

Frontiers in Genome Engineering 2019

25-27 November 2019
Kobe, Japan



WELCOME MESSAGE

We are pleased to announce the 3rd "Frontiers in Genome Engineering" International Conference to be held at the Kobe Convention Center, Hyogo, Japan from November 25 to 27, 2019. The topics of the conference will include but not limited to the use and development of new genome editing technologies for human health as well as agriculture and bioindustry. Following the successful meetings in 2017 and 2018, we are expecting presentations by the world's leading scientists and intense discussions among highly active participants of over 300 people at home and abroad.

KEYNOTE SPEAKERS



Feng Zhang

MIT, USA



Virginijus Siksnys

Vilnius Univ., Lithuania

MEET THE EDITORS

natureresearch

Markus Elsner
Nat. Biotech., Senior Editor

Steve Mao
Science, Senior Editor

INVITED SPEAKERS



Alexis Komor
University of California, USA



Baohui Chen
Zhejiang University, China



Benjamin Kleinstiver
Harvard Medical School, USA



Caixia Gao
Institute of Genetics and
Developmental Biology, CAS,
China



Dave Savage
University of California
Berkeley, USA



Debojyoti Chakraborty
CSIR-Institute of Genomics
and Integrative Biology, India



Hideyuki Okano
Keio University, Japan



Hui Yang
Institute of Neuroscience,
China



Hyongbum Kim
Yonsei University, Korea



Izuho Hatada
Gunma University, Japan



Jacob Corn
ETH Zurich, Switzerland



Jin-Soo Kim
Seoul National University,
Korea



Kathy Niakan
The Francis Crick Institute,
UK



Keiichiro Suzuki
Osaka University, Japan



Keiji Nishida
Kobe University, Japan



Knut Woltjen
CiRA, Japan



Kosuke Yusa
Kyoto University, Japan



Prashant Mali
Jacobs School of
Engineering, USA



Tomoji Mashimo
Osaka University, Japan

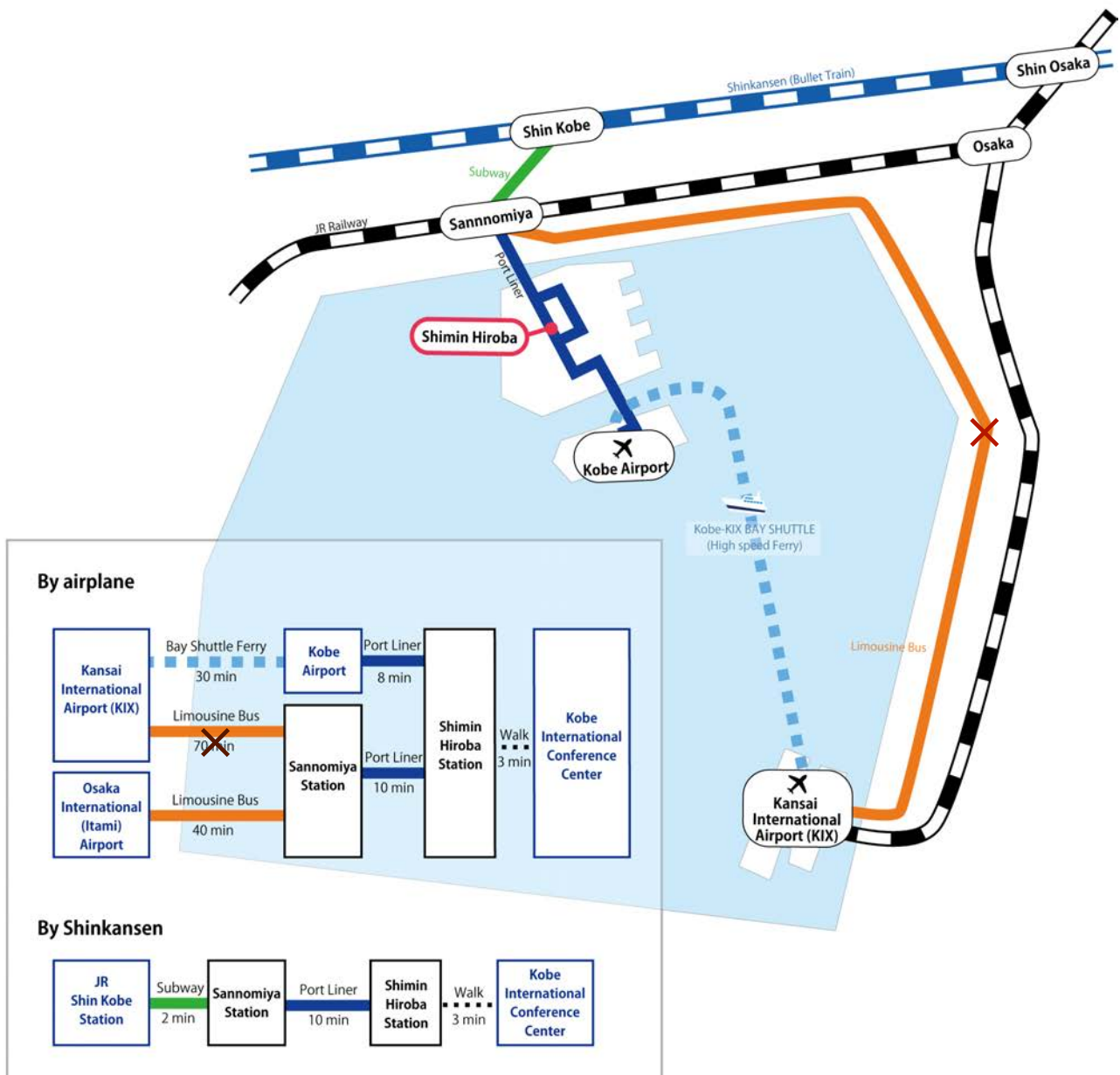


Wensheng Wei
Peking University, China

VENUE

Kobe Convention Center
 (Kobe International Conference Center and Kobe Portpia Hotel)

To Shimin-Hiroba Station



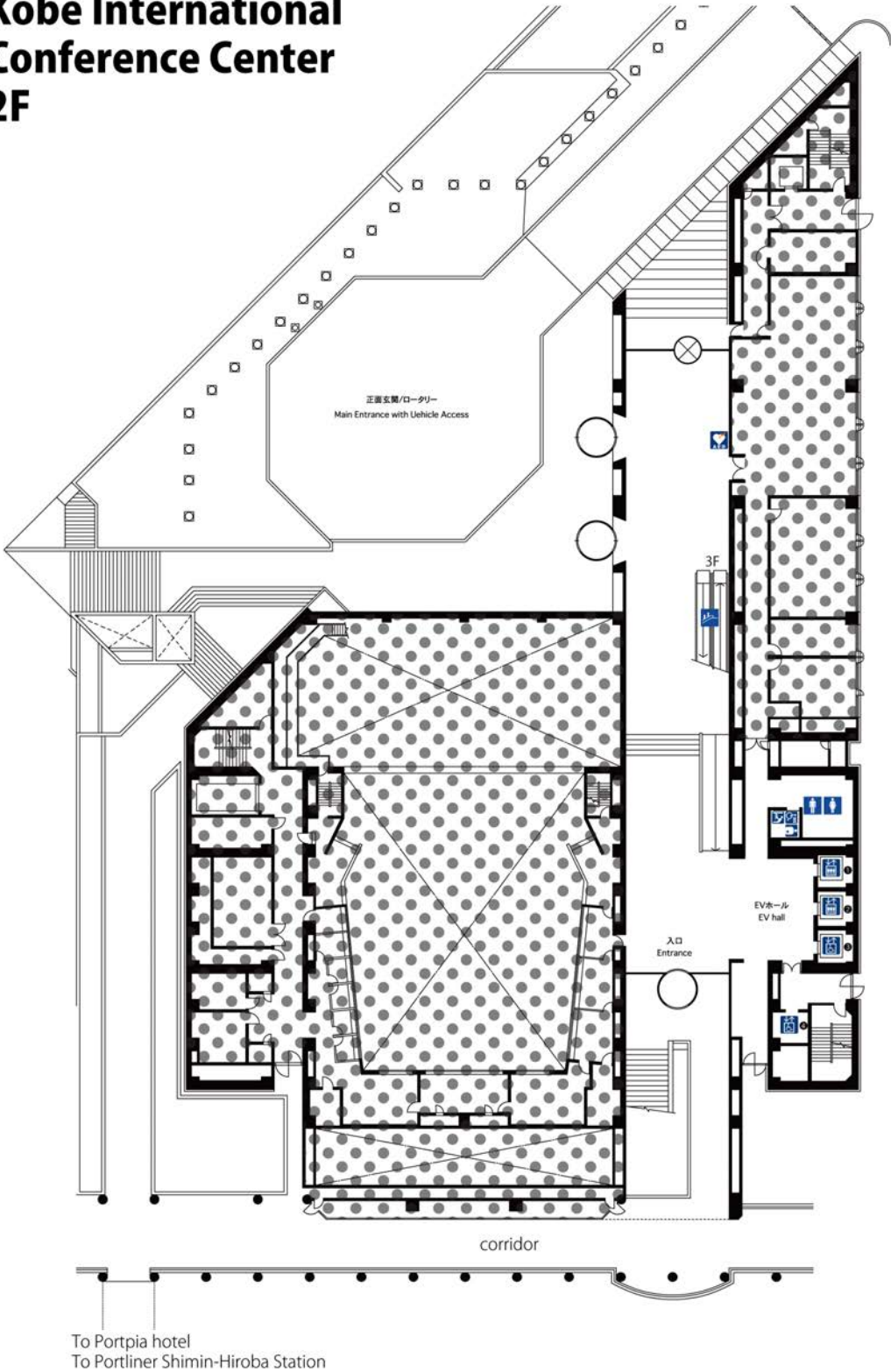
CAUTION!

Due to Hanshin Expressway closure by construction on 20th Nov. to 29th Nov., the operation of Limousine Buses from KIX is scheduled for delay or suspension. Please come with plenty of time or use other transportation systems (Bay Shuttle Ferry or train).

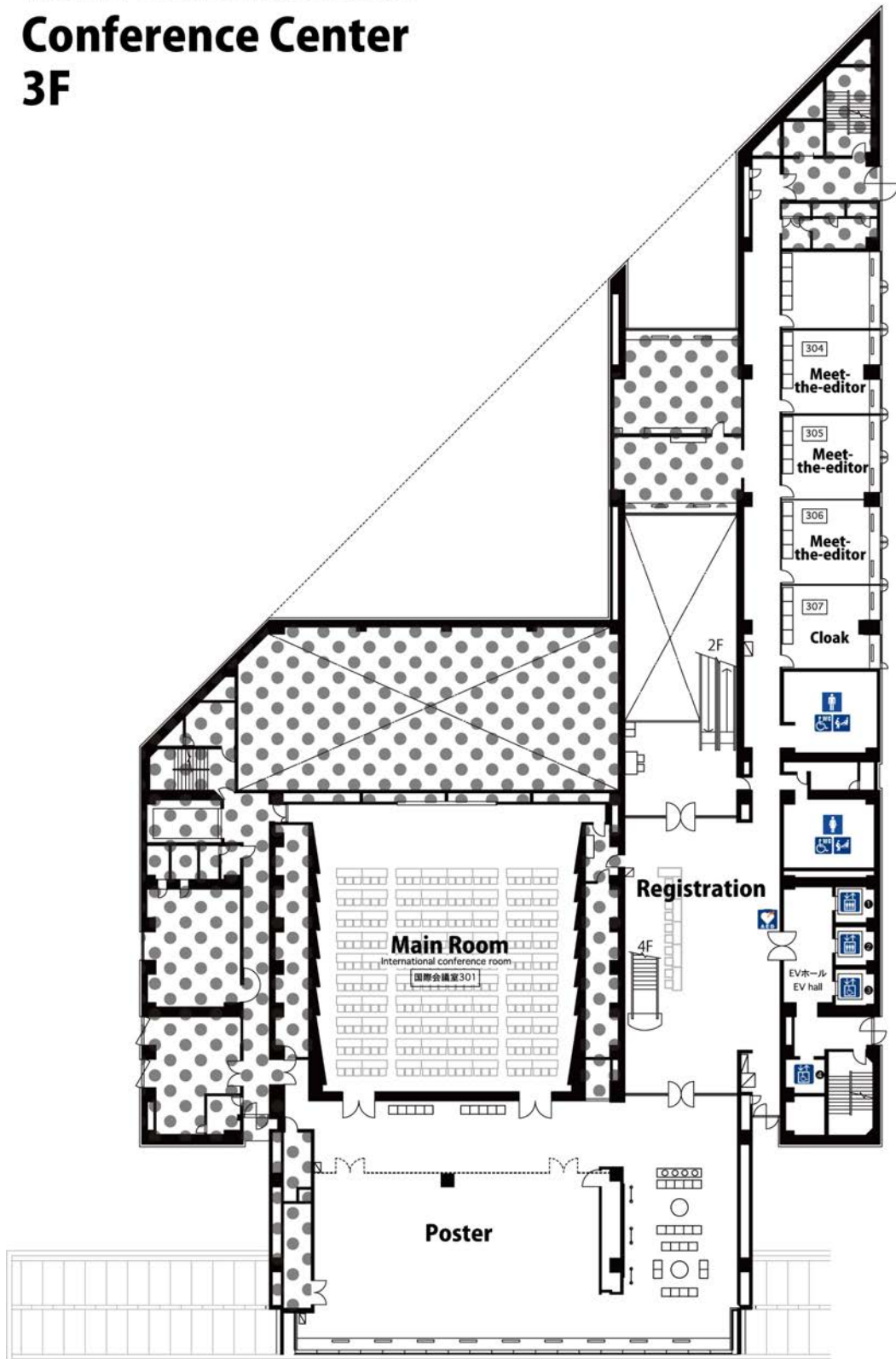
From Shimin-Hiroba Station To Kobe Convention Center



Kobe International Conference Center 2F



Kobe International Conference Center 3F



PROGRAM

| Time | November 25 (Mon) | November 26 (Tue) | November 27 (Wed) |
|-------|---|---|---|
| 9:00 | | Session 1 Technology & Tools -1 (9:00-10:30) Keiji Nishida Tomoji Mashimo Keiichiro Suzuki Kazuki Nakamae | Keynote Lecture (9:00-9:45) Virginijus Siksnys |
| 10:00 | | Coffee break and poster session | Session 4 Regenerative Biology (9:45-11:15) Hideyuki Okano Kathy Niakan Prashant Mali |
| 11:00 | | Session 2 Technology & Tools -2 (10:45-13:00) Baohuai Chen Jin-Soo Kim Dave Savage Osamu Nureki Pranam Chatterjee Nozomu Yachie | Coffee break and poster session |
| 12:00 | | | Session 5 Genome wide screening (11:30-13:00) Kosuke Yusa Hyongbum Kim Wensheng Wei |
| 13:00 | | Lunch and poster session (13:00-14:00) | Lunch and poster session (13:00-13:45) |
| 14:00 | | Poster session and Coffee break (14:00-15:30) | Session 6 Animals and Plants (13:45-15:45) Hui Yang Caixia Gao Hiroaki Saika Lee Hickey Kenta Sumiyama |
| 15:00 | Arrival and Registration | | Coffee break and poster session |
| 16:00 | | Session 3 Technology & Tools -3 (15:30-17:30) Alexis Komor Benjamin Kleinstiver Knut Woltjen Martin Pacesa Yuichiro Miyaoka | Session 7 Therapeutics (15:45-17:30) Izuho Hatada Jacob Corn Debojyoti Charkraborty Yutaka Hanazono |
| 17:00 | Welcome reception (17:00-18:30) | Meet-the-editor Poster session (17:30-18:15) | Meet-the-editor Poster session (17:30-18:15) |
| 18:00 | Welcome and opening remarks | | Closing remarks |
| 19:00 | Keynote Lecture (18:40-19:30) Feng Zhang | | |
| 20:00 | Drinks (19:30-21:30) | Banquet (18:30-21:30) @Kobe Portpia Hotel "KAIRAKU" | |
| 21:00 | | | |

Program

| MONDAY, NOVEMBER 25, 2019 | |
|---|--|
| 14:00-20:00 | Arrival and Registration |
| 17:00-18:30 | Welcome reception |
| 18:30-18:40 | Welcome and opening remarks |
| Keynote lecture | |
| Chair : Osamu Nureki, The University of Tokyo, Japan | |
| 18:40-19:30 | Feng Zhang , MIT, USA Harnessing Nature's Diversity For Gene Editing and Beyond |
| 19:30-21:30 | Drinks |
| | |
| TUESDAY, NOVEMBER 26, 2019 | |
| Session 1: Technology and Tools-1 | |
| Chair : Jin-Soo Kim, Seoul National University, Korea | |
| 9:00-9:15 | Keiji Nishida , Kobe University, Japan Base editing, gene conversion and local diversification without DNA double strand break |
| 9:15-9:45 | Tomoji Mashimo , Osaka University, Japan Type I CRISPR-Cas3 mediated genome editing in human cells |
| 9:45-10:15 | Keiichiro Suzuki , Osaka University, Japan Development of in vivo genome editing technologies and application for genome-editing therapy |
| 10:15-10:30 | Kazuki Nakamae , Hiroshima University, Japan Analysis of genomic and epigenomic features affecting the efficacy of MMEJ-assisted knock-in using machiato |
| 10:30-10:45 | Coffee break and poster session |
| | |
| Session 2: Technology and Tools-2 | |
| Chair : Keiji Nishida, Kobe University, Japan | |
| 10:45-11:15 | Baohui Chen , Zhejiang University, China Live Imaging of the Cellular Genome Using CRISPR Cas9 S systems |
| 11:15-11:45 | Jin-Soo Kim , Seoul National University, Korea Genome-wide target specificity of CRISPR RNA-guided base editors |

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| 11:45-12:15 | Dave Savage , University of California Berkeley, USA High-throughput approaches for engineering CRISPR-Cas proteins |
| 12:15-12:30 | Osamu Nureki , The University of Tokyo, Japan Molecular mechanism of CRISPR and structure-based development of genome editing tool towards medical applications |
| 12:30-12:45 | Pranam Chatterjee , MIT Media Lab, USA Robust genome editing with broad targeting CAS9 variants |
| 12:45-13:00 | Nozomu Yachie , The University of Tokyo, Japan Recording cellular events in DNA |
| Poster Session | |
| 13:00-14:00 | Lunch and poster session |
| 14:00-15:30 | Poster Session and Coffee break |
| Session 3: Technology and Tools-3 | |
| Chair : Caixia Gao, CAS, China | |
| 15:30-16:00 | Alexis Komor , University of California, USA Investigating the Chemical and Cellular Mechanisms of Base Editing |
| 16:00-16:30 | Benjamin Kleinstiver , Harvard Medical School, USA Expanding Genome Editing with Engineered CRISPR Enzymes |
| 16:30-17:00 | Knut Woltjen , CiRA, Japan Templated and template-free precision editing of human gene variants |
| 17:00-17:15 | Martin Pacesa , University of Zurich, Switzerland Structural basis SPCAS9 off-target binding |
| 17:15-17:30 | Yuichiro Miyaoka , Tokyo Metropolitan Institute of Medical Science, Japan Precise deletion mutagenesis by dual CAS12A DNA cleavage |
| 17:30-18:15 | Meet-the-editor and poster session |
| 18:30-21:30 | Banquet Kobe porpia hotel "Kairaku" |

| WEDNESDAY, NOVEMBER 27, 2019 | |
|---|--|
| Keynote lecture | |
| Chair : Akihiko Kondo, Kobe University, Japan | |
| 9:00-9:45 | Virginijus Siksnys , Vilnius University, Lithuania Harnessing bacterial immune system for targeted genome engineering |
| Session 4: Regenerative Biology | |
| Chair : Tomoji Mashimo, Osaka University, Japan | |
| 9:45-10:15 | Hideyuki Okano , Keio University, Japan Non-human primate brain science using genome editing |
| 10:15-10:45 | Kathy Niakan , The Francis Crick Institute, UK Using genome editing and single cell approaches to study early lineage specification in human embryos |
| 10:45-11:15 | Prashant Mali , Jacobs School of Engineering, USA Improving genome interpretation via genome engineering toolsets: new approaches and new challenges |
| 11:15-11:30 | Coffee break and poster session |
| Session 5: Genome wide screening | |
| Chair : Steve Mao, Science | |
| 11:30-12:00 | Kosuke Yusa , Kyoto University, Japan Development and application of CRISPR-knockout screening |
| 12:00-12:30 | Hyongbum Kim , Yonsei University College of Medicine, Korea Deep learning-based prediction of CRISPR-Cpf1 and Cas9 activities |
| 12:30-13:00 | Wensheng Wei , Peking University, China Gene Editing: High-throughput Functional Genomics and Beyond |
| 13:00-13:45 | Lunch and poster session |
| Session 6: Animals and plants | |
| Chair : Markus Elsner, Nature Biotechnology | |
| 13:45-14:15 | Hui Yang , Institute of Neuroscience, China DNA base editing induces substantial DNA&RNA off-target mutations and eliminated by mutagenesis |
| 14:15-14:45 | Caixia Gao , CAS, China Base editing and Crop Improvement |
| 14:45-15:00 | Hiroaki Saika , National Agriculture and Food Research Organization, Japan Targeted deletion of rice retrotransposon |
| 15:00-15:15 | Lee Hickey , The University of Queensland |

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| | Express editing for crop improvement |
| 15:15-15:30 | Kenta Sumiyama , RIKEN, Japan Triple-target CRISPR enabled production of complete bi-allelic double and triple gene knockouts at first generation |
| 15:30-15:45 | Coffee break and poster session |
| Session 7: Therapeutics | |
| | Chair : Nozomu Yachie, The University of Tokyo, Japan |
| 15:45-16:15 | Izuho Hatada , Gunma University, Japan Epigenome editing of animals |
| 16:15-16:45 | Jacob Corn , ETH Zurich, Switzerland Genome editing at work in human cells |
| 16:45-17:15 | Debojyoti Charkraborty , CSIR-Institute of Genomics and Integrative Biology, India Highly precise genome editing using an engineered orthogonal Cas9 protein |
| 17:15-17:30 | Yutaka Hanazono , Jichi Medical University, Japan Feasibility Study of Homologous Recombination-Based Genome-Editing Therapy in a Swine Model of X-SCID |
| 17:30-18:15 | Meet-the-editor and poster session |
| | Closing remarks |

Poster presentations

P01

Seiichi Hirano (The University of Tokyo)

STRUCTURAL BASIS FOR THE PROMISCUOUS PAM RECOGNITION BY *C. DIPHTHERIAE* CAS9

P02

Hiroshi Nishimasu (The University of Tokyo)

STRUCTURE-BASED ENGINEERING OF CRISPR-CAS9

P03

Nahye Kim (Yonsei University College of Medicine)

SPCAS9 ACTIVITY PREDICTION BY DEEPSPCAS9, A DEEP LEARNING-BASED MODEL WITH HIGH GENERALIZATION PERFORMANCE

P04

Ryoya Nakagawa (The University of Tokyo)

BIOCHEMICAL CHARACTERIZATION AND MOLECULAR ENGINEERING OF THE MINIMAL CAS9 FROM *C. JEJUNI*

P05

Hui Kwon Kim (Yonsei University College of Medicine)

HIGH-THROUGHPUT COMPARATIVE ANALYSIS OF xCas9, SpCas9-NG, AND SpCas9 ACTIVITIES IN HUMAN CELLS

P06

Hideto Mori (The University of Tokyo)

SPADE FOR EXPLORING PERIODIC SEQUENCE REPEATS AS POTENTIAL GENOME EDITING MODULES

P07

Keishi Osakabe (Tokushima University)

GENOME EDITING IN PLANTS BY USING A NOVEL GENOME EDITING TOOL, TID

P08

Nina Kurihara (The University of Tokyo)

BIOCHEMICAL ANALYSIS OF CAS12C

P09

Kazuto Yoshimi (Osaka University)

CHARACTERIZATION OF CRISPR-CAS3-MEDIATED GENOME EDITING IN MAMMALIAN CELLS

P10

Naoyuki Miyashita (KINDAI University)

MOLECULAR DYNAMICS SIMULATION STUDY FOR THE DIFFERENCES BETWEEN THE DYNAMICS OF CRISPR CAS3 WITH AND WITHOUT SHORT SINGLE-STRAND DNA

P11

Satoru Takeda (The University of Tokyo)

THE FUNCTIONAL AND STRUCTURAL ANALYSIS OF MINIATURE CRISPR-Cas14a

P12

Lapatrada Taemaitree (Suez University)

Split-and-Click sgRNAs

P13

Atsushi Kunii (Hiroshima University)

POWERFUL GENE ACTIVATION VIA CRISPR-BASED HIERARCHICAL ACCUMULATION OF EFFECTOR DOMAINS

P14

Ha rim Shin (University of Ulsan College of Medicine)

INHIBITION OF HISTONE DEACETYLATION IMPROVE CRISPR-MEDIATED ADENINE BASE EDITING EFFICIENCY

P15

Jonathan Strecker (Broad Institute of MIT and Harvard)

RNA-guided DNA insertion with CRISPR-associated transposases

P16

Takahiro Otabe (The University of Tokyo)

SPLIT-CPF1 SYSTEM AS AN INDUCIBLE GENOME EDITING AND EFFICIENT GENE ACTIVATION

P17

Ji-Eun See (University of Ulsan College of Medicine)

Reporter-based drug screening to improve CRISPR-mediated adenine base editing efficiency

P18

Niels R. Weisbach (ETH Zurich)

MULTIPLEXED GENOME ENGINEERING BY CAS12A AND CRISPR ARRAYS ENCODED ON SINGLE TRANSCRIPTS

P19

Hiroyuki Konishi (Aichi Medical University School of Medicine)

TANDEM PAIRED NICKING USING CAS9 NICKASES PERMITS TARGETED KNOCK-IN WITHOUT SIGNIFICANT INHIBITION BY P53

P20

Yanpeng Wang (Chinese Academy of Sciences)

CYTOSINE, BUT NOT ADENINE, BASE EDITORS INDUCE GENOME-WIDE OFF-TARGET MUTATIONS IN RICE

P21

You Kyeong Joeong (Hanyang University)

Adenine base editors catalyze cytosine conversions in human cells

P22

Changyang Zhou (Chinese Academy of Sciences)

OFF-TARGET RNA MUTATION INDUCED BY DNA BASE EDITING AND ITS ELIMINATION BY MUTAGENESIS

P23

Ju-Chan Park (Seoul National University)

Safe Scarless Cassette-free Selection of Genome-edited Human Pluripotent Stem Cells Using Temporary Drug Resistance

P24

John Yu (Chang Gung Memorial Hospital)

B3GALT5 GENOMIC KNOCKOUT ALTERS GLYCOSPHINGOLIPID PROFILE AND FACILITATES TRANSITION TO HUMAN NAÏVE PLURIPOTENCY

P25

Marco Jost (University of California)

CRISPR-BASED GENETIC SCREENS IN PRIMARY HUMAN DENDRITIC CELLS TO DECIPHER MECHANISMS OF HOST-MICROBIOTA INTERACTIONS

P26

Yan Zhou (Wellcome Sanger Institute)

MEASURING GERMLINE VARIATION OF HUMAN GENE ESSENTIALITY BY GENOME-WIDE CRISPR/CAS9 SCREENING IN INDUCED PLURIPOTENT STEM CELLS

P27

Gue-ho Hwang (Hanyang University)

WEB TOOLS FOR CRISPR: RGENOME.NET

P28

Jun Teramoto (Kobe University)

A COMPUTATIONAL TOOL TO DESIGN UNIQUE GUIDE RNAs FOR GENOME-WIDE BASE EDITING BY TARGET-AID

P29

Ko Ishihara (Epigeneron, Inc.)

A NOVEL SCREENING METHOD FOR GENOME-EDITED CELLS BY OLIGORIBONUCLEOTIDE INTERFERENCE-PCR (ORNi-PCR)

P30

Xiaomin Si (University of Chinese Academy of Sciences)

GENOME EDITING OF UPSTREAM OPEN READING FRAMES ENABLES TRANSLATIONAL CONTROL IN PLANTS

P31

Yuriko Osakabe (Tokushima University)

DEVELOPMENT OF IN PLANTA-REGENERATION SYSTEM FOR PLANT GENOME EDITING

P32

Rui Zhang (Chinese Academy of Sciences, Beijing)

GENERATION OF HERBICIDE TOLERANCE TRAITS IN RICE BY BASE-EDITING

P33

Ayako Okuzaki (Tamagawa University)

CRISPR/Cas9 mediated genome editing of the SP11 gene in Broccoli

P34

Tomoko Miyaji (Tokushima University)

GENOME EDITING OF THE MODEL STRAWBERRY '*FRAGARIA VESCA*' USING PLANT-OPTIMIZED CRISPR/CAS9 SYSTEM

P35

Takuya Tsubota (National Agriculture and Food Research Organization)

DEVELOPMENT OF GENOME EDITING TECHNOLOGIES IN THE SILKWORM

P36

Takaya Abe (RIKEN)

Harnessing the CRISPR/Cas9 System in Mouse Genome Engineering @ LARGE, RIKEN BDR

P37

Naoki Wada (Tokushima University)

Development of a novel genome editing tool, TiD system, for mammalian genome engineering

P38

Shinya Ayabe (RIKEN)

MUTANT MOUSE CREATION IN RIKEN BRC FOR THE INTERNATIONAL MOUSE PHENOTYPING CONSORTIUM

P39

Shuji Takada (National Research Institute for Child Health and Development)

SCREENING OF THE RESPONSIBLE SEQUENCES FOR DISORDERS OF SEX DEVELOPMENT BY GENERATION OF A 70 KB DUPLICATION AND FINE MAPPING USING MOUSE AS A MODEL

P40

Ramu Gopalappa (Yonsei University College of Medicine)

EN BLOC AND SEGMENTAL DELETIONS OF HUMAN XIST REVEAL X CHROMOSOME INACTIVATION-INVOLVING RNA ELEMENTS

P41

Gyeong-Min Gim (Seoul National University)

GERMLINE TRANSMISSION OF CAS9-TRANSGENIC CATTLE AND ITS APPLICATION

P42

Eugene Chung (Institute for Basic Science, Seoul, Republic of Korea)

GENERATION OF CANINE DYSTROPHINOPATHY MODEL BY NUCLEAR TRANSFER USING CRISPR/CAS9-MEDIATED SOMATIC CELLS

P43

Yoshiki Miyasaka (Osaka Univ.)

EFFICIENT AND SIMPLE KNOCK-IN METHODS EXPAND THE POTENTIAL OF ANIMAL MODELS.

P44

Choongil Lee (Seoul National University)

CRISPR-PASS: GENE RESCUE OF NONSENSE MUTATIONS USING ADENINE BASE EDITORS.

P45

Suvd Byambaa (Jichi Medical University)

PHENOTYPICAL CORRECTION OF X-SCID MICE AFTER CRISPR/CAS9-MEDIATED UNIVERSAL GENOME-EDITING THERAPY OF HEMATOPOIETIC STEM CELLS

P46

Sung-ah Hong (Hanyang University)

COL7A1 GENE EDITING IN PATIENT-DERIVED FIBROBLASTS FOR RECESSIVE DYSTROPHIC EPIDERMOLYSIS BULLOSA (RDEB) RESCUE USING NG PAM TARGETABLE ADENINE BASE EDITOR

P47

Takafumi Hiramoto (Jichi Medical University)

THERAPEUTIC GENE CORRECTION OF HUMAN HEMOPHILIA B IPSCS BY BASE-EDITING APPROACH BASED ON AN ENGINEERED CAS9 WITH BROAD PAM FLEXIBILITY

P48

Christopher J. Vavricka (Kobe University)

GENOME-SCALE PREDICTION OF GENE ONTOLOGY FROM YEAST KNOCKOUT MASS FINGERPRINTS

P49

Hiromasa Hara (Jichi Medical University)

ESTABLISHMENT OF SIMULTANEOUS TRIPLE-REPORTER SYSTEM FOR HDR/NEHJ/DSB

