

Schedule	Time	Oral#	Title	Authors
□頭発表 1 2019/9/9 14:30-16:00	14:30 – 14:52	O-1	脂肪由来幹細胞の分化制御に働くエピジェネティック因子のin-silico同定	恭代 山谷, 聖俊 朴 and 謙太 中井
	14:52 – 15:14	O-2	Study of Conformational Changes and Interactions of Calcium Ion Signal Transfer Protein Calmodulin and Calmodulin-binding Domain by Multi-scale and Multi-physics Simulation	Hiromitsu Shimoyama and Yasushige Yonezawa
	15:16 – 15:38	O-3	Analyzing the 3D Chromatin Organization Coordinating with Gene Expression Regulation in B-cell Lymphoma	Luis Augusto Eijy Nagai, Sung-Joon Park and Kenta Nakai
	15:38 – 16:00	O-4	Genotype imputation method by using recurrent neural network	Kaname Kojima, Shu Tadaka, Gen Tamiya and Kengo Kinoshita
□頭発表 2 2019/9/10 14:30-16:00	14:30 – 14:52	O-5	トランスクリプトーム情報とエピゲノム情報の融合解析によるインシリコ・ダイレクトリプログラミング	Ryohei Eguchi, Momoko Hamano, Michio Iwata, Toru Nakamura, Shinya Oki and Yoshihiro Yamanishi
	14:52 – 15:14	O-6	ヒト転写因子の標的遺伝子の特徴とエンハンサー・遺伝子相互作用に関わる転写因子解析	Naoki Osato
	15:16 – 15:38	O-7	Selecting the genes related to breast cancer by combining the unsupervised machine learning and enrichment analysis	Kota Fujisawa and Ryota Miyata
	15:38 – 16:00	O-8	低分子化合物によるデータ駆動型ダイレクトリプログラミング	Toru Nakamura, Michio Iwata, Momoko Hamano, Ryohei Eguchi and Yoshihiro Yamanishi
□頭発表 3 2019/9/10 16:00-17:30	16:00 – 16:22	O-9	Drug Target Excavator: An Integrative Web Tool for Identifying New Potential Drug Targets	Atsushi Hijikata, Masafumi Shionyu and Tsuyoshi Shirai
	16:22 – 16:44	O-10	OpenContami: A Web-based Application for Detecting Microbial Contaminants in Next-generation Sequencing	Sung-Joon Park, Satoru Onizuka, Masahide Seki, Yutaka Suzuki, Takanori Iwata and Kenta Nakai
	16:46 – 17:08	O-11	Toward Constructing Eukaryotic Aminoacyl-tRNA Synthetases Database based on the Phylogenetic and Localization Analysis	Yuki Hamaguchi, Motomu Matsui, Seishiro Aoki and Wataru Iwasaki
	17:08 – 17:30	O-12	singleCellHaystack: A clustering-independent method for predicting differentially expressed genes in single-cell transcriptome data	Alexis Vandenbon and Diego Diez
□頭発表 4 2019/9/10 17:30-19:00	17:30 – 17:52	O-13	Growth-coupled overproduction is theoretically possible for most metabolites in <i>Saccharomyces cerevisiae</i> under anaerobic condition	Takeyuki Tamura
	17:52 – 18:14	O-14	Targeted enzyme gene re-positioning: a computational approach for discovering alternative bacterial enzymes for the synthesis of plant-specific secondary metabolites	祐哉 中村, Shuichi Hirose and Takuji Yamada
	18:16 – 18:38	O-15	The abundance profile of eukaryotic plankton viruses associates with global ocean carbon export efficiency	Hiroto Kaneko, Romain Blanc-Mathieu, Hisashi Endo and Hiroyuki Ogata
	18:38 – 19:00	O-16	Replication dynamics analysis of microbes by whole genome sequence based on directional statistics	Shinya Suzuki and Takuji Yamada