演題一覧表 - Bioinformatics

カテゴリー：
B1 genome & transcriptome
B2 NGS & GWAS
B3 proteins & structure
B4 algorithm & learning
B5 database & software
B6 network & simulation
B7 metabolomics & glycomics & others

ポスター番号	演題	筆頭著者	所属	カテゴリー						
B01_119	Integrated analysis of clinical ChIPSeq data and public databases identified candidate long non-coding RNAs critically involved in gastrointestinal	Reo Maruyama	Sapporo Medical University	B1						
B02_44	GO analysis of gene expression patterns comparison among organs and species	Yasunobu Okamura	Tohoku University	B1						
B03_8	Comprehensive pattern analysis of protein-small ligand molecular interactions in the PDB	Kota Kasahara	Tohoku University			B3				
B04_103	perGENIE: a web application for personal genome interpretation	Kensuke Numakura	Tohoku University	B1						
B05_126	Identification of functional modules in protein networks by near-clique detection algorithm	Shu Tadaka	Tohoku University						B6	
B06_127	Discovery of cis-regulatory elements using a gene coexpression	Satoshi Ito	Tohoku University	B1						
B07_135	Uniformity in the amino acid sequences of soluble ordered proteins	Matsuyuki Shirota	Tohoku University			B3				
B08_140	Different synonymous codon correlations between yeast and human	Kei Hiraya	Tohoku University	B1						
B09_166	Spatial features of genomic characteristics: Trial of visualization by utilizing chromosomal position	Ikuko Motoike	Tohoku University	B1						
B10_112	Variational Bayesian method for inferring transcript isoform abundance from RNA-Seq	Naoki Nariai	Tohoku University	B1						
B11_130	A Tool to detect viral RNA from RNA-seq data	Junya Yamagishi	Tohoku University	B1						
B12_142	Untranslated mRNAs and translated non-coding RNAs	Riu Yamashita	Tohoku University	B1						
B13_90	Database maps and meta-data annotation for strategic research planning in data-driven and omics era	Katsuhiko Murakami	BIRC, AIST					B5		
B14_110	Semantic web service for H-InvDB, integrated database of human genes, transcripts and	Chisato Yamasaki	BIRC, AIST					B5		
B15_121	RAvariome: a literature-based database for human genetic variants associated with	Yoko Nagai	BIRC, AIST					B5		
B16_34	A Predator-Pray model for RNAi dynamics	Takanori Ueda	CytoPathfinder Inc.				B4			
B17_78	A classification of bioinformatics algorithms from the viewpoint of maximizing expected accuracy	Michiaki Hamada	University of Tokyo				B4			
B18_86	Semi-supervised learning approach to predict RNA secondary structure	Haruka Yonemoto	University of Tokyo				B4			
B19_88	An assembling pipeline parallelized by dividing short reads using SlideSort program	Aya Yoshizawa	CBRC, AIST				B4			
B20_111	A method for measuring RNA secondary structure stability and reliability based on	Ryota Mori	University of Tokyo				B4			
B21_13	PBSIM: PacBio reads simulator - toward accurate genome	Yukiteru Ono	Information and Mathematical Science and	B1						
B22_147	PoSSuM: A database for predicting protein-ligand interactions	Kentaro Tomii	CBRC, AIST					B5		
B23_100	Gene-structure-aware multiple protein sequence alignment as a tool for assessment of predicted eukaryotic gene structures	Osamu Gotoh	CBRC, AIST				B4			
B24_137	Mapping middle-to-long RNA-seq reads onto genomic sequence	Chao Zeng	Kyoto University	B1						
B25_108	Recent mitochondrial DNA insertion marks species-specific open chromatin regions in	Junko Tsuji	University of Tokyo	B1						

演題一覧表 – Bioinformatics

カテゴリー： B1 genome & transcriptome
B2 NGS & GWAS
B3 proteins & structure
B4 algorithm & learning
B5 database & software
B6 network & simulation
B7 metabolomics & glycomics & others

ポスター番号	演題	筆頭著者	所属	カテゴリー						
B26_79	Metabolomics of tardigrade Ramazzottius varieornatus reveals dynamic metabolic response during anhydrobiosis	Kazuharu Arakawa	Keio University							B7
B27_84	G-Links: a RESTful gene-centric annotation aggregator	Kazuki Oshita	Keio University					B5		
B28_85	Identification of RNA editing sites in tardigrade transcriptome from RNA-Seq data	Soh Ishiguro	Keio University	B1						
B29_124	Modeling of oxidative stress induced membrane protein clustering in human erythrocytes	Hanae Shimo	Keio University			B3				
B30_150	Identification of Hox genes in the draft genome sequence of Ramazzottius varieornatus	Shiori Komine	Keio University	B1						
B31_152	Web application for pathway visualization with instinctive interface for metagenome data	Nobuaki Kono	Keio University					B5		
B32_20	The FANTOM5 project, a promoter level expression atlas	Hideya Kawaji	Omics Science Center, RIKEN	B1						
B33_38	DiffCorr: an R package to analyze and visualize differential correlations in biological networks	Atsushi Fukushima	Plant Science Center, RIKEN						B6	
B34_17	A new algorithm for metabolic reaction network determination using time-series data	Kansuporn Sriyudthsak	Plant Science Center, RIKEN							B7
B35_15	Performance of Newton-Raphson method for estimating kinetic parameters in S-system type equation models for metabolic reaction network systems	Michio Iwata	Kyushu University				B4			
B36_72	A probabilistic fragment-based protein structure prediction algorithm	David Simoncini	Advanced Science Institute, RIKEN			B3				
B37_83	A RINGS application for iOS platforms	Takaaki	Soka University					B5		
B38_91	New functional development of GlycanBuilder	Takuya Kondo	Soka University					B5		
B39_104	Implementing semantic web in RINGS and FlyGlycoDB	Shunsuke Okazaki	Soka University					B5		
B40_105	3D glycan structure analysis for prediction of the key atomic structures necessary for binding	Akihiro Fujita	Soka University							B7
B42_107	Implementation of glycan fingerprints	Shinichiro Tsuchiya	Soka University							B7
B44_33	Conferring multipotency to the bistable system by overexpression of genes	Daisuke Kiga	Tokyo Institute of Technology						B6	
B45_139	Bioinformatic analysis of interaction of transcription repressor MarR in Escherichia coli with quaternary ammonium compound	Takuya Maeda	Hyogo University of Health Sciences	B1						
B46_76	Efficient approximate classifier of linear graphs having filtered mutual entropy weights defined on a vertex-edge square array	Yuichi Kida	Ohu University				B4			
B47_45	Rapid fabrication of engineered microvasculatures using microfluidic technology	Yukiko Matsunaga	University of Tokyo							B7
B48_37	Metabolic flux and convex polytope	Masamichi Sato	University of Tokyo							B7
B49_35	Period mismatch enhances entrainability in genetic oscillator	Yoshihiko Hasegawa	University of Tokyo						B6	
B50_141	An investigation of structural profiles around target sites of RNA binding proteins	Tsukasa Fukunaga	University of Tokyo				B4			
B51_120	Literature management and recommendation service	Wataru Iwasaki	University of Tokyo					B5		
B52_129	Enumerating DNA-binding motifs from ChIP-seq	Haruka	University of Tokyo	B1						
B53_128	Domain ontology compilation of phytoremediation using ontology learning	Yusuke Komiyama	University of Tokyo					B5		
B54_7	Reference free approach for detecting chromosomal rearrangement	Edward Wijaya	University of Tokyo	B1						

演題一覧表 – Bioinformatics

カテゴリー： B1 genome & transcriptome
B2 NGS & GWAS
B3 proteins & structure
B4 algorithm & learning
B5 database & software
B6 network & simulation
B7 metabolomics & glycomics & others

ポスター番号	演題	筆頭著者	所属	カテゴリー						
B55_114	The conservation of chemical composition in intrinsically disordered regions and its utility in their functional classification	Ashwini Patil	University of Tokyo			B3				
B56_160	Construction of transcriptional regulatory database in Streptomyces and comparative analysis of transcription factor binding sequences	Yuko Makita	Bioinformatics and Systems Engineering Division					B5		
B57_123	SiGN: Large-scale gene network estimation software for K computer and HGC	Yoshinori Tamada	University of Tokyo						B6	
B58_18	Applying the residual cutting method to a coupled perturbed equation	Toshihiko Abe	University of Tokyo				B4			
B59_93	Study for the normalization method for the comparison of multiple ChIP-seq data	Ryuichiro Nakato	University of Tokyo	B1						
B60_146	Molecular dynamics simulation of thermal fluctuation of protein genus	Masanori Yamanaka	Nihon University			B3				
B61_39	Improvement of a homology modeling method with low homologous protein templates	Takashige Yamai	Tokyo University of Science			B3				
B62_136	Classification of kinase group in protein phosphorylation	Kenji Satou	Kanazawa University			B3				
B63_48	Semi-supervised learning on multiple gene networks	Motoki Shiga	Toyohashi University of				B4			
B64_92	GENIES: gene network inference engine in GenomeNet	Masaaki Kotera	Kyoto University					B5		
B65_14	Enumeration of tree-like compounds by breadth first search of a family tree	Yang Zhao	Kyoto University				B4			
B66_42	Completing method for ortholog-based GPR metabolic network by gene essentiality	Takeyuki Tamura	Kyoto University						B6	
B67_116	Time-series analysis of protein dynamics using Kernel method	Mayumi Kamada	Kyoto University				B4			
B68_98	A clustering method for cancer microarray data from mathematical and biological viewpoints	Siliang Yue	Kyoto University	B1						
B69_138	A statistical model for predicting transcription activities based on linear regression	Ying Liu	Kyoto University	B1						
B70_29	Bayes-based inference of gene regulatory network for multiple time series gene expression	Yukito Watanabe	Osaka University						B6	
B71_74	Transcript-type dependent normalization of expression levels in RNA-seq data for non-coding RNA analysis	Tomoshige Ohno	Osaka University	B1						
B72_115	Comparison of gene expressions measured by RNA-seq and microarray for transcriptome analysis of adipose tissues	Sugiyama Masakazu	Osaka University	B1						
B73_132	Two-stage method to infer gene regulatory network utilizing Link Prediction	Sho Ohsuga	Osaka University						B6	
B74_133	Estimation of dynamic gene regulatory networks for cell differentiation by splitting time course	Tomoyoshi Nakayama	Osaka University						B6	
B75_19	Transcription regulation in heart development	Keisuke Nimura	Osaka University	B1						
B76_57	Efficiently discriminating typical time series patterns in omics data based on functional t-test	Mitsunori Kayano	Obihiro University of Agriculture and Veterinary Medicine				B4			
B77_40	Local conformation changes of proteins in the DNA interfaces	Tomoko Sunami	Japan Atomic Energy Agency			B3				
B78_97	Comparative metatranscriptomic analysis of microbial communities associated with an extreme environment	He Huang	Ehime University	B1						

演題一覧表 – Bioinformatics

カテゴリー： B1 genome & transcriptome
B2 NGS & GWAS
B3 proteins & structure
B4 algorithm & learning
B5 database & software
B6 network & simulation
B7 metabolomics & glycomics & others

ポスター番号	演題	筆頭著者	所属	カテゴリー						
B79_67	Analysis of transcriptional regulation network of yeast	Kzumasa Yada	Kyushu Institute of Technology						B6	
B80_68	Integration of structural and biochemical information into protein interaction network	Yuji Kawakami	Kyushu Institute of Technology						B6	
B81_69	Decision tree for guiding the treatment selection to improve pregnancy rate	Shizuka Nishinoaki	Kyushu Institute of Technology				B4			
B82_89	Analysis of domain and non-domain interactions in protein-protein interaction network	Satoshi Komori	Kyushu Institute of Technology						B6	
B83_31	CADLIVE: Mathematical model construction on MATLAB	Kentaro Inoue	Kyushu Institute of Technology						B6	
B84_96	Web-based interactive rendering of anchor alignments on multiple genomes	Yasunori Osana	University of the Ryukyus					B5		
B85_149	Web 2.0 electronic laboratory notebook (Elegance) for biomedical research community on sharing, co-working and inspiriting	Shu-Hwa Chen	Academia Sinica					B5		
B86_95	ValidNESs: an integrated, up-to-date database and prediction tool for proteins containing leucine-rich nuclear	Szu-Chin Fu	National Taiwan University					B5		
B87_148	Variant caller comparison	Mari Miyamoto	CLC bio Japan Inc.		B2					
B88_81	Pathway Studio®: Information extraction from the literature, knowledge inference, network and pathway analysis	Takayuki Taniya	Elsevier Japan K.K.						B6	
B89_9	A streamlined approach to identify genetic interactions across diverse NGS data sets	Benjamin Adamczyk	Genedata USA Inc.		B2					