

Accepted Posters

- P001 GC Content Provides New Insights into Exon Recognition *Eddo Kim, Amir Goren, Maayan Amit, Gil Ast*
- P002 Immigrants to the Nucleus; Analysis of Mitochondrial-like Fragments in Human Genome *Junko Tsuji, Paul Horton*
- P003 How (not) to align Genomes *Martin C. Frith, Michiaki Hamada, Paul Horton*
- P004 Expression Profile in Various Stages of Gametogenesis Correlates with the Alu Distribution Pattern in Human Genome *Hiroki Ashida, Toutai Mituyama, Kiyoshi Asai*
- P005 Properties of the Word Set for Estimating Similarities between Prokaryotic Genomes in Linguistic Approach *Keishin Hanya, Satoshi Mizuta*
- P006 Comparative Genomic Analysis of Unicellular to Seed Plants by Using Gene Functions of *A.thaliana* *Mai Kawazoe, Hiroki Takahashi, Masayoshi Wada, Aki Hirai, Kensuke Nakamura, Md. Altaf-Ul-Amin, Shigehiko Kanaya*
- P007 The Evolution of Metazoan Mitochondrial Genome and Latent Biological Mechanisms *Haidong Tan, Masaharu Seno*
- P008 Detection of Mosaic Structure of Syntenic Segments in Marine Cyanobacterial Genomes *Naobumi V. Sasaki, Naoki Sato*
- P009 Contribution of Mobile Genetic Elements on Variation in Gene Content among Bacteria *Haruo Suzuki, Michael J. Stanhope*
- P010 Comparative Analysis of Information Contents Relevant to Intron Recognition in Many Species *Hiroaki Iwata, Osamu Gotoh*
- P011 Plant Gene Identification Based on Cross-Species Mapping of Full-Length cDNAs *Naoki Amano, Tsuyoshi Tanaka, Hisataka Numa, Hiroaki Sakai, Takeshi Itoh*
- P012 Integrated Transcriptional Regulatory Networks Identify Differences in Iron Regulation Across and within *Yersinia* Species *Xin-Yi Chua, James Hogan*
- P013 The Functional Diversity of GPCR Genes Observed from Comparative Genome Analysis. *Makiko Suwa, Yukiteru Ono, Wataru Fujibuchi*
- P014 A Method for Extracting Optimal Sequence Related to Biological Activity *Tatsuya Noshio, Ko Kato, Hiroki Takahashi, Md. Altaf-Ul-Amin, Shigehiko Kanaya*
- P015 Evolution of Human Phosphorylation Sites *Dong Seon Kim, Yoonsoo Hahn*
- P016 Prediction of the *O*-glycosylation by Support Vector Machine and Independent Component Analysis for Amino Acid Sequence around *O*-glycosylation *Yukiko Nakajima, Kazutoshi Sakakibara, Masahiro Ito, Ikuko Nishikawa*
- P017 Detection of Tissue-Specific Genes and Computational Analysis of Testis-Specific Gene Expression Regulatory Regions *Akifumi Yamashita, Naohisa Goto, Seiji Nishiguchi, Kazunori Shimada, Hiromichi Yamanishi, Teruo Yasunaga*
- P018 Pairwise RNA Pseudoknotted Structure Prediction Based on Stochastic Grammar *Nobuyoshi Mizoguchi, Yuki Kato, Hiroyuki Seki*
- P019 The Effect Read Length has on the Performance of Adaptive Seeds for Sequence Alignment *Raymond Wan, Szymon M. Kielbasa, Paul Horton, Martin C. Frith*
- P020 Prediction of Eukaryotic Translation Initiation Sites Using Machine Learning *Yoko Ishino*
- P021 Selectivity of Cis-Element Data and its Analysis with an Informatics Approach *Yuya Yamazaki, Tomonori Suzuki, Satoru Miyazaki*

- P022 Comprehensive Analysis of Polyketide Synthase Families *Yugo Shimizu, Masaaki Kotera, Toshiaki Tokimatsu, Masahiro Hattori, Susumu Goto, Minoru Kanehisa*
- P023 A Multi-Objective Genetic Algorithm for Pairwise RNA Sequence Alignment *Akito Taneda*
- P024 Molecular Evolutionary Analysis of Primary Immunodeficiency Associated Genes *Tomotaka Koyama, Katsuhiko Mineta, Toshinori Endo*
- P025 Inference of Geographic Transmission Probability of Influenza Viruses from a Large Phylogenetic Tree *Fumiaki Yanagihashi, Kimihito Ito, Hiroki Arimura*
- P026 New trend of Biodiversity Informatics Based on Global Biodiversity Information Facility (GBIF) and Barcode of Life (BoL) *Yasumasa Shigemoto, Yoshikazu Kuwana, Hideaki Sugawara*
- P027 Analysis of Plant UGT Family Sequences and Substrate Specificity *Yosuke Nishimura, Toshiaki Tokimatsu, Masaaki Kotera, Susumu Goto, Minoru Kanehisa*
- P028 Complicated Evolutionary History of Wild and Cultivated Asian Rice Disclosed by Gene Tree Incongruence Analysis *Ching-chia Yang, Hiroaki Sakai, Takeshi Itoh*
- P029 TANGLE: an Integrated Server for Protein Backbone Torsion Angle Prediction *Jiangning Song, Hao Tan, Khalid Mahmood, Geoffrey Webb, Tatsuya Akutsu, James Whisstock*
- P030 Analysis of Glycan Recognition Sites of Viruses *Shota Yamada, Sayaka Takase, Kiyoko F. Aoki-Kinoshita*
- P031 Development of a New Glycan Score Matrix *Yukie Akune, Kiyoko F. Aoki-Kinoshita*
- P032 Identifying Functional Motifs on Protein Surfaces by Structural Alignment with Sequence Information *Zhi-Ping Liu, Ling-Yun Wu, Yong Wang, Takashi Yamamoto, Xiang-Sun Zhang, Luonan Chen*
- P033 Improvement of All-to-All Protein-Protein Interaction Prediction System MEGADOCK *Masahito Ohue, Yusuke Matsuzaki, Yuri Matsuzaki, Yutaka Akiyama*
- P034 Classification of Protein Fragments with a Graph Spectral Technique *Jun-ichi Ito, Junichi Higo, Kentaro Tomii*
- P035 Classification and Identification of Indiscernible Metal Binding Sites of Proteins *Yuki Sakashita, Jun-ichi Ito, Kiyoshi Asai, Kentaro Tomii*
- T001/P036 Dynamic Programming Algorithms for RNA Structure Prediction with Binding Sites *Unyane Poolsap, Yuki Kato, Tatsuya Akutsu*
- P037 Identification of DNA Methylation Which Leads to Differences of Gene Interaction Network between Cell Types *Michio Kamiya, Kenji Satou, Yoichi Yamada*
- P038 Gene-Expression-Based Disease Class Classification Using Probit Model *Hideyuki Takahashi, Toshimasa Yamazaki, Hiroki Sasaki*
- P039 Finding Informative Genes Related to Alzheimer Disease using Supervised Independent Component Analysis *Faezeh Dorri, Houshang Hassibi, Seyed Hassan Paylakhi, Elahe Elahi*
- P040 Correction and Integration of Normalized Microarray Data *Takashi Yoneya, Tatsuya Miyazawa*
- P041 Microarray-Based Classification of Seed-Specific Gene Expression for Pigmentation in Colored Rice *Changkug Kim, Unghan Yoon, Dowon Yun, Gangseob Lee, Yonghwan Kim*
- P042 Annotating Gene Functions by Spectral Clustering for Combining Gene Expressions and Sequences *Limin Li, Motoki Shiga, Wai-ki Ching, Hiroshi Mamitsuka*
- P043 Molecular Network Analysis Suggests Aberrant CREB-Mediated Gene Regulation in the Alzheimer's Disease Hippocampus *Jun-ichi Satoh, Shinya Obayashi, Hiroko Tabunoki*

- P044 Analyzing Histone Codes by a Computational Approach *Yayoi Natsume-Kitatani, Motoki Shiga, Hiroshi Mamitsuka*
- P045 Genome-Wide Three-Way Gene Interactions from Transcript and Genotype Data *Mitsunori Kayano, Ichigaku Takigawa, Motoki Shiga, Koji Tsuda, Hiroshi Mamitsuka*
- P046 Prevailing Cancer Transcriptional Networks Revealed by Meta-Analysis of Cancer Transcriptomes *Atsushi Niida, Seiya Imoto, Masao Nagasaki, Rui Yamaguchi, Satoru Miyano*
- P047 Subspace Clustering of Gene Expression Data with Prior Knowledge *Yoko Omura, Jun Sese*
- P048 Cytokine Productions and Gene Expressions Caused by Mechanical Stretching of Normal Human Pulmonary Artery Endothelial Cells *Kozue Kobayashi, Masumi Tanaka, Hidenori Inaoka, Satoru Nebuya, Yutaka Fukuoka, Hirotsuke Kobayashi, Makoto Noshiro*
- P049 Data Analysis of Genomic Alteration by Environmental Toxicant *Yu Ri An, Seung Jun Kim, Hye-Won Park, Jong Pil Youn, Jung Mi Ha, Moon-Ju Oh, Seung Yong Lee, Jung-Hwa Oh, Seok-Joo Yoon, Seung Yong Hwang*
- P050 Co-Expression Analysis in Close Physical Proximity Using Tumor Data *Hidenori Inaoka, Yutaka Fukuoka, Makoto Noshiro*
- P051 Distinguishing Tumors from Normal by Cell Surface Marker with Spherical SOM *Yuh Sugii, Ling Chen, Heizo Tokutaka, Masaharu Seno*
- P052 *Aspergillus Niger*: Mapping Fungal Specific Zinc-Finger Transcription Factors to Gene Co-Expression Networks *Benjamin M. Nitsche, Vera Meyer, Arthur F.J. Ram*
- P053 Comparison of Transcriptional Regulatory Network Based on Cis-Module Database *Shizu Akasaka, Tomoko Urushibara, Tomonori Suzuki, Satoru Miyazaki*
- P054 Quality Control and Reproducibility in DNA Microarray Experiments *André Fujita, João Sato, Fernando H.L da Silva, Maria C. Galvão, Mari C. Sogayar, Satoru Miyano*
- P055 A Statistical Method of Analyzing Global Gene Expression Data Obtained from Experiments Using Japanese Herbal Medicine *Masayuki Shojo, Akira Katoh, Tatsuhiko Ikeda, Yuka Ninomiya, Masatomo Sakurai, Tomoyuki Hayasaki, Toshihiko Hanawa, Hiroki Takahashi, Md. Altaf-Ul-Amin, Kyosuke Nomoto, Shigehiko Kanaya*
- P056 A Web Tool for Expression Pattern-Based Data Retrieval and Relevant Network Discovery from vast Public Microarray Database *Chunlai Feng, Michihiro Araki, Ryo Kunimoto, Akiko Tamon, Hiroki Makiguchi, Satoshi Nijima, Gozoh Tsujimoto, Yasushi Okuno*
- P057 A Method of Estimation of Crosstalk Genes with Multiple Time-Series Gene Expression Profiles *Kiyoshi Yoshizawa, Shigeto Seno, Yoichi Takenaka, Hideo Matsuda*
- P058 Reinterpretation of the Database Search Result Using Trans-Proteomics Pipeline in Mass Spectrometry-Based Proteomics *Kyung-Hoon Kwon, Sang Kwang Lee, Kun Cho, Gun Wook Park, Byeong Soo Kang, Young Mok Park*
- P059 Time and Space Efficient Implementation of Robust Biclustering Algorithm (ROBA) *Muhammad Ibrahim, Nasimul Noman, Hitoshi Iba*
- P060 A Study of Different Rule Selection Strategies for Rule Based SNP Imputation *Yue Wang, Guimei Liu, Limsoon Wong*
- P061 Discovering CNVs from Read Depth Analysis of Next Generation Sequencing Data *Alexej Abyzov, Alexander Eckehart Urban, Michael Snyder, Mark Gerstein*
- P062 Accurate Assignment of Short Pyrosequencing Reads in a 16S rRNA Taxonomy *José C. Clemente, Jesper Jansson, Gabriel Valiente*
- P063 Bayesian Analysis of Perturbed *Escherichia coli* metabolism *Seung Min Yoo, Hyun Uk Kim, Tae Yong Kim, Sang Yup Lee*

- P064 Adjustable Diffusion Matrix-Based Spectral Clustering for Protein-Protein Interaction Network
Kentaro Inoue, Hiroyuki Kurata
- P065 Novel Robustness Analysis Reveals Remarkable Robustness of Dual Feedback Loops in a Circadian Clock
Kazuhiro Maeda, Hiroyuki Kurata
- P066 Module Decomposition and Integration Method Optimizes a Large-Scale Cell Cycle Model
Daichi Nitta, Hiroyuki Kurata
- P067 Metabolite Essentiality Analysis Using Genome-Scale Metabolic Networks of Pathogens for the Drug Discovery
Sang Yup Lee, Hyun Uk Kim, Tae Yong Kim
- P068 Metabolic Network Reconstruction and Pathway Analysis of *Mannheimia Succiniciproducens*
Seung Min Yoo, Tae Yong Kim, Hyung Rok Choi, Sang Yup Lee
- P069 Proteome Analysis of the Succinic Acid Producer *Mannheimia Succiniciproducens* and Byproduct Elimination Strategy
Yu Hyun Lee, Jeong Wook Lee, Meehee Kim, Sang Yup Lee
- P070 Adaptive Response to Low Level of an Alkylating Agent in *Escherichia coli* K-12 and *ada* Mutant Strains by Transcriptome and Proteome Analyses
Yu Hyun Lee, Mee-Jung Han, Jong Hwan Baek, Sang Yup Lee, Meehee Kim
- P071 Genome-Wide Mutational and Expression Analyses of Evolved *Escherichia Coli* Strains Under Ethanol Stress
Takaaki Horinouchi, Kuniyasu Tamaoka, Chikara Furusawa, Takashi Hirasawa, Naoaki Ono, Shingo Suzuki, Tetsuya Yomo, Hiroshi Shimizu
- P072 Modeling of Early Sporulation in *Bacillus Subtilis* with Hybrid Functional Petri net
Jin Hwan Do, Masao Nagasaki, Satoru Miyano
- P073 Model Analysis of Helper T Cell Differentiation with Transcriptional Factor's Interactions in Th0
Satoshi Yamada, Akihiko Yoshimura
- P074 Systematic Identification of Differential Expression Networks in Chemosensitive and Chemoresistant Ovarian Cancer
Shih-Yi Chao, A-Mei Huang
- P075 Comparing Biological Networks via Graph Compression
Morihiro Hayashida, Tatsuya Akutsu
- P076 Prediction of Transcriptional Patterns of Gene Deletion Mutants by Modified Control Effective Flux
Quanyu Zhao, Hiroyuki Kurata
- P077 Construction of Transcriptional Regulatory Network during Rice Anther Development
Luo-nan Chen, Wenjuan Zhang, Takashi Yamamoto, Shunsuke Okuzumi, Zhiping Liu
- P078 Elucidation of Metabolic Pathway under the Influence of Gene Regulatory Network
Yuta Hamano, Kozo Nishida, Takuya Morimoto, Hiroki Takahashi, Md Altaf-Ul-Amin, Shigehiko Kanaya
- P079 Kinetic Modeling of Central Metabolic Pathway for Phenotype MicroArray Analysis
Yusaku Mazaki, Hirotada Mori, Masahiro Ito, Yukako Tohsato
- P080 A Method for the Inference of Gene Regulatory Networks based on Dynamic Bayesian Network with Clustering of Time-Series Subsequences
Yuya Shuto, Shigeto Seno, Yoichi Takenaka, Hideo Matsuda
- T002/P081 Dissecting Protein-Protein Interaction-Mediated Cross-Talk Pathways in Hepatocellular Carcinoma
Chia-Hung Liu, Chun-Nan Hsu, Cheng-Yan Kao, Minoru Kanehisa, Susumu Goto, Chi-Ying F. Huang
- P082 Estimating Dynamic Gene Networks Under Different Biological Conditions
Teppey Shimamura, Seiya Imoto, Rui Yamaguchi, Masao Nagasaki, Satoru Miyano
- P083 Cancer Related Pathways are Enriched Among Common Human Targets in Viruses-Human Interactions
Dai-Shin Chen, Wen-Chih Cheng, Wan-Jing Lu, Chen-hsiung Chan

- P084 Effective Multi-Scale Graph Navigation System Powered by Fast and Biologically Meaningful Hierarchical Clustering *Thanet Praneenarat, Wataru Iwasaki, Toshihisa Takagi*
- P085 Robustness Analysis on Lateral Propagation Mechanism of EGF Signaling by L_2 -induced Gain *Makoto Ogawa, Takashi Nakakuki*
- T004/P086 A Parallel Algorithm for Estimating Genome-Wide Gene Networks using Nonparametric Bayesian Networks *Yoshinori Tamada, Seiya Imoto, Hiromitsu Araki, Masao Nagasaki, Satoru Miyano*
- P087 Active State Transition Diagram Analysis from Time Course Simulation Data: an HFPNe Approach *Chen Li, Masao Nagasaki, Ayumu Saito, Satoru Miyano*
- P088 Network Based Analysis of Hepatitis C Virus Infection *Lokesh Tripathi, Kohji Moriishi, Yoshio Mori, Yoshiharu Matsuura, Yi-an Chen, Kenji Mizuguchi*
- P089 Gene Network Comparison by State Space Models Based on Time Course Microarray Data *Kaname Kojima, Rui Yamaguchi, Seiya Imoto, Mai Yamauchi, Masao Nagasaki, Ryo Yoshida, Tepei Shimamura, Kazuko Ueno, Tomoyuki Higuchi, Noriko Gotoh, Satoru Miyano*
- P090 Sensitivity Analysis of MAPK-Induced Transcription Control of Fos Protein by using L_2 -induced Gain *Hiroki Ishiyama, Takashi Nakakuki*
- P091 PGFeval: Software Tool and Web Server for Evaluation and Visualization of Proteogenomic Features *Mohamed Helmy, Masaru Tomita, Yasushi Ishihama*
- P092 Pathway Projector: an Interactive Pathway Browser with Zoomable User Interface *Nobuaki Kono, Kazuharu Arakawa, Ryu Ogawa, Nobuhiro Kido, Kazuki Oshita, Keita Ikegami, Satoshi Tamaki, Masaru Tomita*
- P093 Temporal Gene Expression Patterns Reveal Mass Conservation in TNF- α Signaling *Ken-taro Hayashi, Masaru Tomita, Masa Tsuchiya, Kumar Selvarajoo*
- P094 Reconstruction and Analysis of Integrated Metabolic Reaction Network of *Bacillus Subtilis* *Kozo Nishida, Hiroki Takahashi, Kensuke Nakamura, Md Altaf-Ul Amin, Shigehiko Kanaya*
- P095 Quantitative Cell Division Dynamics Information from Early *C.elegans* Embryos *Koji Kyoda, Eru Adachi, Junko Kuramochi, Kumiko Shimada, Shuichi Onami*
- P096 Robustness of Attractor in Complex Networks with Scale-Free Topology III *Shu-ichi Kinoshita, Kazumoto Iguchi, Hiroaki S. Yamada*
- P097 Gene Function Prediction via Discriminative Graph Embedding *Canh Hao Nguyen, Hiroshi Mamitsuka*
- P098 Using Local Reaction Structure to Build a Global Metabolic Network Classifier *Timothy Hancock, Hiroshi Mamitsuka*
- P099 REST/SOAP Web Service API for G-language System *Kazuharu Arakawa, Nobuhiro Kido, Kazuki Oshita, Masaru Tomita*
- P100 Efficient Computation of Impact Degrees for Multiple Reactions in Metabolic Networks with Cycles *Yang Cong, Takeyuki Tamura, Tatsuya Akutsu, Wai-Ki Ching*
- P101 Improvements to Profile PSTMM for Glycan Recognition Profile Prediction *Sakiko Kaiya, Masae Hosoda, Kiyoko F. Aoki-Kinoshita*
- P102 Semantic Classification of Nouns in UMLS Using Google Web 1T 5-gram *Aika Myosho, Kenji Nakano, Yoichi Yamada, Kenji Satou*
- P103 KBWS: an EMBASSY Package for Effective Utilization of Bioinformatics Web Services *Kazuki Oshita, Kazuharu Arakawa, Masaru Tomita*
- P104 Classification of Adrenergic Receptors Using the Multi-Dimensional Method *Yasuhito Inoue, Yuki Kinoshita, Jyunpei Seki, Ryosuke Hanbayashi*

- P105 Classification of Neuroimaging Figures toward Automatic Figure Annotation System *Natsu Ishii, Asako Koike, Toshihisa Takagi*
- P106 Biomedical Figure Search Using Combination of Bag of Keypoints and Bag of Words *Asako Koike, Natsu Ishii, Toshihisa Takagi*
- P107 Mining Significant Substructure-Substructure Pairs in Structural Associations *Ichigaku Takigawa, Koji Tsuda, Hiroshi Mamitsuka*
- P108 Graph Summarization for Finding Relations of Protein Functions *Aika Terada, Jun Sese*
- P109 Reliable Augmentation of Protein Interaction Data with Interologs for Protein Function Prediction *Chern Han Yong, Limsoon Wong*
- P110 A New Approach to Analyzing DNA Microarray Data Using Principal Component Analysis *Jun-ichi Sagara, Hideaki Koike, Yasunobu Terabayashi, Motoaki Sano, Noriko Yamane, Noriko Yamane, Mitsuko Dohmoto, Ken Oda, Eiji Ohshima, Kuniharu Tachibana, Yoshimasa Higa, Shinichi Ohashi, Masayuki Machida*
- P111 FUJI Database Provides Functional and Structural Annotation of Proteins On Demand *Kei-ichi Homma, Hideaki Sugawara*
- P112 MetalMine: a Database of Functional Metal-Binding Sites in Proteins *Kensuke Nakamura, Aki Hirai, Hiroki Takayashi, Md. Altaf-Ul-Amin, Shigehiko Kanaya*
- P113 On-the-Fly Link Generation for Workflows in Biology *Yeondae Kwon, Yasumasa Shigemoto, Yoshikazu Kuwana, Hideaki Sugawara*
- P114 CaMPDB: a Resource for Calpain and Modulatory Proteolysis *David A. du Verle, Ichigaku Takigawa, Yasuko Ono, Hiroyuki Sorimachi, Hiroshi Mamitsuka*
- P115 Incorporation of New Data and Development of User Management and Feedback System in RINGS *Junichi Araki, Masatoshi Shimahara, Anna Kokubu, Kiyoko F. Aoki-Kinoshita*
- P116 Consecutive Update of the Microbial Genome Re-Annotation Database, GTPS *Takehide Kosuge, Yasumasa Shigemoto, Yoshikazu Kuwana, Hideaki Sugawara*
- P117 SDOPDB: Comparative Standardized-Protocol Database for Mouse Phenotyping Analyses *Nobuhiko Tanaka, Kazunori Waki, Hideki Kaneda, Tomohiro Suzuki, Ikuko Yamada, Tamio Furuse, Kimio Kobayashi, Hiromi Motegi, Hideaki Toki, Maki Inoue, Osamu Minowa, Tetsuo Noda, Keizo Takao, Tsuyoshi Miyakawa, Tsuyoshi Koide, Shigeharu Wakana, Hiroshi Masuya*
- P118 FlyGlycoDB: a Database of Glycan-Related Genes and Proteins in Drosophila *Kiyoshi Tadahisa, Shoko Nishihara, Kiyoko F. Aoki-Kinoshita*
- P119 Omics Data Analysis Using SOP (Search of Omics Pathway) Web Tool *Seung Yong Lee, Jun-Sub Kim, Seung-Jun Kim, Ji-Hoon Kim, Hye-Won Park, Yu Ri An, Moon-Ju Oh, Seung Yong Hwang*
- T003/P120 DDBJ Read Archive and DDBJ Read Annotation Pipeline: An Archive Database and an Analytical Tool for Next-Generation Sequence Data *Eli Kaminuma, Yuichi Kodama, Satoshi Saruhashi, Takeshi Konno, Takako Mochizuki, Hidemasa Bono, Hideaki Sugawara, Kousaku Okubo, Toshihisa Takagi, Yasukazu Nakamura*
- P121 CyanoClust: Protein Cluster Database for Comparative genomics of Cyanobacteria and Plastids *Naoki Sato, Naobumi V. Sasaki*
- P122 Evaluating Protein Sequence Signatures Inferred from Protein-Protein Interaction Data Using Gene Ontology Annotations *Osamu Maruyama, Hideki Hirakawa, Takao Iwayanagi, Yoshiko Ishida, Shizu Takeda, Jun Otomo, Satoru Kuhara*

- P123 Creation and Management of Information Platform in Targeted Proteins Research Program *Hisashi Mizutani, Takao Iwayanagi, Keiichi Homma, Yoshie Ohno, Miyuki Konishi, Haruki Nakamura, Junko Sato, Akihito Kaneko, Tomoakira Kawai, Hideaki Sugawara*
- P124 Reclassification of Oxidoreductase Subclasses Based on the Relationships of Reductants and Oxidants *Masaaki Kotera, Toshiaki Tokimatsu, Zen-ichi Nakagawa, Yuki Moriya, Masahiro Hattori, Susumu Goto, Minoru Kanehisa*
- P125 INOH Pathway Database *Noriko Sakai, Satoko Sakai, Hiromi Nakamura, Ken-ichiro Fukuda, Toshihisa Takagi*
- P126 The New Version of *MutationView* : Enhanced Search Function and Significant Increase in the Number of Gene Entries *Masafumi Ohtsubo, Kouichi Kawaguchi, Katsue Adachi, Tomoyoshi Horisawa, Nobuyoshi Shimizu, Shinsei Minoshima*
- P127 Structural Clustering of Plant Secondary Metabolite to Estimate Compound Classes Reflecting their Biosynthetic Pathway *Toshiaki Tokimatsu, Masaaki Kotera, Susumu Goto, Shigehiko Kanaya, Minoru Kanehisa*
- P128 A Trial to Develop a Integrative Database of Mouse Phenotype Related Information *Hiroshi Masuya, Norio Kobayashi, Nobuhiko Tanaka, Kazunori Waki, Kouji Kozaki, Shigeharu Wakana, Riichiro Mizoguchi, Tetsuro Toyoda*
- P129 The Ontology-Based Data Processing System for International Integration, Ontology and Data Mining of Mouse Phenome Information *Kazunori Waki, Hiroshi Masuya*
- P130 DMPD: Dynamic Macrophage Pathway Database *Ayumu Saito, Masao Nagasaki, Andre Fujita, Kazuko Ueno, Emi Ikeda, Satoru Miyano*
- P131 An Automatic Glyco-Work ow Generator in RINGS *Daisuke Shinmachi, Kiyoko F. Aoki-Kinoshita*
- P132 Constrained Clustering for Discovering High Binding Affinity Glycan Substructures *Haruna Terai, Jun Sese*
- P133 A Method for Extraction of the Active Compound Groups which Have Strong Relationship between Structure and Activity *Takahiro Kishimoto, Shigeto Seno, Yoichi Takenaka, Hideo Matsuda*
- P134 Extracting Common Substructures of GPCR Ligands *Bekir Erguner, Masahiro Hattori, Susumu Goto, Minoru Kanehisa*
- P135 Chemical Continuity of Reaction Centers along Successive Metabolic Reactions *Masahiro Hattori, Masaaki Kotera, Ai Muto, Susumu Goto, Minoru Kanehisa*
- P136 Applied Method of Extending Van Krevelen Diagrams for Exhaustive Analysis of Metabolites *Kaori Matsuda, Md Altaf-Ul-Amin, Kensuke Nakamura, Hiroki Takahashi, Daisaku Ohta, Shigehiko Kanaya*
- P137 Structural Similarity-Based Approach to Characterize Crude Drug Components *Ai Muto, Minoru Kanehisa*
- P138 Constructing Database of Epilepsy Genes and Mutations for Development of Genetic Diagnosis System *Shuichi Yoshida, Kazuaki Kanai, Toshio Shimizu, Sunao Kaneko*
- P139 Molecular Evolutionary Origins of the Adaptive Immune System in Gnathostomata *Jun-ichi Kaneta, Masumi Itoh, Kanako O. Koyanagi, Hidemi Watanabe*
- P140 Spatiotemporal Sequence Analysis of Influenza Virus Sequences *Chih-Jen Tai, Tzu-Wen Chen, Po-An Cheng, Chen-hsiung Chan*