

Accepted Software Demonstrations

- S001 Microbial Genome Annotation Pipeline (MiGAP) for Diverse Users *Hideaki Sugawara, Akira Ohyama, Hiroshi Mori, Ken Kurokawa*
- S002 Bridging the Gap between Biologists and Bioinformaticians with Subio Platform *Akio Tanabe, Fumio Naito, Taro Fukasa, Shiro Terashima*
- S003 cyto-Hubba: a Cytoscape Plug-in for Hub Object Analysis in Network Biology *Shu-Hwa Chen, Chia-Hao Chin, Hsin-Hung Wu, Chin-Wen Ho, Ming-Tat Ko, Chung-Yen Lin*
- S004 Extended CADLIVE: Multi-User Framework and Data Integrator *Sayaka Tomeda, Shinpei Tonami, Kentaro Inoue, Kazuhiro Maeda, Hiroyuki Kurata*
- S005 Cell Illustrator Online 4.0: A Platform for Systems Biology *Masao Nagasaki, Kazuko Ueno, Emi Ikeda, Chen Li, Kaname Kojima, Ayumu Saito, Satoru Miyano*
- S006 New Functions of MassBank: Mass Spectral Database for Metabolome Analysis - Peak Search by Formula, Web API and Database Maintenance - *Hisayuki Horai, Masanori Arita, Yoshito Nihei, Tasuku Ikeda, Yuya Ojima, Takaaki Nishioka*
- S007 COPICAT: A Software System for Predicting Interactions between Chemical Compounds and Proteins by Using Two-Layer Support Vector Machine *Masahiro Yokota, Nobuyoshi Nagamine, Yohei Sugawara, Kris Popendorf, Miho Uchida, Tatsuo Kitahashi, Takashi Komori, Yasubumi Sakakibara*
- S008 Pathway Prediction Focusing on Inclusive Relation of Substructures *Kenichi Tanaka, Kensuke Nakamura, Tamio Saito, Hiroyuki Osada, Hiroki Takahashi, Aki Hirai, Shigehiko Kanaya, Md. Altaf-Ul-Amin*