysis of Gene Expression Data from Promoter Models to Signaling Pathways, *Alexander Kel, Holger Karas, Nico Voss, Tagir Waleev, Edgar Wingender*
- S07 Cell Illustrator3.0: A Platform for Biopathway Modeling and Simulation, *Masao Nagasaki, Atsushi Doi, Ayumu Saito, Emi Ikeda, Kazuko Ueno, Euna Jeong, ChristopherJ. Savoie, Satoru Miyano*
- S08 Ajax for Networks and Ontologies, *Kinya Okada, Takahisa Furukawa, Kiyoshi Asai*

Posters

- P001 Serial Regulation on Cell Cycle System in *S.cerevisiae*, *Sachiyo Aburatani, Katsuhisa Horimoto*
- P002 Efficient Inferring Method for Extracting Reliable Interactions from Time Series of Gene Expression Profile, *Masahiko Nakatsui, Takanori Ueda, Maki Yukihiro, Isao Ono, Masahiro Okamoto*
- P003 Emerging Needs for Restructuring Biomedical Knowledge and Education System, *Tsuguchika Kaminuma, Masumi Yukawa, Yoshitomo Tanaka, Takako Takai-Igarashi, Yoshihiro Takemoto, Hiroshi Tanaka*
- P004 Relation between Cell Division and Gene Expression by Using Single Cell Tracking System, *Kazumi Hakamada, Satoshi Fujita, Jun Miyake*
- P005 Identification of Apoptosis-Induced Gene Networks from Time Course Expression Profiles with Replicated Measurements, *Osamu Hirose, Ryo Yoshida, Seiya Imoto, Satoru Miyano*
- P006 p53 Pathways to Simulate the p53 Transcriptional Activity, *Atsushi Doi, Masao Nagasaki, Kazuko Ueno, Hiroshi Matsuno, Satoru Miyano*
- P007 An S-System Application for Mammalian Circadian Clock System, *Daisuke Tominaga, Katsuhisa Horimoto*
- P008 Noise-Induced Robust Synchronization in a Multicellular System, *Ruiqi Wang, Luonan Chen, Kazuyuki Aihara*
- P009 Mathematical Modeling of G1/S Phase in the Cell Cycle with Involving the p53/Mdm2 Network, *Kazunari Iwamoto, Yoshihiko Tashima, Hiroyuki Hamada, Yukihiro Eguchi, Masahiro Okamoto*
- P010 Sensitivity Analysis for the *E.coli* Nitrogen Assimilation System, *Koichi Masaki, Hiroyuki Kurata*
- P011 Analysis for the Conflict between G2/M Phase Arrest in the Cell Cycle and Apoptosis Induction, *Yoshihiko Tashima, Yu Kisaka, Hiroyuki Hamada, Taizo Hanai, Yukihiro Eguchi, Masahiro Okamoto*
- P012 Spatio-Temporal Dynamics of Molecules on the Cell Surface Studied by Particle Simulation, *Ryuzo Azuma, Hiroshi Kobayashi, Tomoyuki Yamamoto, Akihiko Konagaya*
- P013 Consistency of the Transition Theory in Computer Simulation of a Genetic Toggle Switch, *Tomohiro Ushikubo, Masaki Sasai*
- P014 Regulation of Metabolic Networks By Small Molecule Metabolites, *Alex Gutteridge, Minoru Kanehisa, Susumu Goto*
- P015 The Finitely Numerable Effect in the Coupled Molecular Motor Model, *Kazunari Mouri, Tetsuya Shimokawa*
- P016 A Steady-State Approximation-Based Solver for Stiff Biochemical Models, *Emi Shiraishi, Hiroyuki Kurata*
- P017 Genomic Data Assimilation for a Hybrid Functional Petri Net Model of Circadian Rhythm with Time Course Gene Expression Data, *Masao Nagasaki, Rui Yamaguchi, Ryo Yoshida, Seiya Imoto, Atsushi Doi, Yoshinori Tamada, Hiroshi Matsuno, Satoru Miyano, Tomoyuki Higuchi*
- P018 Cell Fate Simulation of ASE Cell in *Caenorhabditis elegans* Using Hybrid Functional Petri Net with Extension, *Ayumu Saito, Masao Nagasaki, Atsushi Doi, Kazuko Ueno, Satoru Miyano*
- P019 A Cluster Identification Method without Using a Threshold of Correlation Coefficient in Hierarchical Cluster Analysis, *Yuki Miyata, Yoichi Yamada, Ken-ichiro Muramoto*
- P020 Cluster Analysis of Transcription Factor Binding Sites in the Promoter Regions of Cardiac Genes in Failing Hearts , *Masaharu Nakayama, Hiroko Tada, Yasuhide Asaumi, Hiroaki Shimokawa*

- P021 Module Discovery in Gene Expression Data Using Closed Itemset Mining Algorithm, *Yoshifumi Okada, Wataru Fujibuchi, Paul Horton*
- P022 A Gene Clustering Method Using Gene Expression Data and Gene Networks, *Motoki Shiga, Ichigaku Takigawa, Hiroshi Mamitsuka*
- P023 Applying Gaussian Distribution-Dependent Criteria to Decision Trees for High-Dimensional Microarray Data, *Raymond Wan, Ichigaku Takigawa, Hiroshi Mamitsuka*
- P024 Computational Analysis of Global Expression Profiles in Mouse Natural Antisense Transcripts, *Yuki Okada, Koji Numata, Rintaro Saito, Hidenori Kiyosawa, Akio Kanai, Masaru Tomita*
- P025 Quantitative Control of Early Transcription by ERK and Akt Signal Transduction, *Takashi Nakakuki, Kaori Ide, Takeshi Nagashima, Kaoru Takahashi, Noriko Yumoto, Mariko Hatakeyama*
- P026 Prediction of Ligand- and ErbB Receptor-Specific Transcription Factors from Time-Course Gene Expression Data of Cancer Cells, *Takeshi Nagashima, Jun Horiuchi, Kenji Nakano, Kaori Ide, Kaoru Takahashi, Mariko Hatakeyama*
- P027 Modeling of Extracellular Matrix Degradation Processes in Cancer Metastasis Using Covariance Structure Analysis, *Akiko Hatano, Kaoru Mogushi, Hiroshi Tanaka*
- P028 Gene Expression Profiling of Hepatocellular Carcinoma Using Independent Component Analysis, *Satoshi Nagaie, Kaoru Mogushi, Hiroshi Tanaka*
- P029 ROKU: An Improved Method for the Detection of Tissue-Specific Expression Patterns, *Koji Kadota, Jiazhen Ye, Yuji Nakai, Tohru Terada, Kentaro Shimizu*
- P030 Identification of Tissue Specific Transcription Factors Using Microarray Gene Expression Data, *Larisa Kiseleva, Ekaterina Shelest, Edgar Wingender, Paul Horton*
- P031 Profiling Prostate Cancer Signatures by Statistical Analysis of mRNA Isoform Expression, *T.Murlidharan Nair, Hai-Ri Li, Xiang-Dong Fu*
- P032 A Comparative Study of Exploratory Analysis versus Statistical Analysis for Oligo-DNA Microarrays, *Kenichiro Kanda, Kaoru Azumi, Nori Satoh, Sorin V. Sabau*
- P033 Genome-Wide Detection of Human Copy Number Variations Using High-Density DNA Oligonucleotide Arrays, *Daisuke Komura, Shumpei Ishikawa, Fan Shen, Kunihiko Nishimura, Sigeo Ihara, Hiroshi Nakamura, Keith W. Jones, Jing Huang, Hiroyuki Aburatani*
- P034 Experimental Design for Time-Series Microarray Analysis, *Ryosuke Ito, Hiroki Takahashi, Taku Oshima, Naotake Ogasawara, Md. Altaf-Ul-Amin, Ken Kurokawa, Shigehiko Kanaya*
- P035 New Gene Filtering Method Using S2N' Based on the Concept of PART Filtering Method, *Hiro Takahashi, Hiroyuki Honda*
- P036 Gene Alignment for Cell Division Cycle Microarray Experiments without Sinusoidal Fittings, *Y-h. Taguchi*
- P037 Power Spectra of Bird-Influenza A Virus (BIV) ssRNA Base Sequences : Possibility of Cooperative Genes or Interferences, *Eisei Takushi, Hiroyuki Sakamoto, Mitsuhiro Seino*
- P038 Gene Finding for Microbial Metagenomics, *Jungho Park, Hideki Noguchi, Toshihisa Takagi*
- P039 Conservation of Regulation Systems in Firmicutes, *Nicolas Sierro, Kenta Nakai*
- P040 Comprehensive Detection of Terminal Oligo-Pyrimidine (TOP)Genes in the Human Genome, *Riu Yamashita, Yutaka Suzuki, Hiroyuki Wakaguri, Sumio Sugano, Kenta Nakai*
- P041 Autoimmune Diseases and Evolutionary Trace of the T-Cell Epitopes, *Wataru Honda, Shuichi Kawashima, Minoru Kanehisa*

- P042 Analysis of Tissue Specific Expression Patterns of Isozymes, *Masataka Takarabe, Akira Tsuchida, Masashi Fujita, Shujiro Okuda, Akiyasu C. Yoshizawa, Takuji Yamada, Masumi Itoh, Susumu Goto, Minoru Kanehisa*
- P043 A Web Application for Identification of Glycosaminoglycan (GAG) Binding Motifs in *Plasmodium Falciparum*, *Nelson Hayes, Johan Normark, Daniel Nilsson, Craig Wheelock, Mats Wahlgren, Susumu Goto*
- P044 Analysis of the Sub-Telomeric Region of the Malaria Parasite *P. Falciparum* Using aCGH Data, *Diego Diez, Ulf Ribacke, Craig Wheelock, Mats Wahlgren, Susumu Goto*
- P045 Proteins with Charge Periodicity of 28 Residues in Amino Acid Sequences from Total Genomes, *Runcong Ke, Shigeki Mitaku*
- P046 Characteristic Distribution of GC Contents for Proteins with Charge Periodicity of 28 Residues, *Ryusuke Sawada, Runcong Ke, Noriyuki Sakiyama, Shigeki Mitaku*
- P047 Analysis and Estimation for the Substituted Sequences of DNA Sequences for *Saccharomyces Cerevisiae* with a Kind of Markov Model, *Mitsuhiro Seino, Hiroyuki Sakamoto*
- P048 Stochastic Local Genome Alignment and Comprehensive Search for Conserved Gene Clusters, *Tsuyoshi Hachiya, Yasubumi Sakakibara*
- P049 Computational Analysis of Human mRNAs Regulated by GRSF-1, a Positive Regulator of *Influenza Virus*, *Hikaru Taniguchi, Kosuke Fujishima, Yuka Watanabe, Yuko Osada, Masaru Tomita, Rintaro Saito, Akio Kanai*
- P050 Significant Deviation in the Configuration of Tandem Repeats in Prokaryotic Genomes, *Shintaro Hirayama, Satoshi Mizuta*
- P051 RNA Base Pairing Probability Alignment by Genetic Algorithm, *Akito Taneda*
- P052 Detailed Analysis of Reentrant Loops and Neighboring Sites in Alpha-Helical Transmembrane Proteins, *Kinya Matsushiro, Wataru Nakahata, Satoshi Mizuta*
- P053 Distribution of Relative Mutation Frequency, *Hyunchul Kim, Masaru Tomita*
- P054 MotifCombinator: A Web Tool to Search for Combinations of Cis-Regulatory Motifs, *Mamoru Kato, Tatsuhiko Tsunoda*
- P055 Frame-Cluster Mapping: Genomewide Analysis for Detection of Localized Signal Regions, *Kou Amano, Hidemitsu Nakamura, Hisataka Numa, Yosiaki Nagamura, Hiroaki Ichikawa, Kaoru Fukami-Kobayashi*
- P056 Analysis of *Aspergillus oryzae* tRNA Genes Using Multivariate Analysis, *Jun-Ichi Sagara*
- P057 Analysis of Amino Acid Sequence by Self Organization Maps, *Takeshi Takahashi, Hiroshi Dozono*
- P058 Prediction of Transcription Factor Binding Sites in *Saccharomyces cerevisiae*, *Takuya Ueno, Hidetoshi Kono, Sarai Akinori*
- P059 Structural Breakpoint Prediction and its Application Based on Dimers in Amino Acid Sequence, *Yoshihide Makino, Nobuya Itoh*
- P060 *Ab-initio* Identification of Promoter Elements in Antimicrobial Peptide-Coding Genes, *Manisha Brahmachary, Christian Schönbach, Liang Yang, Enli Huang, Sin Lam Tan, Rajesh Chowdhary, S.P.T Krishnan, Chin-Yo Lin, David A Hume, Chikatoshi Kai, Jun Kawai, Piero Carninci, Yoshihide Hayashizaki, Vladimir B Bajic*
- P061 Structural Analysis on Functional Epitope, *Jian Huang, Minoru Kanehisa*
- P062 A GP Based Algorithm for HP-Model Problem, *Takahiro Yabuki, Hitoshi Iba*

- P063 Combining Molecular Dynamics Simulation with a Graph Theoretical Approach to Study Protein Complex Flexibility, *AbdulRajjak Shaikh, Mohamed Ismael, Pei Qiang, Hideyuki Tsuboi, Michihisa Koyama, Nozomu Hatakeyama, Akira Endou, Hiromitsu Takaba, Momoji Kubo, Eiichiro Ichiishi, Carlos A. Del Carpio, Akira Miyamoto*
- P064 Inferring Domain Combination Pattern and Its Biological Meaning via Association Rules, *Sukhoon Jung, Dong-soo Han, Sung-doke Lee*
- P065 A Novel Method to Determine the Assembling Space between Two Protein Subunits, *Miki Maeda, Hiroya Nobori*
- P066 Biomolecular Computations toward Enzyme-Catalyzed Transformations of Non-Natural Organic Compounds: *Ab initio* Fragment Molecular Orbital Calculations, *Takahisa Tanaka, Takatomo Kimura, Yoichiro Yagi, Yoshinobu Naoshima*
- P067 Can Brownian Dynamics be a Useful Tool for Structure-Based Drug Design?, *Akifumi Oda, Hisao Matsuzaki, Noriyuki Yamaotsu, Shuichi Hirono*
- P068 A Benchmark Study of the “Soft Docking” Module of MIAx, Using a Set of Unbound Proteins, *Pei Qiang, Mohamed Ismael, Abdul Rajjak Shaikh, Hideyuki Tsuboi, Michihisa Koyama, Nozomu Hatakeyama, Akira Endou, Hiromitsu Takaba, Momoji Kubo, Eiichiro Ichiishi, Carlos A. Del Carpio, Akira Miyamoto*
- P069 Supervised Consensus Scoring Methods for Structure-Based Drug Design, *Reiji Teramoto, Hiroaki Fukunishi*
- P070 Scoring Analysis of DNA Binding Sites of DNA Binding Proteins, *Reika Okihara, Yukako Sakatsuji, Ayumi Suzuki, Ichiro Yamato, Satoru Miyazaki*
- P071 Classification of Protein-DNA Complexes Based on Structural Descriptors, *Ponraj Prabakaran, Shandar Ahmad, M. Michael Gromiha, Maria G. Singarayan, Akinori Sarai*
- P072 Comparative Analysis of Amino Acid Residues and Structures between RNase HII and Argonaute Proteins from *Pyrococcus furiosus*, *Sayaka Kitamura, Kosuke Fujishima, Asako Sato, Arun Krishnan, Masaru Tomita, Akio Kanai*
- P073 Mulet: A Practical Multiple Alignment Tool for Structural RNA Sequences, *Hisanori Kiryu, Yasuo Tabei, Taishin Kin, Kiyoshi Asai*
- P074 fRNadb: A Platform for Mining/Annotating Functional RNA Candidates from Non-Coding RNA Sequences, *Taishin Kin, Kouichirou Yamada, Goro Terai, Hiroaki Okida, Yasuhiko Yoshinari, Yukiteru Ono, Aya Kojima, Takashi Komori, Kiyoshi Asai*
- P075 RNamine: Frequent Stem Pattern Miner from RNAs, *Michiaki Hamada, Koji Tsuda, Taku Kudo, Taishin Kin, Kiyoshi Asai*
- P076 An Evolving Zipper Automaton for RNA Secondary Structure Prediction: Improvement by Sequence Homology Inclusion, *Carlos A. Del Carpio M., Mohamed Ismael, Eiichiro Ichiishi, Hideyuki Tsuboi, Michihisa Koyama, Nozomu Hatakeyama, Akira Endou, Hiromitsu Takaba, Momoji Kubo, Akira Miyamoto*
- P077 Comprehensive Analysis of miRNA Effect to the Transcripts, *Keishin Nishida, Riu Yamashita, Kengo Kinoshita, Kenta Nakai*
- P078 Multiple Alignment of RNAs by Maximizing the Sum of the Matching Probability of Stem Fragments, *Yasuo Tabei, Hisanori Kiryu, Taishin Kin, Kiyoshi Asai*
- P079 Phylogenetic Analysis of Essential Genes by Using ORI-GENE, *Hirotooshi Kawano, Hideaki Mizuno, Akinori Sarai*
- P080 Evidence for ‘ Introns-Late ’ from Intron Phase Distribution, *Hung Dinh Nguyen, Maki Yoshihama, Naoya Kenmochi*
- P081 Algebraic Evolution of the Genetic Code, *Takashi Kawamura*

- P082 Distance Structure of Homologous Gene Cluster in *Cyanobacteria*, *Naobumi Sasaki, Naoki Sato*
- P083 Tracing Back Xenobiotic Responsive and NR Mediated Pathways/Networks, *Yoshitomo Tanaka, Masumi Yukawa, Hiroshi Tanaka, Tsuguchika Kaminuma*
- P084 Analyses of the Nutrient Dependency of Parasites to Hosts Using KEGG Database, *Ai Muto, Masahiro Hattori, Wataru Honda, Minoru Kanehisa*
- P085 Identification of Novel Types of Prokaryotic Retroelements Based on Gene Neighborhood and Protein Architecture, *Kenji K. Kojima, Minoru Kanehisa*
- P086 Comprehensive Analysis of Domain Architectures of Transmembrane Proteins, *Syu-ichi Yoshida, Yoshihiro Yamazaki, Takuhiro Nishio, Sunao Kaneko, Toshio Shimizu*
- P087 Gene Expression Profile Analysis for Circadian Promoter Activities of Cyanobacterial Bioluminescent Reporter Strains Using Non-Metric Multidimensional Scaling, *Tokitaka Oyama, Hiroshi Ito, Takao Kondo, Y-h. Taguchi*
- P088 Comparative Sequence Analysis between Human and Mouse: Promoter Conservation and Protein Conservation, *Hirokazu Chiba, Riu Yamashita, Kengo Kinoshita, Kenta Nakai*
- P089 Whole-Genome Functional Linkage Network Construction in the Domain Level by Probabilistic Model, *Yong Wang, Rui-Sheng Wang, Xiang-Sun Zhang, Luonan Chen*
- P090 Systematic Analysis of Functional SNP with Type 2 Diabetes Mellitus (T2DM) in the Korean Population, *Hyo-Jeong Ban, Keun-Joon Park, Ji-Hong Kim, Hyun-Woo Han*
- P091 Analysis of Disease-Associated Mutations and SNP in Relationship with Protein Structure, *Taku Ashikari, Hidetoshi Kono, Akinori Sarai*
- P092 Adaptive Threshold for Detecting Significant Fold Changes in Microarray Data, *Hide-nori Inaoka, Yutaka Fukuoka*
- P093 Precise Correlation between MLV Integration Sites and Transcription Start Sites in the Human Genome, *Yoshiaki Tanaka, Riu Yamashita, Kengo Kinoshita, Kenta Nakai*
- P094 Hierarchical Bayes Approach to Array CGH Data Normalization, *Shigeyuki Oba, Shin Ishii*
- P095 Development of a Platform for Functional Genomics under the Generation Challenge Programme (GCP), *Masaru Takeya, Kohji Suzuki, Koji Doi, Shoshi Kikuchi, Richard Bruskiwich*
- P096 Annotating Genes with Labelled and Unlabelled Data, *Xing-Ming Zhao, Luonan Chen, Kazuyuki Aihara*
- P097 Developing SVM Classifier for GPI-(Like)-Anchored Proteins Prediction, *Wei Cao, Shugo Nakamura, Kentaro Shimizu*
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