

Poster Session A
Sunday, April 2, 2006

5:30pm-7:30pm

Balcony, First Floor

(Session A posters will be displayed all day Sunday and Monday)

- A1 **Alexa, Adrian** *University of Saarlandes*
 “Scoring of Functional Groups from Gene Expression Data by Decorrelating GO Graph Structure”
- A2 **Alexe, Gabriela** *IBM Thomas J. Watson Research Center*
 “Data Perturbation Independent Diagnosis and Validation of Breast Cancer Subtypes Using Clustering and Patterns”
- A3 **Asano, Tetsuo** *Japan Advanced Institute of Science and Technology*
 “Template Matrices for Perfect Phylogeny Haplotyping and Site Consistency”
- A4 **Babor, Mariana** *Weizmann Institute of Science*
 “Searching for soft metal binding sites in protein structures”
- A5 **Beane, Jennifer** *Boston University*
 “Airway Gene Expression: A Clinically Relevant Diagnostic in Smokers with Suspect Lung Cancer”
- A6 **Ben-Shimon, Avraham** *Weizmann Institute of Science*
 “Looking at Enzymes from the Inside Out: The Proximity of Catalytic Residues to the Molecular Centroid Can be Used for Detection of Active Sites and Enzyme Ligand Interfaces”
- A7 **Berman, Piotr** *The Pennsylvania State University*
 “Consistent sets of secondary structures in proteins”
- A8 **Boeva, Valentina** *Moscow State University*
 “Vestigial Minisatellites in Human Genome”
- A9 **Brown, Clive G.** *Solexa ltd.*
 “Informatics for next-generation DNA sequencing using Single Molecule Clusters and Sequencing-by-synthesis (SBS)”

- A10 **Cheng, Jill** *Affymetrix*
 “Identification of Transcriptional Regulation Complexes By Integrated Analysis of Chromatin IP and RNA Expression Data Generated With Genome Tiling Arrays”
- A11 **Cho, Min-su** *ISTECH Inc*
 “GenPlex : component-wise DNA Chip Data Analysis Pipeline”
- A12 **Choo, Siew Woh** *Genome Institute of Singapore*
 “Comprehensive Analysis of Processed Pseudogenes by Pair-End-diTag(PET) Sequencing Approach”
- A13 **Chung, Myungguen** *Electronics and Telecommunications Research Institute, Daejeon*
 “The Wrapping Method of Ontology for Biological Database Integration”
- A14 **Ciriello, Giovanni** *University of Padova*
 “High-Performance Protein Structure Comparison”
- A15 **Clote, Peter** *Boston College*
 “Combinatorics of locally optimal secondary structures of RNA”
- A16 **Clote, Peter** *Boston College*
 “Energy landscape of k-point mutants of an RNA sequence”
- A17 **Cora, Davide** *University of Torino*
 “Statistical analysis of DNA motifs in humanmouse 3-utr regions leads to the detection of miRNA targets genes”
- A18 **Ding, Chris** *University of California*
 “Finding Cliques in Protein Interaction Networks via Transitive Closure of a Weighted Graph”
- A19 **Dutkowski, Janusz** *Warsaw University*
 “Biomarker selection method based on rank aggregation”
- A20 **Eden, Eran** *Technion, Haifa*
 “Discovering Sequence Motifs in ChIP-chip data”
- A21 **Ferrazzi, Fulvia** *University of Pavia*
 “A Bayesian Approach to Identify Feedback Loops in Gene Regulation”

- A22 **Fogolari, Federico** *University of Udine*
 “A comparison of different free energy estimators for model quality evaluation”
- A23 **Fornasari, Maria Silvina** *Universidad Nacional de Quilmes*
 “Conformational diversity and evolutionary sequence divergence of proteins”
- A24 **Fourati, Ahmed** *Center of Biotechnology of Sfax*
 “Combining multiple models for prokaryotic promoter prediction”
- A25 **Frenkel-Morgenstern, Milana** *Weizmann Institute of Science* ..
 “Intra-protein contact prediction using a structurally derived pair-to-pair substitution matrix”
- A26 **Davidovich, Ofir** *Tel-Aviv University*
 “An integrated software tool for genotype analysis”
- A27 **Gassend, Blaise** *MIT*
 “Learning Biophysically-Motivated Parameters for Alpha Helix Prediction”
- A28 **Gavish, Matan** *Tel Aviv University*
 “Genetic Code Symmetry and Efficient Design of GC-Constrained Coding Sequences”
- A29 **Gramada, Apostol** *University of California San Diego*
 “Multipolar Representation of Protein Shape”
- A30 **Gross, Samuel** *Stanford University*
 “CONTRAST: De Novo Gene Prediction Using a Semi-Markov Conditional Random Field”
- A31 **Halperin, Yonit** *Tel-Aviv University*
 “The amadeus Motif Discovery Tool”
- A32 **Höglund, Annette** *Eberhard Karls University Tübingen*
 “MultiLoc: prediction of protein subcellular localization using N-terminal targeting sequences, sequence motifs, and amino acid composition”
- A33 **Horton, Paul** *AIST, Japan*
 “Protein Subcellular Localization Prediction with WoLF PSORT”

- A34 **Huang, Jing** *Affymetrix*
 “CARAT: A Novel Method for Allelic Detection of DNA Copy Number Changes using High Density Oligonucleotide Arrays”
- A35 **Jourdan, Laetitia** *INRIA Futurs*
 “An online engine for peptide mass fingerprinting from spectrum”
- A36 **Jung, Ho-Youl** *Electronics and Telecommunications Research Institute, Daejeon*
 “Integrated System for Gene Expression Clustering and Regulatory Network Inference”
- A37 **Keane, Andy** *University of Southampton*
 “Evolution and Learning”
- A38 **Kermany, Amir Raji** *Concordia University*
 “A Stochastic Model of Changes in the Haplotype Block Structure of Chromosomes”
- A39 **Kitakami, Jun’ichi** *University of Tokyo*
 “Dynamics of Bibliographic Interactions in Temporal Gene Expression”
- A40 **Kurbatova, Natalja** *University of Latvia*
 “Protein structures comparison based on evolutionary changes”
- A41 **Lecca, Paola** *University of Trento*
 “A stochastic description of the molecular mechanisms of hereditary parkinsonism”
- A42 **Lee, Daesang** *SmallSoft Co. Ltd.*
 “An Integrated System for Microbial Genome Annotation and Pathway Mapping Analysis”
- A43 **Lee, Wei-Po** *National University of Kaohsiung*
 “Motif constituents in the yeast protein interaction network discovered through the asymmetric functional annotation”
- A44 **Lee, Young-Bok** *Yonsei University College of Medicine*
 “SNPAnalyzer: a web-based one-stop tools for SNP analysis”
- A45 **Leonard, Julie** *BD Technologies*
 “Connected Subgraphs of the Human Receptome”

- A46 **Lu, Zhi** *University of Rochester*
 “Designing siRNA using improved RNA Secondary Structure Prediction”
- A47 **Kristoffersen, Anja Bråthen** *University of Oslo*
 “Detecting unknown genetic modifications”
- A48 **Li, Mingkun** *DOE Joint Genome Institute*
 “A Statistical Monitoring and Diagnosis System for High-Throughput DNA Sequencing”
- A49 **Maetschke, Stefan** *Queensland University of Technology*
 “BioPatML - an XML pattern description language for amino acid and nucleotide sequences”
- A50 **Maglietta, Rosalia** *ISSIA- CNR*
 “Automated Diagnosis of Colon Cancer by varying the number of genes”
- A51 **Makosa, Ewa Maria** *Warsaw University*
 “A novel boosting technique applied to mass spectrometry data”
- A52 **Markowitz, Florian** *Max Planck Institute for Molecular Genetics*
 “Pleiotropic hierarchies from high-dimensional phenotyping by RNA interference”
- A53 **Martignetti, Loredana** *University of Torino*
 “Comparative regulatory genomics: evidence for a power law distribution of the length of conserved non-coding blocks”
- A54 **McClure, Marcella** *Montana State University*
 “Automated identification and annotation of Retroviral agents in eukaryotic genomes”
- A55 **McDowall, Jennifer** *EMBL-EBI*
 “InterPro: a Powerful Resource for Protein Functional and Structural Annotation”
- A56 **Merico, Daniele** *University of Milano*
 “Functional Correlation Maps: a method for functional data-mining”

- A57 **Nielsen, Fiona Gwendolyn Ginn** *University of Southern Denmark*
 “Predicting Direction of Transcription from Histone Acetylation Patterns”
- A58 **Ning, Kang** *National University of Singapore*
 “De novo Peptide Sequencing for Multi-charge Mass Spectra based on Strong Tags”
- A59 **Ning, Kang** *National University of Singapore*
 “The distribution and deposition method for the multiple oligo nucleotide arrays”
- A60 **Onge, Bob St.** *Stanford University*
 “Automated Pathway Reconstruction From Quantitative Phenotyping of Combinatorial Gene Deletions”
- A61 **Palopoli, Nicolas** *Universidad Nacional de Quilmes*
 “3D Model quality assessment using a structurally constrained model of evolution”
- A62 **Paluszewski, Martin** *University of Copenhagen*
 “Protein Structure Prediction Using Tabu Search and HSE Measure”
- A63 **Perco, Paul** *Medical University of Vienna*
 “discoveryBASE - virtual protein lead discovery workflow”
- A64 **Plewczynski, Dariusz** *University of Warsaw*
 “Target Specific Compound Identification using Support Vector Machine”
- A65 **Rao, J. Sunil** *Case Western Reserve University*
 “BAMarray Software for Microarray Analysis”
- A66 **Rapberger, Ronald** *University of Vienna*
 “Proteome-scale virtual screening for immunogenic bacterial proteins”
- A67 **Reshef, Dan** *Ben-Gurion University of the Negev*
 “Identifying Functional Sites in Enzyme Structures using Energy Functions”

- A68 **Rosselló, Francesc** *University of the Balearic Islands*
 “Alignment-Free Comparison of Metabolic Pathways”
- A69 **Ruklisa, Dace** *University of Latvia*
 “Finite State Linear Model and Reverse Engineering of Gene Regulatory Networks”
- A70 **Ryo, Jin Ho** *ISTECH Inc.*
 “SNPWizard :a web-based SNP data management system”
- A71 **Sanchez-Baez, Eliany** *University of Rochester*
 “Molecular Dynamics Free Energy Perturbation of tRNA-Asp: Understanding SHAPE Reactivity”
- A72 **Saraswath, Abhiman** *Karolinska Institutet*
 “Prediction of Adaptive Evolution in Protein Families”
- A73 **Saul, Zachary M.** *University of California*
 “Methods for Random Modularization of Networks”
- A74 **Su, Wen-Hui** *Institute of Biomedical Sciences, Taipei*
 “OncoDB.HCC: an integrated oncogenomic database of human hepatocellular carcinoma revealed cancer genes and genomic biology”
- A75 **Suetsugu, Yoshitaka** *National Institute of Agrobiological Sciences*
 “Direct Physical Mapping Method and its Application”
- A76 **Swidan, Firas** *Israel Institute of Technology*
 “MAGIC: an Integrative and Accurate Method for Comparative Genome Mapping”
- A77 **Shah, Vishal** *Boston University*
 “Differences in Smoke-Induced Airway Gene Expression Between African-American and Caucasian Smokers”
- A78 **Tae, Hongseok** *SmallSoft Co.*
 “An analysis system of modular polyketide synthases”
- A79 **Taneri, Bahar** *Scripps Genome Center*
 “Pathological Alternative Splicing in Cancer Tissues”

- A80 **Tendulkar, Ashish** *Kanwal Rekhi School of Information Technology*
 “Structure and sequence variations in beta-strand subclasses revealed via Gaussian mixture modeling”
- A81 **Tininini, Leonardo** *CNR-IASI*
 “CollHaps: haplotpye inference by collapse rules”
- A82 **Tonazzini, Anna** *Istituto di Scienza e Tecnologie dell’Informazione - CNR*
 “Joint correction of cross-talk and peak spreading in DNA electropherograms”
- A83 **Tsiporkova, Elena** *Ghent University*
 “Gene Networks of Parallel Aggregation Processes Inducing Additive and Dominance Phenomena”
- A84 **Tsutsumi, Shuichi** *University of Tokyo*
 “High-resolute Map of DNA Methylation in Human Genome Using Tiling Arrays”
- A85 **Tuller, Tamir** *Tel Aviv University*
 “Regulation and Genomic Arrangement of microRNA Genes”
- A86 **Tyagi, Rahul** *University of Rochester*
 “Prediction of Coaxial Stacking Configuration of Helices in RNA Multi-branch Loops”
- A87 **Ulitsky, Igor** *Tel Aviv University*
 “MetaReg application: a graphical interface for modeling and evaluation of biological systems”
- A88 **Shimomura, Michihiko** *Mitsubishi Space Software Co. Ltd.*
 “Silkworm EST clustering based on BLAST and PhredPhrap”
- A89 **Viksna, Juris** *University of Latvia*
 “Gene Duplication Models and Reconstruction of Network Evolution from Network Structure”
- A90 **Vives, Sergi** *Barcelona University*
 “Clustering and reliability for two color spotted microarray experiments”

- A91 **Snir, Yair** *Sheba Medical Center, Tel-Hashomer*
 “An Integrative Model for Reconstruction of Drug-Related Regulatory Pathways”
- A92 **Wilczynski, Bartek** *Polish Academy of Sciences*
 “Regulatory network reconstruction with generalized boolean networks”
- A93 **Yang, Lee-Wei** *University of Pittsburgh*
 “oGNM: Online Computation of Protein Dynamics Using Gaussian Network Model”
- A94 **Ziman, Mel** *Edith Cowan University*
 “Determination of the Role of Pax7 in Childhood Rhabdomyosarcoma using In Silico Biology”

Poster Session B

Tuesday, April 4, 2006

4:00pm-6:00pm

Balcony, First Floor

(Session B posters will be displayed all day Tuesday and Wednesday)

- B1 **Adam, Zaky** *University of Ottawa*
 “Model-free Phylogenomics Using Common Intervals”
- B2 **Ameur, Adam** *Uppsala University*
 “Base pair localization of in vivo transcription factor binding from low resolution ChIP-chip data”
- B3 **Andersson, Robin** *Uppsala University*
 “A Segmental Maximum A Posteriori Approach for Array-CGH Copy Number Profiling”
- B4 **Arnaout, Ramy** *Broad Institute*
 “Googling Network Biology”
- B5 **Ausiello, Gabriele** *University of Rome Tor Vergata*
 “Local Structure Comparison for Protein Functional Annotation”
- B6 **Bauer, Sebastian** *Charité University Hospital*
 “Feature Selection for Strings Kernels in the Maximum Entropy Framework”

- B7 **Bhanot, Gyan** *IBM Thomas J. Watson Research Center*
 “Clustering, Patterns, Trees and Common Origins: An Analysis of Complete mtDNA Sequences”
- B8 **Blackburne, Benjamin Patrick** *National Institute for Medical Research, London*
 “Changing patterns of selective pressure in Human Influenza H3”
- B9 **Brilli, Matteo** *University of Florence*
 “Plasmidome evolution by network analysis”
- B10 **Chen, Chien-Yu** *National Taiwan University*
 “Removing Noisy Relations to Reduce the Side-Effect of Exploiting Homology Transitivity”
- B11 **Chiarugi, Davide** *University of Siena*
 “Simulating complex biological properties using ViCe”
- B12 **Climescu-Haulica, Adriana** *CEA-DRDC, Grenoble*
 “A Stochastic Differential Equation Model for Transcriptional Regulatory Networks”
- B13 **Corsi, Claudio** *University of Pisa*
 “The BioPrompt-box”
- B14 **Csuros, Miklos** *University of Montreal*
 “Reticular alignment: a new heuristic for multiple sequence alignment using transducers and suboptimal alignments”
- B15 **Dalkic, Ertugrul** *Bilkent University*
 “Non-random component dynamics of highly modulated gene networks derived from zebrafish time-series microarray data”
- B16 **de Jong, Edwin** *Utrecht University*
 “A comparison of gene interaction measures”
- B17 **Do, Chuong B.** *Stanford University*
 “A Discriminative Learning Model for RNA Secondary Structure Prediction”

- B18 **Fuchsberger, Christian** *Institute of Genetic Medicine, EURAC Bolzen*
 “Quality Assessment for Mass Spectrometry Proteomic Data during Alignment using Background Knowledge”
- B19 **Garutti, Claudio** *University of Padova*
 “Protein Functional Recognition Using a Spin-Image Representation”
- B20 **Halachev, Konstantin** *Max-Planck-Institut für Informatik*
 “EpiGRAPH: A toolkit for (epi-) genomic relationship analysis and prediction in human”
- B21 **Haldermans, Philippe** *Hasselt University*
 “Using Linear Mixed Models as scatterplot smoother for Normalization of cDNA Microarrays”
- B22 **Hallgrimsdottir, Ingileif** *University of Oxford*
 “Correct estimation of p-values in disease-marker association studies”
- B23 **Han, Sang-Ik** *Honam Agricultural Research Institute, NICS, Jeonbuk*
 “An Integrated Data Mining Approach to Analyze Gene Expression of Barley Powdery Mildew”
- B24 **Hsu, Chen-Ming** *Yuan Ze University*
 “Identification of Hot Regions in Protein-Protein Interactions by Sequential Pattern Mining”
- B25 **Huang, Tao-Wei** *National Taiwan University*
 “Reconstruction of Human Protein Interologs by Evolutionary Conserved Network”
- B26 **Hvidsten, Torgeir R.** *Uppsala University*
 “Learning regulatory binding site modules from sequence and expression data”
- B27 **Hyland, Fiona** *Applied Biosystems, Foster City*
 “Low Linkage Disequilibrium among 1840 SNPs in Over 200 Drug Metabolizing Enzymes Underlines the Necessity of Directly Genotyping Putative Functional Variants”

- B28 **Kel, Alexander** *BIOBASE GmbH*
 “ExPlain: explaining gene expression data by knowledge-driven promoter and regulatory network analysis”
- B29 **Khrebtukova, Irina** *Solexa Inc.*
 “Bioinformatic Tools for Genome-Wide Applications of Next-Generation DNA Sequencing”
- B30 **Kierczak, Marcin** *Uppsala University*
 “Rough sets-based classifiers for prediction of HIV resistance to nucleoside reverse transcriptase inhibitors”
- B31 **Kim, Haseong** *Seoul National University*
 “Regression Based Gene Regulatory Network”
- B32 **Kim, Hyunsoo** *Georgia Institute of Technology*
 “Missing Value Estimation for DNA Microarray Gene Expression Data by Alternating Least Squares”
- B33 **Kiseleva, Larisa** *Computational Biology Research Center, AIST, Japan*
 “Cell typing by expression profile: a new look at an old problem”
- B34 **Kleffe, Jürgen** *Institute of Molecular Biology and Biochemistry, Berlin*
 “Memory efficient and simultaneous identification of similar substrings in large sets of sequences”
- B35 **Kleffe, Jürgen** *Institute of Molecular Biology and Biochemistry, Berlin*
 “Annotation of *M.truncatula* based on strong similarity to proteins of other plants”
- B36 **Kontijevskis, Aleksejs** *Uppsala University*
 “Novel Insights into Complexity of HIV-1 Protease Specificity”
- B37 **Lai, Weil** *Harvard-Partners Center for Genetics and Genomics* ..
 “Combining Segmentation and Smoothing Algorithms for Analysis of Array CGH Data”

- B38 **Lanave, Cecilia** *ITB CNR Bari*
 “Comparative Genomics of OXPHOS gene families”
- B39 **Lanzeni, Stefano** *University of Milan-Bicocca*
 “Can physically infeasible fluxes compromise steady state flux distributions of entire metabolisms? An empiricist investigation”
- B40 **Lassmann, Timo** *Karolinska Institutet*
 “Automatic assessment of alignment quality”
- B41 **Lee, Marianne M.** *Ohio State University*
 “Distant Homology Detection Using a Length and Structure-based Sequence Alignment Tool (LESTAT)”
- B42 **Lexa, Matej** *Masaryk University*
 “Improvements in PCR simulation”
- B43 **Lexa, Matej** *Masaryk University*
 “Segmentation of protein sequences: are they written in biological language?”
- B44 **Liao, Wei-Chao** *National Yang Ming University*
 “Distinct Grouping and Genome Organization among Escherichia coli Bacteriophages”
- B45 **Lilburn, Timothy G.** *American Type Culture Collection*
 “Towards an integrated view of the emergence of Yersinia pestis”
- B46 **Lim, Jaesoo** *Electronics and Telecommunications Research Institute, Daejeon*
 “Effects of Training Algorithms and Chunk Features on Biomedical NER using Maximum Entropy Models”
- B47 **Lim, Joon-Ho** *Electronics and Telecommunications Research Institute, Daejeon*
 “Species Classification for Mapping Protein Strings to Swiss-Prot”
- B48 **Lin, Kuang** *Biomathematics and Statistics Scotland, JCMB*
 “Promoter Detection with an Extended K-means Algorithm Integrating Gene Expression Profiles and Sequence Information”

- B49 **Lin, Yu-Hsuan** *National Yang Ming University*
 “Phylogenetic Analysis with Metabolic Profiles”
- B50 **Lingner, Thomas** *Georg-August-Universität Göttingen*
 “Remote Homology Detection using Oligomer Distances and Hyperparameter-free Kernels”
- B51 **Lo, Eric Wei-xuan** *National Yang-Ming University*
 “Distinct conservation of regulatory elements in all sequenced mitochondrial genomes”
- B52 **Lorenz, Peter** *University of Rostock*
 “Modelling of transcriptional networks based on the analysis of KRAB zinc finger protein functions”
- B53 **Ma, Tao** *Georgia Institute of Technology*
 “Development of a System for High-Throughput BioMarker Discovery Using Evolutionary Techniques”
- B54 **Margelevicius, Mindaugas** *Institute of Biotechnology, Vilnius* ..
 “A Psi-Blast based tool to assess alignment reliability through an intermediate sequence search”
- B55 **McCoy, Nigel** *National University of Ireland Galway*
 “Gene Prediction and Genome Based Clustering in Whole-Genome Shotgun Sequenced Metagenomic Assemblies using the Self Organising Map”
- B56 **Menconi, Giulia** *University of Bologna*
 “Exploring the properties of a eukaryotic gene by using a complexity-based algorithm”
- B57 **Metpally, Raghu-Prasad Rao** *National centre for biological sciences, Bangalore*
 “Genome Inventory and Analysis of Nuclear Receptor Superfamily in *Tetraodon nigroviridis*: Insights into Sequence Diversity and Evolution”
- B58 **Miklos, Istvan** *Eötvös University*
 “Efficient sampling of transpositions and inverted transpositions for Bayesian MCMC”

- B59 **Mohtashemi, Mojdeh** *MIT*
 “Using Gene Expression Profiles to Predict Chemosensitivity”
- B60 **Morris, Quaid** *University of Toronto*
 “A Bayesian algorithm for untangling biological networks: degree distributions count”
- B61 **Movaghar, Afshin Fayyaz** *University of Toulouse 2*
 “Significance Statistics for Gapped Local Alignments”
- B62 **Nalbantoglu, Ufuk** *University of Nebraska-Lincoln*
 “A Compact Method for Identification of Exons”
- B63 **Novak, Adam** *Eötvös University,*
 “Structure Projector: protein secondary structure prediction from Bayesian distribution of multiple alignments”
- B64 **Ou, Yu-Yen** *Yuan-Ze University*
 “Using QuickRBF and PSSM profiles to Predict Outer Membrane Proteins”
- B65 **Panjovich, Alejandro** *Pontificia Universidad Católica de Chile*
 “Structure-specific statistical potentials for fold assessment of three-dimensional protein models”
- B66 **Pozzoli, Uberto** *Scientific Institute IRCCS E. Medea*
 “Expression levels and gene function influence transposon occurrence in mammalian introns”
- B67 **Quo, Chang** *Georgia Institute of Technology*
 “An Approach to Intelligent Parameter Selection for Sphingolipid Pathway Modeling”
- B68 **Reinhardt, Ralf** *Protagen AG*
 “A Proteome database system for managing Proteome data and MS interpretation”
- B69 **Romualdi, Chiara** *University of Padova*
 “Meta-analysis on Rhabdomyosarcoma identifies common dysregulated metabolic pathways”

- B70 **Roy, Sushmita** *University of New Mexico*
 “Cell Population Deconvolution using Particle filters”
- B71 **Sacchi, Lucia** *University of Pavia*
 “TA-based classification of transcriptional phenotypes”
- B72 **Scalabrin, Simone** *University of Udine*
 “Stem-loop Structure Search (without using lowest common ancestor)”
- B73 **Seetin, Matthew** *University of Rochester*
 “Efficiently Measuring Folding Free Energies of with Computational Pulling Experiments”
- B74 **Sekijima, Masakazu** *Computational Biology Research Center (CBRC) /AIST*
 “Unfolding Simulation of Prion Protein: analysis of dynamics”
- B75 **Sellamuthu, Sivakumar** *Wayne State University*
 “Onto-Translate: Resolving name space issues in the existing biological annotation databases”
- B76 **Shefi-Novershtern, Noa** *Hebrew University*
 “Stochastic Integrative Modeling of Transcription Regulation”
- B77 **Siehs, Christian** *University of Vienna*
 “Autoantigens and differential gene expression in ovarian cancer”
- B78 **Srinivasan, Balaji** *Stanford University*
 “A Protein Recommender For Interactome Validation”
- B79 **Steigele, Stephan** *University of Tübingen*
 “Computational Prediction and Annotation of Structured RNAs in Yeasts”
- B80 **Stoka, Veronika** *J. Stefan Institute*
 “Phylogenetic relationship and modeling of human cathepsins O and W”
- B81 **Swenson, Krister M.** *University of New Mexico*
 “Identifying Orthologs: Cycle Splitting on the Breakpoint Graph”

- B82 **Tabach, Yuval** *Weizmann Institute of Science*
 “The promoters of human cell cycle genes integrate signals from two tumor suppressive pathways during cellular transformation”
- B83 **Valkenburg, Dirk** *Hasselt University*
 “An algorithm to process and analyse COFRADIC data”
- B84 **Valkenburg, Dirk** *Hasselt University*
 “Monoisotopic peak finding using a Poisson approximation in COFRADIC setting”
- B85 **Van de Plas, Raf** *Katholieke Universiteit Leuven*
 “Detecting chemically distinct anatomical regions in rat nerve tissue using Imaging Mass Spectrometry”
- B86 **Vilardell, Mireia** *Pompeu Fabra University*
 “Array-CGH data: Could we predict dye-bias effect?”
- B87 **Wang, San-Yuan** *Providence University*
 “Constrained Multiple RNA Secondary Structure Alignment”
- B88 **Westholm, Jakub Orzechowski** *Uppsala University*
 “Combinatorial regulation of glucose repression in *Saccharomyces cerevisiae*”
- B89 **Wrede, Paul** *Institute for Molecular Biology and Bioinformatics, Berlin*
 “Agent-based optimisation: Generating MHC I peptides with desired binding behaviour”
- B90 **Xu, Yanlong** *Louisiana State University*
 “All-atom model to simulate protein evolution”
- B91 **Yang, Chih-Hsien** *National Yang Ming University*
 “Duplication Modules in Photosynthetic Cyanobacterial Proteomes”
- B92 **Zantoni, Marco** *University of Udine*
 “TFBS discovery fixing layouts”
- B93 **Zheng, Chunfang** *University of Ottawa*
 “Rearrangement of Noisy Genomes”