

| Schedule | Time | | Highlight # | Title | Authors |
|--|-------|---------|-------------|--|--|
| ハイライト トラック1 2019/9/9 14:30-16:00 | 14:30 | — 14:52 | H-1 | Nucleotide Archival Format (NAF) enables efficient lossless reference-free compression of DNA sequences | Kirill Kryukov, Mahoko Ueda, So Nakagawa and Tadashi Imanishi |
| | 14:52 | — 15:14 | H-2 | 有用化合物を生産・増産する代謝ネットワークの設計 | Takeyuki Tamura |
| | 15:16 | — 15:38 | H-3 | Metagenomic and metabolomic analyses reveal dynamic shifts in gut microbiota along the adenoma-carcinoma sequence in colorectal cancer | Sayaka Mizutani, Shinichi Yachida, Hirotsugu Shiroma, Satoshi Shiba and Takuji Yamada |
| | 15:38 | — 16:00 | H-4 | Comprehensive evaluation of structural variation detection algorithms for whole genome sequencing. | Shunichi Kosugi |
| ハイライト トラック2 2019/9/10 17:30-19:00 | 17:30 | — 17:52 | H-5 | Machine-Learning-Guided Mutagenesis for Directed Evolution of Fluorescent Proteins | Yutaka Saito, Misaki Oikawa, Hikaru Nakazawa, Teppei Niide, Tomoshi Kameda, Koji Tsuda and Mitsuo Umetsu |
| | 17:52 | — 18:14 | H-6 | Latent environment allocation of microbial community data | Koichi Higashi |
| | 18:16 | — 18:38 | H-7 | 制約付き最適化に基づくパラメータ推定を用いた大腸菌アンモニア輸送-同化の動力学モデリング | Kazuhiro Maeda, Hans Westerhoff, Hiroyuki Kurata and Fred Boogerd |
| | 18:38 | — 19:00 | H-8 | 新規のTensor-train分解アルゴリズムによる、多様なヒト細胞における薬物応答トランスクリプトームの予測 | Michio Iwata, Longhao Yuan, Qibin Zhao, Yasuo Tabei, Francois Berenger, Ryusuke Sawada, Sayaka Akiyoshi, Momoko Hamano and Yoshihiro Yamanishi |