Poster ID (発表番号)	Authors	Title
	Daichi Shigemizu, Fuyuki Miya, Shintaro Akiyama, Shujiro Okuda, Keith Boroevich, Akihiro Fujimoto, Hidewaki Nakagawa, Kouichi Ozaki, Shumpei Niida, Yonehiro Kanemura, Nobuhiko Okamoto, Shinji Saitoh, Mitsuhiro Kato, Mami Yamasaki, Tatsuo Matsunaga, Hideki Mutai, Kenjiro	疾患原因変異発見のための正確な中間サイズインデル検出法の開発
01-1	Kosaki and Tatsuhiko Tsunoda Kazunori Yamada and Kengo Kinoshita	Development of de novo generator of amino acid sequence profile using
01-2		LSTM framework
O1-3	Toshiyuki Yokoyama, Yoshitaka Sakamoto, Masahide Seki, Yutaka Suzuki and Masahiro Kasahara	グラフゲノムブラウザ
01-4	Takafumi Chishima, Junichi Iwakiri and Michiaki Hamada	Identification of Transposable Elements which contribute to tissue specific expression of IncRNAs
O2-1	Michio Iwata, Ryusuke Sawada, Yasuo Tabei and Yoshihiro Yamanishi	遺伝子発現プロファイルのディジーゾーム解析による疾患間の関連性理解 と創薬応用
O2-2	Chao Zeng, Tsukasa Fukunaga and Michiaki Hamada	Integrative analysis of multiple ribosome profiling datasets reveals widespread IncRNA-ribosome interaction in mammals
O2-3	Kuo-Ching Liang and Yasubumi Sakakibara	MetaVelvet-DL: a MetaVelvet deep learning extension for de novo metagenomics assembly
O2-4	Yumi Kawamura, Shinsuke Koyama and Ryo Yoshida	Inverse prediction for transcription elongation rates with total RNA sequencing
	Toru Nagasaka	Additional Effect and Frequecy Spectrum of ResNet and MLP on CNN in
P01	Shujiro Okuda, Yu Watanabe, Yuki Moriya, Shin Kawano, Tadashi Yamamoto, Masaki Matsumoto, Tomoyo Takami, Daiki Kobayashi, Norie Araki, Akiyasu C. Yoshizawa, Tsuyoshi Tabata, Naoyuki Sugiyama, Satoshi Tanaka, Susumu Goto	Cell Image Analysis jPOST: Integrated database for proteomes
P02	and Yasushi Ishihama Md. Mehedi Hasan and Hiroyuki Kurata	A critical evaluation of bioinformatics tools for the prediction of protein
P03	Kai Chiharu and Uchiyama Yoshikazu	succinylation sites Computer-Aided Diagnosis Scheme Based on Radiogenomics For the
P04	•	Detection of Alzheimer 's Disease Computer-Aided Treatment Strategy Scheme Based on Radiogenomics For
P05	Kouno Yumiko and Uchiyama Yoshikazu	the Prognosis Prediction of Glioblastoma Patient
P06	Jun Yasuda, Kazuki Kumada, Soichi Ogishima, Keita lida, Hideki Tokunaga, Yusuke Shibuya, Nobuo Yaegashi and Masayuki Yamamoto	Variants of uncertain significance of the cancer predisposing genes in two thousand Japanese whole genome sequencing data
P07	Teppei Ogawa, Hiroki Makiguchi and	Development of Extension Pathway for Human-Specific Metabolic Reaction
P08	Michihiro Araki Mei Takeda, Junichi Iwakiri and Michiaki Hamada	Estimation of mapping parameters for PAR-CLIP data using LAST-TRAIN
P09	Yuta Arizono, Tsukasa Fukunaga and Michiaki Hamada	Classification of Chromatin States with Hierarchical Hidden Markov Model
P10	Yuji Ota, Kosuke Shido, Kaname Kojima, Kenshi Yamasaki, Masao Nagasaki and Setsuya Aiba	The first step to the artificial intelligence (AI) diagnosis of skin cancer.
P11	Daiki Sato and Masakado Kawata	Interactive effects of the VMAT1 genotype with life environments and
P12	Mitsunori Kayano, Sayuri Higaki and Shumpei Niida	experience of the Great East Japan Earthquake on mental states Plasma microRNA biomarker detection for mild cognitive impairment using differential correlation analysis
P13	Wataru Okada, Takeshi Chujo, Tetsuro Hirose and Michiaki Hamada	Selection of novel arcRNA candidates from RNA-seq data and search for common local secondary structure motifs
P14	Yusuke Matsuyama and Takashi Ishida	Ensemble multiple molecular fingerprints for improvement of ligand base drug discovery
P15	Kaneko, Genki Yoshikawa and Hiroyuki	Biogeography of nucleocytoplasmic large DNA viruses in the ocean
P16	Ogata Yuki Takeda and Michiaki Hamada	Analysis of histone modifications using latent feature models
P17	Shinichi Higashimoto and Kiyoko F. Aoki-	Rebuilding of RINGS to implement microservice architecture
P18	Kinoshita Taisuke Hori, Daiki Sato, Takashi Makino and Masakado Kawata	The evolution of the noncoding-sequence in the human duplicated regions
P19	Takuya Aramaki, Romain Blanc-Mathieu, Hisashi Endo, Susumu Goto, Minoru	Protein function annotation by hidden Markov model
P20	Kanehisa and Hiroyuki Ogata Tatsuya Sakaguchi and Yuichi Higashimoto	Meta-Analysis of Microarrays to Search PEDF-Related Genes
P21	Ibuki Mishina and Michiaki Hamada	Privacy-preserving profile HMM using homomorphic encrypt system toward
	Yuki Mizuochi, Haruo Suzuki, Kohei Ito,	secure genome analysis Genome analysis of Tepidibacillus sp. HK-1: an arsenic-metabolizing

P23	Yosuke Kondo and Satoru Miyazaki	Gene evolutionary analysis by use of the genome-wide influenza virus database
P24		The Desktop Application for Gene Analytics on Cloud Computing (AWS)
F 24	and Yuichi Shiraishi Shinichiro Tsuchiya, Aoki Nobuyuki P, Daisuke Shinmachi, Masaaki Matsubara,	GlycanBuilder 2.0 to support WURCS and SNFG
P25	Issaku Yamada, Aoki-Kinoshita Kiyoko F and Hisashi Narimatsu	
P26	Yiqian Zhang and Michiaki Hamada	Prediction of mRNA m6A sites in the mammalian genome
P27	Shunichi Kosugi, Yukihide Momozawa, Michiaki Kubo and Yoichiro Kamatani	Structural variations in whole genome sequencing data from 1300 disease genomes
P28	Yutaka Saito and Toutai Mituyama	Cosearge: an exploratory approach reveals spatial gene co-localization beyond topologically associated domains
P29	Francois Berenger and Yoshihiro Yamanishi	A new rotation-translation invariant molecular descriptor for Ligand-Based Virtual Screening and beyond
	Seiichi Omura, Kazuaki Shimizu, Miyuki Morikawa, Motoi Kuwahara, Takashi Kawamura, Tsutomu Mori, Susumu Kusunoki	Exploratory Factor Analysis Determines Latent Factors Associated with Distinct Sets of Anti-Glycolipid Antibodies in Guillain-Barré Syndrome
P30	and Ikuo Tsunoda	
D0.4	Akari Nishii, Hirotsugu Shiroma, Sayaka Mizutani, Keigo Masuda, Pande Putu Erawijantari, Hikaru Watanabe and Takuji	Metagenomic and metabolomic analysis of human gut microbiota in familial adenomatous polyposis
P31	Yamada Ying Chen, Tomoya Mori, Tsuyoshi Kato,	Forecasting coral reef system through multiple-kernel support vector
P32	Junko Yamane, Yoshikatsu Nakano, Hiroyuki Fujimura, Shoichiro Suda, Toru Maruyama, Michihiro Ito, Haruko Takeyama and Wataru	
F32	Fujibuchi Manato Akiyama, Yasubumi Sakakibara and	RNA secondary structure prediction using deep learning
P33	Kengo Sato Hiroshi Dozono	Looking for the global features of DNA sequences -Correlation Coefficient of
P34		Oligo-nucleotides
P35	Hirotaka Matsumoto, Hisanori Kiryu, Yasuhiro Kojima and Itoshi Nikaido	The analysis of spatial gene regulation based on reaction-diffusion system in Drosophila early embryogenesis
P36	Ai Okada, Kenichi Chiba, Satoru Miyano and Yuichi Shiraishi	Automatic generation of cancer genome interactive report via paplot
P37	Masashi Tsubaki	Molecular Representation Learning with Graph Neural Networks
P38	Wataru Tanaka and Masanori Arita	Physicochemical Prediction of Metabolite Fragmentation in Tandem Mass Spectrometry toward Comprehensive Metabolite Identification
P39	Satoshi Ito, Yasunobu Terabayashi, Ryo Shintani, Takuya Fuchikami, Satoshi Kira, Masamitsu Shimada and Masanari Kitagawa	High quality and cost-effective de novo assembly using linked-reads sequencing
P40	Yuki Kuriya, Akira Ohyama and Michihiro Araki	Construction of metabolic model using genomic sequence and reaction database for improving valuable chemical productions by microorganisms
D44	Kohei Ito, Tsubasa Watabe, Masafumi Harada, Ken Kobayashi, Mototsugu Sato, Haruki Ishida, Honami Ando, Shinji Fukuda,	Microbial communities of university campuses in Japan.
P41	Masaru Tomita and Haruo Suzuki Harazono Yoritaka and Kasahara Masahiro	Towards detection of human genomes structural variations using long reads
P42	Dai Watabe, Hiroshi Yuasa, Naoki Osada	Molecular analysis suggested that bottle gourds were derived from Asia
P43	and Toshinori Endo Wessam Mohamed, Ryosuke Omori and	based on traditionally conserved cultivars by local tribes Estimating human-to-human transmissibility of H5N1 influenza A virus using
P44	Kimihito Ito	nucleotide sequences
P45	Masaki Kawamoto, Toshinori Endo, Masayoshi Fukasawa, Kentaro Hanada and Naoki Osada	Whole genome sequence analysis of liver cancer-derived cell lines HuH-7 and Huh7.5.1-8
P46	Shun Kodate and Kengo Kinoshita	Sleeping Beauties in Biomedicine: quantitative publication analysis with citations and words
P47	Natsuhiro Ichinose, Tetsushi Yada and Hiroshi Wada	Dissimilarity between indegree and outdegree distributions in human gene regulatory networks
P48	Shu Saikawa and Masahiro Kasahara	Analysis of "uncallable" regions in the human reference genome associated with gene annotation and segmental duplication
P49	Naoki Osato	Characteristics of functional enrichment of human putative transcriptional target genes
P50	Alexis Vandenbon	Determining the key factors for accurate inference of gene co-expression networks
P51	Masaki Ikeda, Toshinori Endo and Naoki Osada	Comprehensive search and evolutionary study of simian endogenous retrovirus in the genome sequences of the Old World monkeys
P52	Osamu Maruyama	Regularizing protein complexes by mutually exclusive protein-protein interactions
P53	Rei Kajitani, Dai Yoshimura, Miki Okuno, Atsushi Toyoda and Takehiko Itoh	Platanus2: a de novo haplotype assembler enabling comprehensive accesses to divergent heterozygous region.
P54	Masanori Yamanaka	Energy level statistics and random matrix theory in proteogenesis
P55	Yuta Yamate and Takuji Yamada	FuncTree 2: Visualization and Analysis tool for omics data based on Biological Functional Tree
P56	Yuichi Aoki, Takeshi Obayashi, Ikuko N	Relationship between Evolutionary Oldness of Protein-coding Gene and
1 30	Motoike and Kengo Kinoshita	Genetic Diversity in Homo sapiens

	Masahito Ohue, Takanori Hayashi, Keisuke	MEGADOCK-Web: an integrated database of high-throughput structure-
	Yanagisawa, Yuri Matsuzaki and Yutaka	based protein-protein interaction predictions
P57	Akiyama	
	Sangeetha Ratnayake, Toshinori Endo and	Predicting Disease Causality of Mutations in Human Beta Globin Gene
P58	Naoki Osada	
	Kazuki Izawa, Marina Yamasawa, Masahito	Comparative metagenomic analysis between periodontitis and healthy
	Ohue, Takashi Ishida, Kazuyuki Ishihara and	dental plaque based on taxonomic composition and functional gene
P59	Yutaka Akiyama	categories
	Naoki Wakui, Ryunosuke Yoshino, Nobuaki	Exploring the selectivity of inhibitor complexes with Bcl-2 and Bcl-XL: a
	Yasuo, Masahito Ohue and Masakazu	molecular dynamics simulation approach
P60	Sekijima	
P61	Soichi Ogishima, Satoshi Nagaie, Satoshi	Integrated database "dbTMM" for genomic prospective cohort study in
	Mizuno, Keita Iida, Naoko Kasahara, Hiroshi	Tohoku Medical Megabank for promotion of development of genomic
	Tanaka and Tommo Dbtmm Project	medicine
	Tamami Komatsu, Naoki Osada and	Extrapolation of genes involved in eusociality of Apis mellifera
P62	Toshinori Endo	
P63	Fumie Ono, Shinji Kohsaka, Ryo Kanada,	Conformational difference in drug efficiency on EGFR mutations based on
	Biao Ma, Mayumi Kamada, Mitsugu Araki,	protein structural analysis.
	Hiroyuki Mano and Yasushi Okuno	
P64	Reika Endo, Naoki Osada and Toshinori	The clustering of G protein coupled receptors using convolutional neural
	Endo	network
	Kazuhiro Satomura, Naoki Osada and	Compensatory back mutation in mitochondrial genome of primates
P65	Toshinori Endo	
P66	Kensuke Manaka and Takuji Yamada	Development of a pipeline for predicting new genes encoding for orphan
		enzymes from metagenomes
P67	Tsukasa Nakamura and Kentaro Tomii	Large-scale analysis of protein pockets using a fast and efficient comparison
		method with a reduced vector representation
D00	Matsuyuki Shirota	Towards a more comprehensive interpretations of personal genomes based
P68		on structural bioinformatics
P69	Yutaro Konta and Hisanori Kiryu	Inferring tumor progression process using population genetics model