Poster Presentation

P01

"OrthoReD: Fast, and Accurate Orthology Prediction Tool with Low Computational Requirement"

Kai Battenberg (RIKEN Center for Sustainable Resource Science, Japan)

P02

"SonicParanoid: Fast, Accurate and Easy Orthology Inference"

Salvatore Cosentino (The University of Tokyo, Japan)

P03

"Orthology matters when inferring difficult phylogenies - an example on the Lophotrochozoa"

David Dylus (University of Lausanne, Switzerland)

P04

"Homoeolog Inference Methods Relying on Best-Bidirectional Hit Miss Many Duplicated and Non-Positional Pairs"

Natasha Glover (University of Lausanne/ Swiss Institute of Bioinformatics, Switzerland)

P05

"Construction of a Data Link System for Integrating Plant Genomic Information" Hisako Ichihara (Osaka University, Japan)

P06

"Molecular Evolution of Expanded Cnidarian Opsins"

Junichi Imoto (National Institute of Genetics, Japan)

P07

"Cnidarian Phylogenomics to Understand the Origin of the Bilateria"

MeiFang Lin (Okinawa Institute of Science and Technology, Japan)

P08

"Evidence of non-tandemly repeated rDNAs and their intragenomic heterogeneity in *Rhizophagus irregularis*"

Taro Maeda (National Institute for Basic Biology, Japan)

P09

"Domainoid: Domain-oriented orthology inference"

Emma Persson (Stockholm University, Sweden)

P10

"Alignment-free and Inparalogs-aware Orthology Placement using Hierarchical Orthologous Groups"

Victor Rossier (Stockholm University, Sweden)

P11

"Comparative Genome Analysis Of The Abiotic And Biotic Stress Tolerant Legume Genus \emph{Vigna} "

Hiroaki Sakai (National Agriculture and Food Research Organization, Japan)

P12

"A novel multiple sequence alignment method based on the distribution of possible alignments: cs-FORTE"

Yu Yamamori/ Kentaro Tomii (National Institute of Advanced Industrial Science and Technology (AIST), Japan)

P13

"Coexistence of multiple obligate endosymbionts in the aphid, *Ceratovacuna japonica*" Shunta Yorimoto (National Institute for Basic Biology/SOKENDAI, Japan)