第 25 回 日本 RNA 学会年会 ポスター発表

Poster Presentations of the 25th RNA Japan Meeting in TOKYO

ポスターセッション（1）奇数番号発表（Odd numbers） 6 月 26 日(水曜日) 13:00-14:30
ポスターセッション（2）偶数番号発表（Even numbers）6 月 27 日(木曜日) 13:00-14:30
㊫ : 筆頭著者が学生会員 First author is student member

P-001 (EMBO Poster Clinic)
Deep learning based end-to-end classification and absolute quantification of E. Coli cellular tRNAs using nanopore sequencing
○ Bhaskar Dasgupta[1], Mai Maeda[2], Ryo Noguchi [2], Tsutomu Suzuki[2], Hiroki Ueda[1]
([1]RCAST, Univ. of Tokyo, [2]Dept. of ChemBio., Sch. of Eng., Univ. of Tokyo)

㊫ **P-002 (EMBO Poster Clinic)**
Structural optimization of tRNA anticodon stem toward translational synthesis of natural nonribosomal peptides
○Ryoichi Hirashima[1], Takayuki Katoh[1], Hiroaki Suga[1]
([1] Department of Chemistry, Graduate School of Science, The University of Tokyo)

P-003 (EMBO Poster Clinic)
Extracellular biomolecule-responsive translational regulation system for synthetic mRNAs
○Hideyuki Nakanishi[1, 2] and Keiji Itaka[1, 2]
([1] Institute of Biomaterials and Bioengineering, Tokyo Medical and Dental University, [2] Center for Infectious Disease Education and Research (CiDER), Osaka University)

P-004 (EMBO Poster Clinic)

Exploring a Nucleoprotein Origin of Life through Ribozyme-Assisted In Vitro Evolution of Protein Polymerases

○ Riddhi Gondhalekar[1,2], Shunsuke Tagami[3], Sota Yagi[4], Kosuke Fujishima[1,2,5]
([1]School of Life Science and Technology, Tokyo Institute of Technology; [2]Earth-Life Science Institute, Tokyo Institute of Technology; [3]RIKEN BDR; [4]Faculty of Human Sciences, Waseda University; [5]Graduate School of Media and Governance, Keio University)

P-005 (EMBO Poster Clinic)

Physiological roles of tRNA modification in myoblast differentiation

○Tsaijung Liu[1], Mayuko Takakura[2], Yuta Noda[2], Shinichiro Akichika[2], Shintaro Iwasaki[3], and Tsutomu Suzuki[1, 2]
([1]Department of Bioengineering, School of Engineering, The University of Tokyo, [2]Department of Chemistry and Biotechnology, School of Engineering, The University of Tokyo, [3]The Institute of Physical and Chemical Research (RIKEN))

P-006 (EMBO Poster Clinic)

Recognition and Deubiquitination of Ribosomes for Next Round Translation

○Ken Ikeuchi[1,2,3], Nives Ivic[4], Robert Buschauer[1], Jingdong Cheng[1], Thomas Fröhlich[1], Yoshitaka Matsuo[5], Otto Berninghausen[1], Toshifumi Inada[5], Thomas Becker[1], Roland Beckmann[1]
([1] Gene Center Munich, University of Munich LMU, Germany, [2] Frontier Research Institute for Interdisciplinary Sciences, Tohoku University, [3] Institute of Multidisciplinary Research for Advanced Materials, Tohoku University, [4] Department of Physical Chemistry, Rudjer Boskovic Institute, Croatia, [5] Institute of Medical Science, The University of Tokyo)

P-007 (EMBO Poster Clinic)

Group A streptococcus selectively manipulates host translation

○Hirotaka Toh[1], Takashi Nozawa[2], Ichiro Nakagawa[2], and Shintaro Iwasaki[1,3]
([1] RNA Systems Biochemistry Laboratory, RIKEN Cluster for Pioneering Research,[2] Department of Microbiology, Graduate School of Medicine, Kyoto University,[3] Department of Computational Biology and Medical Sciences, Graduate School of Frontier Sciences, The University of Tokyo)

㊫ **P-008 (EMBO Poster Clinic)**

Regulatory Mechanisms of A-to-I RNA Editing: Modulating Protein Synthesis through Translation Initiation Signals in the 5'-UTR

○Yuki Ogata[1], Masatora Fukuda[1, 2]
([1]Dept. Chem., Graduate School of Science, Fukuoka Univ. [2]Dept. Chem., Fac. Sci., Fukuoka Univ.)

㊫ **P-009 (EMBO Poster Clinic)**

The Analysis of Uncapped mRNA Transcriptome in Trypanosoma Parasites

○Kieu DM Nguyen[1], Yuko Takagi[2], and C. Kiong Ho[1,3]
([1]Human Biology Program, University of Tsukuba, [2] National Institute of Advanced Industrial Science and Technology, [2] Institute of Medicine, University of Tsukuba)

㊫ **P-010 (EMBO Poster Clinic)**

SUMOylated Senataxin suppresses transposable elements in the Drosophila Piwi-piRNA pathway

○Rin Imai, Yaning Wu, Haruhiko Siomi, Kensaku Murano
(Department of Molecular Biology, Keio University School of Medicine Japan)

P-011 (EMBO Poster Clinic)

Elucidation of the role of the N-terminal prion-like domain of SGS3 in plant secondary siRNA biogenesis

○Yuji Fujimoto[1], Yuriki Sakurai[1], Keisuke Shoji[2], Manabu Yoshikawa[3], and Hiro-oki Iwakawa[1]

([1] College of Science, Rikkyo University, [2] Graduate School of Bio-Applications and Systems Engineering, Tokyo University of Agriculture and Technology, [3] Division of Plant and Microbial Sciences, Institute of Agrobiological Sciences, National Agriculture and Food Research Organization)

㊫ **P-012 (EMBO Poster Clinic)**

The regulation of persistent Borna disease virus infection by RNA silencing factors in human cells

○Yuui Naito[1], Yuka Kaneko[1], Rie Koide[2,3], Nicholas F. Parrish[2,3], Tomoko Takahashi[1]

([1]Graduate School of Science and Engineering, Saitama University, [2]Genome Immunobiology RIKEN Hakubi Research Team, Cluster for Pioneering Research, RIKEN, [3]Center for Integrative Medical Sciences, RIKEN)

P-013 (EMBO Poster Clinic)

Short-term metatranscriptional response to warming and cooling of the microbiome in Alaskan permafrost measured by on-site RNA extraction

Lan Anh Catherine Nguyen[1,2], Go Iwahana[3], Kenjiro Tadakuma[4], ○Josephine Galipon[1,5]

([1]Institute for Advanced Biosciences, Keio University, Japan, [2] Systems Biology Program, Graduate School of Media and Governance, Keio University, Japan, [3]International Artic Research Center (IARC), University of Alaska Fairbanks, USA, [4]Graduate School of Engineering Science, Osaka University, Japan, [5]Graduate School of Science and Engineering Yamagata University, Japan)

P-014 (EMBO Poster Clinic)

Molecular mechanism of tRNA hydroxylation and its pathophysiological roles

○Xu Yue[1], Kotaro Tomuro[2,3], Shintaro Iwasaki[2,3], Akiko Ogawa[1], Fan-Yan Wei[1]
([1] Department of Modomics Biology and Medicine, Institute of Development, Aging and Cancer, Tohoku University, Sendai, Miyagi, 980-8575, Japan, [2] RNA Systems Biochemistry Laboratory, RIKEN Cluster for Pioneering Research, Wako, Saitama, 351-0198, Japan, [3] Department of Computational Biology and Medical Sciences, Graduate School of Frontier Sciences, The University of Tokyo, Kashiwa, Chiba 277-8561, Japan.)

P-015 (EMBO Poster Clinic)

Enzymatic Characteristics of Mycoplasma Membrane Nuclease mnuA

○Katsuki Aoyama[1], Yoshika Takenaka[1], Yoshihisa Tomioka[1] and Yasutoshi Akiyama[1]
([1] Department of Pharmaceutical Sciences, Tohoku University)

P-016 (EMBO Poster Clinic)

A potential role of inefficient and non-specific piRNA production from the whole transcriptome

○Keisuke Shoji[1,2,3], Jie Yu[1], Natsuko Izumi[1], Yukihide Tomari[1,2]
([1]Laboratory of RNA Function, Institute for Quantitative Biosciences, The University of Tokyo, [2]Department of Computational Biology and Medical Sciences, Graduate School of Frontier Sciences, The University of Tokyo, [3]Graduate school of Bio-Applications and Systems Engineering, Tokyo University of Agriculture and Technology)

㊫ **P-017**

Thermodynamic and Structural Impacts of Chemical Modifications in the siRNA Seed Region on Off-Target Effects

○ Seongjin An[1], Yoshiaki Kobayashi[2], Kohei Nomura[3], Yasuaki Kimura[3], Hiroshi Abe[3], Akase Dai[4], Misako Aida[5], Kumiko Ui-Tei[1,2]

([1]Graduate School of Frontier Sciences, The University of Tokyo, [2]Graduate School of Science, The University of Tokyo, [3]Graduate School of Science, Nagoya University, [4]AIDI Center, Hiroshima University, [5]Office of Research and Academia-Government-Community Collaboration, Hiroshima University)

㊫ **P-018**

Interferon-inducible ADAR1p150-mediated regulation of gene expression network through microRNA

○Toyotaka Yoshida[1], Yoshimasa Asano [1,2], Shota Azuma[1], Kumiko Ui-Tei [1]

([1] Graduate School of Science, The University of Tokyo, [2] School of Pharmacy, Nihon University)

㊫ **P-019**

siRNAs discriminate single nucleotide differences in PIK3CA

○Toshinori Ohyama[1], Yoshiaki Kobayashi[2], Yoshimasa Asano[2], Susumu Goyama[1], Kumiko Ui-Tei[1,2]

([1]Department of Computational Biology and Medical Sciences, Graduate School of Frontier Science, The University of Tokyo, [2]Department of Biological Sciences, Graduate School of Science, The University of Tokyo)

㊫ **P-020**

Structural and functional analysis of antiphage defense mechanism in the type III-D2 CRISPR-Cas system

○Yoshihisa Mitsuda[1], Junichiro Ishikawa[1], Masahiro Hiraizumi[1,2], Keitaro Yamashita[1,2] and Hiroshi Nishimasu[1,2]

([1] Graduate School of Engineering, The University of Tokyo, [2] Reserch Center for Advanced Science and Technology, The University of Tokyo)

P-021

Paip1 represses translation in a PABP dependent manner

○Kanae Miyazaki[1], Takumi Tomohiro[1], Akira Fukao[1], Tomohiko Aoyama[1] Yuichi Shichino[2], Shintaro Iwasaki[2], Toshinobu Fujiwara[1]
([1]Kindai University, [2]RIKEN)

P-022

Recent Progress of High-Throughput Mutational Analysis for RNA Methylation

Ryota Yamagami, Hina Kubota, Emi Kohno, and ○Hiroyuki Hori
(Graduate School of Science and Engineering, Ehime University, Japan)

P-023

Mutation analysis of a novel domain of ZRSR2 - a responsible gene product in myelodysplastic syndrome.

○Tomoki Chiba[1], Eri Matsumoto[1], So Masaki [1], Satoshi Tanaka[1] and Naoyuki Kataoka[1]
([1]. The University of Tokyo)

P-024

Four-way Decoding with Unmodified Uridine at the Wobble Position in Lactic Acid Bacteria

○Chie Tomikawa[1], Riko Sugita[1], Vincent Guérineau[2], David Touboul[2], Satoko Yoshizawa[3], and Kazuyuki Takai[1]
([1] Graduate School of Science and Engineering, Ehime University, [2] ICSN, CNRS UPR 2301, Université Paris-Saclay, [3] LBPA, CNRS UMR8113, ENS Paris-Saclay, Université Paris-Saclay)

㊫ **P-025**

Identify the effect of R-loop on transcriptional regulatory mechanisms

○Ryotaro Yanoshita[1] , Eito Ichihashi[1], Mai Kubota[1], Chao Zeng[2], Michiaki Hamada[2], Masayuki Sakurai[3]

([1] Graduate School of Biological Sciences, Tokyo University of Science, [2]Waseda University Hamada Laboratory, [3]Research Institute for Biological Science, Tokyo University of Science)

P-026

Dissection of stop codon recognition by mammalian mitochondrial peptide release factors by an in vitro reconstituted mammalian mitochondrial translation system

○Muhoon Lee, Yutong Zhang, Ruiyuan Huang, Nono Takeuchi-Tomita

(Department of Computational Biology and Medical Sciences, Graduate School of Frontier Sciences, University of Tokyo)

㊫ **P-027**

A possible mechanism for the mutually exclusive formation of U-bodies and stress granules

○Kantaro Sugi[1], Shinichi Nakagawa[1,2], Hiroshi Maita[1,2]

([1]Graduate school of life science, Hokkaido University, [2]Faculty of pharmaceutical sciences, Hokkaido University)

P-028

Mechanism of cancer malignancy via chronic inflammation mediated by YAP/TAZ through RNA hierarchy

○Tomoki Chiba[1], Hiroshi Asahara[1]

([1] Department of Systems BioMedicine, Tokyo Medical and Dental University (TMDU))

㊫ **P-029**

Development of practical purification methods for circular mRNA

○Kosuke Fukuchi[1], Shiryu Kajihara[1], Naoko Abe[1], Fumitaka Hashiya[2], Hiroshi Abe[1,3]

([1]Grad. Sch. of Sci., Nagoya Univ., [2]RCMS, Nagoya Univ., [3]iGCORE.)

P-030

Roles of SECIS binding protein 2 (SBP2) in selenoprotein synthesis and neuronal function

Takako Furukawa, ○Yoshika Hayakawa-Yano, Azusa Kondo and Masato Yano

(Graduate School of Medical and Dental Sciences, Niigata University)

P-031

C-terminal IDR domain of ESS2 regulates prostate cancer proliferation

○Ichiro Takada[1], Makoto Makishima[2], Tohru Nakagawa[3], Sayuri Takahashi[1]

([1]Department of Urology, The Institute of Medical Science, The University of Tokyo, [2]Division of Biochemistry, Department of Biomedical Sciences, School of Medicine, Nihon University, [3]Department of Urology, Teikyo University School of Medicine)

P-032

Integrating mRNA-LNP Platforms with Antibody Engineering in Drug Development

○Shun Shimizu[1], Hikaru Koga[1], Naoya Miura[1], Kazuki Sato[1], Haruno Onuma[1], Zenjiro Sampei[1]

([1] Discovery Biologics Dept., Chugai Pharmaceutical Co., Ltd.)

㊫ **P-033**

Deciphering the relationship between 5'UTR and 3'UTR sequence of mRNA

○Kanta Suga[1], Michiaki Hamada[1,2,3],

([1] Faculty of Science and Engineering, Waseda university, [2]. Computational Bio Big-data Open Innovation Laboratory (CBBD-OIL), [3].National Institute of Advanced Industrial Science And Technology (AIST))

P-034

Two secondary structures in SARS-CoV-2 3′ UTR controlling genome replication

○Takako Ohyama[1], Takuo Osawa[1], Shun-ich Sekine[1], Yoshitaka Ishii[1,2]
([1]Center for Biosystems Dynamics Research, RIKEN, [2]School of Life Science and Technology, Tokyo Institute of Technology)

㊫ **P-035**

Relationship between stress granule and microRNA-mediated translation repression using stress granule formation factor

○Mai Miyao[1], Ayumi Mori[1], Takumi Tomohiro[1], Akira Fukao[1], Shungo Adachi[2,3], Tohru Natsume[3], Koji Onomoto[4], Mitsutoshi Yoneyama[4], Toru Suzuki[5], Tadashi Yamamoto[6] and Toshinobu Fujiwara[1]
([1]. Kindai University, [2]. National Cancer Center, [3]. AIST , [4]. Chiba University, [5]. IMSUT, [6]. OIST)

㊫ **P-036**

Exploration and functional analysis of circRNAs regulating inflammatory responses

○Shuya Hiroki[1], Daisuke Ori[1], Norisuke Kano[1], Taro Kawai[1]
([1] Laboratory of Molecular Immunobiology, Graduate School of Science and Technology, Nara Institute of Science and Technology (NAIST))

㊫ **P-037**

Structural and Functional Analyses of Cwf19L1 Protein, a Responsible Gene Product for SCAR17

○Ryota Furukawa[1], So Masaki[1], Satoshi Tanaka[1] and Naoyuki Kataoka[1]
([1] The University of Tokyo)

学 **P-038**

Pseudouridine in the middle of tRNA anticodon facilitates genetic code alteration in arthropod mitochondria

○Naho Akiyama[1], Kazuki Inoue[1], Kenjyo Miyauchi[1], Kensuke Ishiguro[1], Shinichi Yokobori[2], Makoto Ihara[3], Kimitsuna Watanabe[2], and Tsutomu Suzuki[1]
([1]Dept. of Chem.&Biotech., Grad. Sch. of Eng., UTokyo, [2]Tokyo Univ. of Pharm. and Life Sci., [3]Radioisotope Medicine, Nagasaki Univ.)

学 **P-039**

Gene expression alteration in HTLV-1 infected cells by a METTL3/14 inhibitor STM2457

○Rei Higa, Kaoru Uchimaru, Makoto Yamagishi
(Graduate School of Frontier Sciences, The University of Tokyo)

P-040

Development of a strategy to fine-tune the efficiency of mRNA translation based on tRNA modifications

○Daisuke Ando[1,2,3], Sherif Rashad[1,4], Thomas J Begley[5], Peter C Dedon[6], and Kuniyasu Niizuma[1,3,4,7]
([1]Department of Neurosurgical Engineering and Translational Neuroscience, Tohoku University Graduate School of Medicine; [2]Department of Neurology, Tohoku University Graduate School of Medicine; [3]Division of Development and Discovery of Interventional Therapy, Tohoku University Hospital; [4]Department of Neurosurgical Engineering and Translational Neuroscience, Graduate School of Biomedical Engineering, Tohoku University; [5]Department of Biological Sciences, University at Albany; [6]Department of Biological Engineering, Massachusetts Institute of Technology; [7]Department of Neurosurgery, Tohoku University Graduate School of Medicine)

㊫ **P-041**

Crucial roles of the RNA helicase DDX6 in the maintenance of alveolar macrophages

○Asako Kajiya[1], Chihiro Goya[1], Ting Cai[1], Yoshinaga Masanori[1], Michael C Bassik[2], Osamu Takeuchi[1]

([1]Department of Medical Chemistry, Graduate School of Medicine, Kyoto University, [2]Department of Genetics, Stanford University)

㊫ **P-042**

SSA and EFGR pathway inhibitors cause dephosphorylation of PUM1 and stabilize p27 mRNA.

○Mayuko Hotta[1], Midori Shima[1], Fuku Matsuda[1], Daisuke Kaida[1]

([1] School of Medicine, University of Toyama)

P-043

Editing of the polyubiquitin architecture on the collided ribosome maintains persistent RQC activity

Shota Tomomatsu[1,2], ○Yoshitaka Matsuo[1], Fumiaki Ohtake[2], Takuya Tomita[3], Yasushi Saeki[3,4], Toshifumi Inada[1].

([1]Division of RNA and Gene regulation, Institute of Medical Science, The University of Tokyo, [2]Institute for Advanced life Sciences, Hoshi University, [3]Division of protein metabolism, Institute of Medical Science, The University of Tokyo, [4]Protein Metabolism Project, Tokyo Metropolitan Institute of medical Science.)

P-044

p40 induces degradation of BmAgo3 stalled on target RNAs

○Natsuko Izumi[1], Keisuke Shoji[1,2,3], Lumi Negish[4], and Yukihide Tomari[1,2]

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P-045

Atomic structures of human mitochondrial tRNAs toward understanding molecular pathogenesis of mitochondrial diseases

○Sena Niwa[1], Asuteka Nagao[1], Naho Akiyama[1], Nono Tomita[3], Mikako Shirouzu[2], Kensuke Ishiguro[1,2] and Tsutomu Suzuki[1]

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P-046

Selection of novel fluorogenic RNA aptamers by affinity and fluorogenic-based method and their characterization

○Tomotaka Tayama[1], Keisuke Ito[1], Sotaro Uemura[1], and Ryo Iizuka[1]

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P-047

Biochemical methods for transcriptome-wide exploration of RNAs with adenosine cap structure

○Noriko Miyahira[1], Takayuki Ohira[1], and Tsutomu Suzuki[1]

([1] Graduate School of Engineering, The University of Tokyo)

P-048

Exploring architectural RNAs associated to cellular senescence

○Saki Fujiwara[1], Naoko Fujiwara[1], Takeshi Chujo[2], Chao Zeng[3], Michiaki Hamada[3], and Tetsuro Hirose[1,4]

([1] Graduate School of Frontier Biosciences, Osaka University, [2] Graduate school of Medical Sciences, Kumamoto University, [3] Research Institute for Science and Engineering, Waseda University, [4] OTRI, Osaka University)

P-049

Drosophila ovarian somatic cell-specific isoform production triggered by transposon insertion

○Mai Moritoh[1], Toru Morita[2], Chikara Takeuchi[3], Yuka W. Iwasaki[3] and Mikiko C. Siomi[1]

([1] Graduate School of Sciences, The University of Tokyo, [2] School of Medicine, Yokohama City University, [3] Laboratory for Functional Non-coding Genomics, RIKEN Center for Integrative Medical Sciences)

P-050

The molecular and physiological roles of Cnot4 in zebrafish

○Koya Kageyama, Chihiro Hayashida, Yuichiro Mishima

(Faculty of Lifesciences, Kyoto Sangyo University)

P-051

New solution for long RNA synthesis: A combination of chemical synthesis and enzymatic ligation accelerates high quality manufacturing of long RNA

○Masato Sanosaka[1], Natsumi Sakamoto[1], Harei Sakusai[1], Emi Saito[1], and Hirokazu Nankai[1]

([1] Ajinomoto Bio-Pharma Services, GeneDesign, Inc)

P-052

Regulated IRE1-dependent mRNA decay is induced by physiological ER stress in Aspergillus oryzae

○Mizuki Tanaka[1], Silai Zhang[2], Shun Sato[2], Jun-ichi Yokota[2], Yuko Sygiyama[2], Yasuaki Kawarasaki[3], Youhei Yamagata[1], Katsuya Gomi[2], Takahiro Shintani[2]

([1] Tokyo University of Agriculture and Technology, [2] Tohoku University, [3] University of Shizuoka)

P-053

Comprehensive Database for RNA-Targeting Drug Discovery

○Chao Zeng[1], Michiaki Hamada[1,2,3]

([1] Faculty of Science and Engineering, Waseda University, [2] CBBD-OIL, National Institute of Advanced Industrial Science and Technology, [3] Graduate School of Medicine, Nippon Medical School)

P-054

Structural basis for pegRNA-guided reverse transcription by prime editor

○Yutaro Shuto[1], Ryoya Nakagwa[1], Shiyou Zhu[2,3,4,5,6], Hoki Mizuki[1], Satoshi N. Omura[1], Hisato Hirano[1], Yuzuru Itoh[1], Feng Zhang[2,3,4,5,6] & Osamu Nureki[1]

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P-055

Elucidation of roles for RNA metabolic regulation in wound-induced cell dedifferentiation

Emy Saetre[1,2,*], Ola Rosengren[1,2,*], Akira Iwase[3], and ○Misato Ohtani[1,3,4]

([1] Graduate School of Science, The University of Tokyo, [2] Chalmers University of Technology, [3] RIKEN, CSRS, [4] Division of Biological Science, NAIST)

P-056

Role of the loop region aligned with RNA-binding motifs in target specificity of bacterial Cold-shock protein

Satoshi Hasegawa[1,2], Rerina Inose[1], Mizuki Igarashi[1,3], Megumi Tsurumaki[1], Motofumi Saito[1], Tatsuo Yanagisawa[4], Akio Kanai[1,2,3] and ○Teppe Morita[1,3]

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P-057

Roles of N^6-methyladenosine readers and writers in the development of Marchantia polymorpha

○Chihiro Furumizu[1], Hiroko Kajiyama[2], Shinichiro Sawa[3]

([1] Graduate School of Integrated Sciences for Life, Hiroshima University, [2] School of Engineering, Hiroshima University, [3] International Research Center for Agricultural and Environmental Biology, Kumamoto University)

P-058

Mapping the functional element of the sex-determining RNA in the crustacean Daphnia magna using DMS-MaPseq and mutational analysis

○Nikko Adhitama[1,2], Christelle Alexa Garcia Perez[1], Yasuhiko Kato[1,2], Hajime Watanabe[1,2]

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㊫ **P-059**

pre-mRNA splicing links photosynthesis activity to lateral root morphogenesis in plants

○Natsu Takayanagi[1], Toshihiro Arae[1], Takayuki Shimizu[2], Mitsuhiro Aida[3], Hidehiro Fukaki[4], Tatsuru Masuda[5], Misato Ohtani[1,6,7]

([1]Graduate School of Frontier Sciences, The University of Tokyo, [2] Faculty of Science and Graduate School of Science, Nara Women's University, [3] FAST, Kumamoto University, [4] Graduate School of Science, Kobe University,[5] Graduate School of Art and Sciences, The University of Tokyo, [6] Division of Biological Science, NAIST, [7]CSRS, RIKEN)

P-060

Candidate Identification of Mobile RNAs and Their Related Genes in Pollen

○Kazuki Motomura[1,2], Ayumi Matsumoto[1], Shigeo S. Sugano[3], Ayumi Saito[1], Marin Komojiri[4], Mayuko Sato[5], Mayumi Wakazaki[5], Daichi Susaki[6], SooJung Yang[1], Yuriko Kibayashi[1], Tetsu Kinoshita[6], Kiminori Toyooka[5], Tetsuya Higashiyama[7], Daisuke Maruyama[6], and Atsushi Takeda[8]

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P-061

Detection and quantification of multiple tRNA modification status by nanopore sequencing

○Yosei Hanzawa[1], Ryo Noguchi[1], Takayuki Ohira[1], and Tsutomu Suzuki[1]

([1] Department of Chemistry and Biotechnology, Graduate School of Engineering, The University of Tokyo)

P-062

PNUTs, a transcription terminator, represses transposable elements in the Piwi-piRNA pathway

○Yaning Wu, Rin Imai, Haruhiko Siomi, Kensaku Murano

(Department of Molecular Biology, Keio University School of Medicine)

P-063

Effect of the conformational equilibrium in the microRNA precursor pre-miR-21 on the activity of a maturation-inhibitor L50

○Yuhei Nishimura[1], Yuji Tokunaga[1], and Koh Takeuchi[1]

([1] Graduate School of Pharmaceutical Sciences, The University of Tokyo)

㊫ **P-064**

The third biosynthesis pathway of 4-thiouridine in tRNA

Yuzuru Sugio[1], ○Sota Yamasaki[1], Junya Ueda[1], Ryo Isogai[1], Natsumi Matsumoto[1], Minoru Hayashi[1], Ryota Yamagami[1], Akira Hirata[2], Chie Tomikawa[1], Satoshi Ohno[3], Takuya Kawamura[1], Takashi Yokogawa[3], and Hiroyuki Hori[1]
([1]Graduate School of Science and Engineering, Ehime University, [2]Graduate School of Technology, Industrial and Social Science, Tokushima University, [3]Faculty of Engineering, Gifu University)

P-065

Sulfolobales TmcA1 and TmcA2 are ac^{4}C writers that acetylate distinct RNA substrates and differently contribute to thermal adaptation

○Takayuki Ohira[1], Masaki Takegawa[1], Kensuke Ishiguro[1], Ryo Matsuda[2], Norio Kurosawa[2], and Tsutomu Suzuki[1]
([1] Graduate School of Engineering, The University of Tokyo, [2] Graduate school of Science and Engineering, Soka University)

㊫ **P-066**

Spatiotemporal regulation of methanol-inducible mRNAs in the methylotrophic yeast Candida boidinii

○Fuka Sekioka, Kosuke Shiraishi, Miho Akagi, Akari Habata, Hiroya Yurimoto and Yasuyoshi Sakai
([1] Graduate School of Agriculture, Kyoto University)

P-067

General remarks of the promoter element 2 regulating genome replication of paramyxoviruses and filoviruses

Shoichi Ashida[1], ○Yusuke Matsumoto[1]
([1] Transboundary Animal Diseases Research Center, Joint Faculty of Veterinary Medicine, Kagoshima University)

P-068

Functionalization of chemically modified mRNA using engineered RNA and RNA binding protein

○Tatsuyuki Yoshii[1], Masumi Ohshima[2], Hirohide Saito[1,2]

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Structural insights into the complex of m^{6}A methyltransferase METTL16 and U6 snRNA

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㊫ **P-070**

Structural analysis of the 5'-UTR of OsMac3 mRNA which involved in the efficient translation

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㊫ **P-071**

Roles of the deadenylase complexes, Ccr4-Not and Pan2-Pan3, in yeast cell growth

○Nozomi Endo and Kenji Irie

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P-072

Circadian variation of miRNAs in mouse plasma

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㊫ **P-073**

Development of translational enhancement technique using designer PPR (Pentatricopeptide Repeat) proteins

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P-074

AtCAF1i/k, deadenylases in Arabidopsis, are important for de novo shoot organogenesis

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P-075

mRNA-specific translational repression by hnRNPU

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㊫ **P-076**

Lysine-transfer reaction mechanism by the complex of ArcS and RaSEA for archaeosine biosynthesis in tRNA.

○Shu Fujita[1], Yuzuru Sugio[1], Takuya Kawamura[1], Ryota Yamagami[1], Natsuhisa Oka[2], Akira Hirata[3], Takashi Yokogawa[2], and Hiroyuki Hori[1]

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P-077

A universal tool for characterization of RNA discovered by SELEX

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P-078

Elucidating the role of Vasa in the accumulation of transposon transcripts in Vasa bodies

○Mizuki Fukuda[1], Hiroya Yamazaki[1], and Mikiko.C.Siomi[1]

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P-079

ANP32A is a critical host factor for Borna disease virus replication and contributes to host tropism

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P-080

Overexpression of pigq gene restores the blood cell counts in a zebrafish model of Diamond-Blackfan anemia

○Tamayo Uechi[1], Mariko Nagatomo[1], Maki Yoshihama[1], Yukari Nakajima[1], Yutaka Suzuki[2], Naoya Kenmochi[1]

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P-081

Translational regulation mediated by ligand-induced tRNA activation

○Ren Nakazaki[1], Asuteka Nagao[1], Kensuke Ishiguro[1], Takeshi Yokoyama[2], Yoshikazu Tanaka[2] & Tsutomu Suzuki[1]

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P-082

Sequence characterization and prediction of semi-extractable RNAs

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P-083

Glycosylated queuosines in tRNAs optimize translational rate and post-embryonic growth

○K. Ishiguro[1,2], X. Zhao[1], D. Ma[1], H. Saito[3,4], S. Akichika[1], I. Matsuzawa[1], M. Mito[3], T. Irie[5], K. Ishibashi[5], K. Wakabayashi[5], Y. Sakaguchi[1], T. Yokoyama[2,6], Y. Mishima[5], M. Shirouzu[2], S. Iwasaki[3], Ta. Suzuki[1], Ts. Suzuki[1]

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P-084

TRMT10A dysfunction perturbs codon translation of initiator methionine and glutamine and impairs brain functions in mice

○Roland Tresky[1], Yuta Miyamoto[1], Yu Nagayoshi[1], Yasushi Yabuki[2], Kimi Araki[3], Yukie Takahashi[1], Yoshihiro Komohara[1], Huicong Ge[1], Kayo Nishiguchi[1], Takaichi Fukuda[1], Hitomi Kaneko[1], Nobuko Maeda[1], Jin Matsuura[1], Shintaro Iwasaki[4], Kourin Sakakida[1], Norifumi Shioda[2], Fan-Yan Wei[5], Kazuhito Tomizawa[1], and ○Takeshi Chujo[1]

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P-085

Deciphering the functions of the RNA helicase DDX6 in the nucleus of human cells

Chia-Yu Shih[1], Jui-Hsuan Liang[1], Jo-Hsi Huang[1], Yun-Chi Chen[1], Heng-Yi Lin[1], and ○Chia-Ying Chu[1,2]

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P-086

RNaseX25-mediated RNA degradation during early embryonic development

○Shiho Makino[1], Yoshinori Ohsumi[2], Takashi Fukaya[1]

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㊫ **P-087**

Structure analysis of small non-coding RNAs, CeR-2a and CeR-2b, involved in rRNA processing in C. elegans

○Hayato Sugawara[1], Miu Tsumagari[1], Yudai Usami[1], Chisato Ushida[2] and Gota Kawai[1]

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P-088

SRP9 migrates nucleus and regulates gene expression through binding to various non-coding RNAs

○Tomoaki Hara[1], Sikun Meng[1], Hiromichi Sato[1,2], Kazuki Sasaki[1,2], Yasuko Arao[1], Yoshiko Saito[1], Ken Ofusa[1,3], Daisuke Motooka[4], Yuichiro Doki[2], Hidetoshi Eguchi[2] and Hideshi Ishii[1]

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㊫ **P-089**

Generation of a conditional Xist knockdown mouse model using Cas7-11

○Nao Watanabe[1], Maho Hashimoto[1], Tomoki Chiba[1], Hiroshi Asahara[1]

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P-090

HSATIII-derived proteins are novel components of a protein complex potentially associated with actin cytoskeleton dynamics

○Kensuke Ninomiya[1], Shungo Adachi[2], Tetsuro Hirose[1, 3]

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㊫ **P-091**

Mechanisms of mRNA-independent translation reaction in mammalian cells

○Shuhei Ebine[1], Takuya Tomita[2], Petr Tesina[3], Robert Buschauer[3], Matthias Thoms[3], Yoshitaka Matsuo[1], Roland Beckmann[3], Yasushi Saeki[2], Toshifumi Inada[1]

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㊫ **P-092**

Analysis of changes in the structure and function of germ granules by Nanos during Drosophila embryogenesis

○Yasuhiro Kozono[1], Miho Asaoka[2], Makoto Hayashi[3] and Satoru Kobayashi[2]

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P-093

Structural basis for the interaction between the UUCG stem-loop of human U1 snRNA and the ubiquitin like domain of the SF3A1 subunit in U2 snRNP

○Kanako Kuwasako[1], Shin-ichi Terawaki[2], Masayuki Takizawa[1], Madoka Kitamura[1], Yutaka Muto[1] and Nobukazu Nameki[3]

([1] Faculty of Pharmacy and Research Institute of Pharmaceutical Sciences, Musashino University, [2] Proteo-Science Center, Ehime University, [3] Graduate School of Science and Technology, Gunma University)

㊫ **P-094**

TRBP regulates RLR-mediated antiviral innate immune signal

○Monami Sakai[1], Koji Onomoto[1], Miyu Watanabe[1], Tomoko Takahashi[2,3], Kumiko Ui-Tei[3,4], Mitsutoshi Yoneyama[1,5]

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P-095

ER protein Kinectin 1 regulates cellular localization of multi-tRNA synthetase complex in a variant-specific manner

○Masaki Hosogane[1], Sue Yi Siao[2], Atsushi Hatano[3], Masaki Matsumoto[3] and Keiko Nakayama[1]

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P-096

Possible regulation of piRNA target transposons via DNA methylation-independent mechanism

○Hiromi Yamada[1], Chikara Takeuchi[1,2], and Yuka W. Iwasaki[1]

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㊫ **P-097**

A novel Drosha isoform specifically expressed in embryonic stem cells and germ line cells in mice

○Yuji Shimizu[1], Ren Shimamoto[1], Ayako Isotani[1], and Katsutomo Okamura[1]

([1] Division of Biological Science, Nara Institute of Science and Technology)

P-098

Single molecule detection of tRNA modifications by signal alignment of nanopore sequencing data

○Ryo Noguchi[1], Mai Maeda[1], Qiuyu Wang[1], Bhaskar Dasgupta[2], Hiroki Ueda[2], Tsutomu Suzuki[1]

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P-099

Analysis of the interaction between m^6Am methyltransferase PCIF1/CAPAM and translational repressor PAIP2

○Chihiro Oyama[1], Ryoya Kano[1], Shiori Toyama[1], Haruki Ikezawa[1], Chihiro Ikeda[1], Shiho Ito[1], Ai Sugita[1], Aki Tanaka[1], Yoshiaki Ohkuma[2], Shinichiro Akichika[3], Tsutomu Suzuki[3], Yutaka Hirose[1]

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P-100

Structural Analysis of stem-loop RNAs involved in the regulation of immunity and their interaction with Regnase-1

○Shiho Nakao[1], Yuna Shimizu[2], Hinano Kobayashi[1], Gota Kawai[1,2]

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P-101

Application of the B. subtilis ultra-transformation system to tRNA study.

○Akiko Soma[1], Ritsuho Yamakawa[1], Fujio Kawamura[1], Tsukasa Kouchi[1], Genki Akanuma[2], Yuma Okubo[1]

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Cap specific m^{6}A methyltransferase PCIF1/CAPAM modulates type I IFN responses

○Ryoya Kano[1], Chihiro Oyama[1], Chihiro Ikeda[1], Ai Sugita[1], Hiroyasu Ishiguro[1], Aki Tanaka[1], Akiko Inujima[2], Keiichi Koizumi[3], Shinichiro Akichika[4], Tsutomu Suzuki[4], Yoshiaki Tabuchi[5], Yoshiaki Ohkuma[6], Yutaka Hirose[1]
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P-103

Single molecule detection of human mitochondrial tRNA modification by nanopore sequencing

○Qiuyu Wang[1], Ryo Noguchi[1], Ena Tomoda[1], Tsutomu Suzuki[1]
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The MTR4/hnRNPK complex-mediated degradation of aberrant polyadenylated RNAs with multiple exons

○Xinyue Gao[1,2], Kenzui Taniue[1], Anzu Sugawara[1], Chao Zeng[3], Han Han[1,2], Masahide Seki[4], Yutaka Suzuki[4], Michiaki Hamada[3,5], Nobuyoshi Akimitsu[1,2]
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㊫ **P-105**

Exploring the landscape of tRNA modifications in ageing

○Longteng Zhang[1], Raja Norazireen Raja Ahmad[1], Lin Liu[1], Yue Xu[1], Shigeru Matsuda[1], Haruna Tani[1], Akiko Ogawa[1], Fan-Yan Wei[1]

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P-106

Insights into the role of eukaryotic translation initiation factor 3 (eIF3) on Hepatitis C virus IRES-mediated translation

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P-107

Oligonucleotide Chemical Ligation Reactions Aimed at Long RNA Production

○Harei Sakurai[1], Yu Hirano[2], Naoshi Kojima[2], Masato Sanosaka[1], Emi Saito[1], Hirokazu Nankai[1] and Yasuo Komatsu[2]

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P-108

Translation-dependent Degradation of Small Ribosomal Subunits

○Sihan Li[1], Okuto Shounai[2], Toshifumi Inada[1]

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P-109

Structural polymorphism of the nucleic acids in pentanucleotide repeats associated with the neurological disorder CANVAS

○Kenta Kudo, Karin Hori, Norifumi Shioda
(Department of Genomic Neurology, Institute of Molecular Embryology and Genetics (IMEG), Kumamoto University)

P-110

Identification of mouse cardiac-specific Ttn splicing isoforms targetd by wild-type and mutant Rbm20 using Long-read sequencing

○Yuri Yamasu[1,2], Marina Ohno-Togo[1], Eichi Watabe[1], Hidehito Kuroyanagi[2]
([1] Tokyo Medical and Dental University, [2] University of the Ryukyus)

P-111

tRNA modifications orchestrate the translational response to mitochondrial stress.

○Sherif Rashad, MD. Shadi Al-Mesitef. Abdulrahman Mousa. Kuniyasu Niizuma, MD, PhD.
(Department of Neurosurgical Engineering and Translational Neuroscience, Graduate School of Biomedical Engineering, Tohoku University, Sendai, Japan.)

P-112

CUG repeat RNA promotes proteasomal degradation of MBNL1

○ Yoshitaka Aoki[1], Ai Ohki[1], Motoaki Yanaizu[1], Yoshihiro Kino[1]
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Translational regulation of haploid-specific mRNAs during spermatogenesis

○Yuka Isono, Hideto Tanaka, Shin-ichi Kashiwabara
(Institute of Life and Environmental Sciences, University of Tsukuba)

P-114

The 3' additional and promoter sequences of Borna disease virus 1 genome coordinately regulate viral transcription and replication.

○Takehiro Kanda[1,2], Keizo Tomonag[1,2,3]

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P-115

Self-alkylating ribozymes available with N1 methyl pseudouridine RNA

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P-116

SSA Stabilizes c-Myc mRNA

○Fuku Matsuda[1], Midori Shima[1], Mayuko Hotta[1], Daisuke Kaida[1]

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Mechanistic insights into the roles of the UFM1 E3 ligase complex in ufmylation and ribosome-associated protein quality control

○Sota Ito[1], Ryosuke Ishimura[2], Gaoxin Mao[2], Satoko Komatsu-Hirota[2], Nobuo N Noda[3], Masaaki Komatsu[2] and Toshifumi Inada[1]

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P-118

Elucidation of the molecular mechanism for ribosomal protein eS7A ubiquitination that contributes to Unfolded Protein Response

○Nichika Sato[1,2], Yasuko Matsuki[3], Yu Nakano[3], Yoshitaka Matsuo[2], Toru Yoshihisa[4] and Toshifumi Inada[1,2]

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P-119

Nanopore direct RNA sequencing reveals the METTL2A-mediated 3-methylcytidine sites on poly(A) RNAs

○Shuhei Mitsutomi [1,2], Kenzui Taniue [2,3], Anzu Sugawara [2], Nobuyoshi Akimitsu [2]

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P-120

RNA G-quadruplexes facilitates Tau phase transition in vitro.

○Ginji Komiya[1,2]、Norifumi Shioda[1,2]、Yasushi Yabuki[1,2]

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P-121

Enhancing Purification of Messenger RNA Drug Substances: Exploring Macroporous Resin Particles for Improved Separation from Immunostimulatory dsRNA Impurities

○Yuki Higuchi[1], Saoko Nozawa[1], Akinari Awatani[1, 2], Takashi Sekida[2], Taeko Nakajima[1]

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Molecular basis for activation of plant organellar C-to-U RNA editosome

Tenghua Wang[1], ○Mizuki Takenaka[1]

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RNA binding protein RBPU maintains cancer stem like status in triple negative breast cancer

○Yutaro Uchida[1], Ryota Kurimoto[1], Tomoki Chiba[1], Takahide Matsushima[1], Yasuto Takeuchi[2], Noriko Gotoh[2], Hiroshi Asahara[1, 3]

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Demystifying the m6A epitranscriptome: a novel deep neural network-based method for long-read sequencing data

○Boyi Yu[1], Genta Nagae[2], Yutaka Midorikawa[3], Kenji Tatsuno[2], Bhaskar Dasgupta[1], Satoshi Ota[2], Hiroyuki Aburatani[2], Hiroki Ueda[1]

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㊫ **P-125**

A subset of primordial germ cells exhibit impaired function of piRNA machinery in Drosophila embryos.

○Kyohei Mikami[1,2], Masaki Masukawa[1,2] and Satoru Kobayashi[1,2].

([1] Degree Program in Life and Earth Sciences, Graduate School of Science and Technology, University of Tsukuba, [2] Life Science Center for Survival Dynamics, University of Tsukuba.)

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mRNA therapeutics development strategy with optimized mRNA design for effective target protein expression

○Akiko Yanagiya[1], Rena Akahori[1], Hiroaki Murakami[1], Azusa Tanaka[1], Yanwen Feng[1], Hayato Sato[1], Naoki Matsumoto[1], Daichi Matsuura[1], Jun Nihira[1], Tetsuo Yoshida[2], Yuki Hasegawa[2], Kazuyuki Nakashima[1]

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㊫ **P-127**

Circular RNA synthesis from circular DNA template

○Yui Yoneda[1], Masayuki Suetsugu[1]

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Identifying and characterizing host cellular proteins binding to the non-polyadenylated 3'-untranslated region of LCMV mRNA

○Mei Hashizume[1], Ayako Takashima[1], Keiko Shindo[1], Masaharu Iwasaki[1,2,3,4]

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㊫ **P-129**

Phosphorylation of human TNRC6A modulates Argonaute binding responsible for RNA silencing activity

○Li Shen,[3] Masataka Suzawa,[1] Hiroko Kozuka-Hata,[2] Masaaki Oyama,[2] Kumiko Ui-Tei[1,3,*]

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Ongoing Participation Report on RNA 3D structure prediction at CASP16: Usage and limitations of AlphaFold3

○Junichi Iwakiri[1], Takumi Otagaki[1], Kazuteru Yamamura[1], Shunsuke Sumi[2,3], Jiro Kondo[4] and Kengo Sato[5]

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㊫ **P-131**

A random walk approach to cluster and integrate spatial transcriptomics data

○Reiichi Sugihara[1], Yuki Kato[1,2] and Yukio Kawahara[1,2]

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Organ-specific gene expression control using DNA origami-based nanodevices

○Yuxiang Liu[1,6], Ruixuan Wang[1,6], Qimingxing Chen[1], Yan Chang[1], Qi Chen[1], Kodai Fukumoto[2,3], Bingxun Wang[1], Jianchen Yu[1], Changfeng Luo[1], Jiayuan Ma[1], Xiaoxia Chen[1], Yuko Murayama[3], Kenichi Umeda[4], Noriyuki Kodera[4], Yoshie Harada[2], Shun-ichi Sekine[3], Jianfeng Li[1,5 *] and Hisashi Tadakuma[1,5 *]

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Structural analysis of a stem-loop in the intergenic region of Plautia stali intestine virus genome RNA

○Kousei Sakaguchi[1], Ryo Okubo[2], and Gota Kawai[1,2]

([1]Graduate School of Advanced Engineering, [2]Faculty of Advanced Engineering, Chiba Institute of Technology)

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Development of a Method for Simultaneous Detection of Multiple RNA Modifications Using Nanopore Sequencing

○Hiroki Ueda[1], Bo-yi Yu [1], Keisuke Yamada[2], Akihide Yoshimi[3], Genta Nagae[2], Hiroyuki Aburatani, [2]

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