# Program

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**Day 1 November 18th (Mon)**

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| Noon – | Registration (ACROS Fukuoka 4F) |
| 14:00 – 18:30 | Opening Remarks, Plenary lecture and Session 1-3 |
| 19:00 – 21:00 | Welcome Reception (Hotel The Lively Fukuoka Hakata, Banquet Rooms) |

**Day 2 November 19th (Tue)**

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| 8:30 – 12:01 | Session 4-6 |
| 12:01 – 14:00 | Group Photo Shooting, Lunch, and Free Discussion |
| 14:00 – 17:24 | Session 7-9 |
| 17:30 – 19: 30 | Poster Session 1 |
| | Odd numbers: 17:30-18:30 |
| | Even numbers 18:30-19:30 |

**Day 3 November 20th (Wed)**

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| 8:30 – 12:04 | Session 10-12 |
| 12:25 – 18:15 | Lunch and Excursion |
| 19:00 – 21:00 | Banquet (Nishitetsu Grand Hotel, 2F, Banquet Room) |

**Day 4 November 21st (Thu)**

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| 8:30 – 12:04 | Session 13-15 |
| 12:04 – 14:00 | Lunch and Free Discussion |
| 14:00 – 17:24 | Session 16-18 |
| 17:30 – 19: 30 | Poster Session 2 |
| | Odd numbers: 17:30-18:30 |
| | Even numbers 18:30-19:30 |

**Day 5 November 22nd (Fri)**

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| 8:30 – 11:50 | Session 19-20 |
| 11:50 – 12:00 | Poster Awards and Closing Remarks |

# Day 1 (18 Nov. 2024)

## 12:00- Registration (ACROS Fukuoka 4F)

## 14:00-14:15 Opening remarks

## 14:15-14:45 Plenary lecture

**A Central Role for Okazaki Fragments in Checkpoint-Dependent Replication Fork Stabilisation**

Agostina Bertolin[1,2], Berta Canal[1,2], John Diffley[1]

[1] The Francis Crick Institute [2]equal contribution, alphabetically listed by surname

## 14:45-15:45 Session 1 (Chairs: Yasunori Noguchi & John Diffley)

14:45-15:05 Session 1-1

**TRESLIN-MTBP defines the initiation zones of DNA replication in human cells**

Xiaoxuan Zhu[1], Atabek Bektash[1,2], Yuki Hatoyama[1,2], Sachiko Sakamoto[1], Chun-Long Chen[4], Yasukazu Daigaku[5], Masato Kanemaki[1,2,3]

[1]National Institute of Genetics, [2]SOKENDAI, [3]The University of Tokyo, [4]Institut Curie, [5]Cancer Institute of JFCR

15:05-15:25 Session 1-2

**Regulation of replication timing and chromatin architecture by nuclear membrane tethering of Rif1**

Hisao Masai[1], Tomohiro Iguchi[1], Sayuri Ito[1], Naoko Kakusho[1], Asako Sakaue-Sawano[2], Asami Oji[3], Hisasshi Miura[3], Mikihiro Shibata[4], Masatoshi Takagi[2], Izumi Noda[2], Kenji Moriyama[1], Ichiro HIratani[3], Atsushi Miyawaki[2], Hiroyuki Sasanuma[1]

[1]Tokyo Metropolitan Institute of Medical Science, [2]Biotechnological Optics Research Team, RAP, RIKEN, [3]RIKEN Center for Biosystems Dynam Res, Lab for Dev Epigenet, [4]Kanazawa University, NanoLSI, Kanazawa, Japan

15:25-15:45 Session 1-3

**Interactions between replication origins and transcription**

Marie-Noelle Prioleau[1], Caroline Doncarli[1], Juliette Mandelbrojt[1], Jeremy Poulet-Benedetti[1], Theo Baret[1]

[1]University Paris Cité, CNRS, Institut Jacques Monod

15:45-16:05 Coffee break

## 16:05-17:35 Session 2(Chairs: Shin-ichiro Hiraga & Huilin Li)

16:05-16:25 Session 2-1

**Cryo-EM Reveals How DNA-Encircling Rings Are Loaded and Unloaded by ATPase machines**

Huilin Li[1]

[1]Van Andel Institute

16:25-16:45 Session 2-2

**Flexible usage of diverse DNA polymerases and its implications for mutagenesis**

Lewis Bainbridge[2], Yuji Masuda[1], Mami Takahashi[2], Tamiko Minamisawa[2], Chikahide Masutani[1], Yasukazu Daigaku[2]

[1]Research Institute of Environmental Medicine, Nagoya University, [2]Cancer Institute, Japanese Foundation for Cancer Research

16:45-17:05 Session 2-3

**CFAP20 salvages arrested RNAPII from the path of co-directional replisomes**

Martijn Luijsterburg[1]

[1]Leiden University Medical Center, Leiden, The Netherlands

17:05-17:15 Session 2-4

**Identification of atypical replication origin in the metallothionein-encoding repeats in the budding yeast Saccharomyces cerevisiae**

Seiji Tanaka[1]

[1]School of Engineering Science, Kochi University of Technology

17:15-17:25 Session 2-5

**The structure-specific nuclease Rad27/FEN-1 maintains the stability of the ribosomal RNA gene locus.**

Mariko Sasaki[1]

[1]National Institute of Genetics

17:25-17:35 Session 2-6

**When DNA becomes its own enemy: Reconstitution of DNA-induced replication stalling**

Gideon Coster[1], Sophie Williams[1,2], Corella Casas-Delucchi[1], Manuel Daza-Martin[1,3], Federica Raguseo[4,5], Dilek Guneri[6], Yunxuan Li[7], Masashi Minamino[2], Emma Fletcher[8], Joseph Yeeles[8], Ulrich Keyser[7], Waller Zoë[6], Marco Di Antonio[2,4,5]

[1]The Institute of Cancer Research, London, UK, [2]The Francis Crick Institute, London, UK, [3]IPBLN, Gradana, Spain, [4]Chemistry Department, Imperial College London, MSRH, London, UK, [5]Institute of Chemical Biology, MSRH, London, UK, [6]UCL, School of Pharmacy, London, UK, [7]Cavendish Laboratory, University of Cambridge, Cambridge, UK, [8]MRC Laboratory of Molecular Biology, Cambridge, UK

17:35-17:45 Short break

## 17:45-18:30 Session 3 (5-min Short talks)

17:45-17:50 Session 3-1

**Strand asymmetry of DNA damage tolerance mechanisms**

Juan Carlos Martínez-Cañas[1], Dolores Jurado-Santiago[2], Mohammed al Mamun[2], Esther Morafraile[2], María Sacristán[1], Katsuhiko Shirahige[3], Avelino Bueno[1], Rodrigo Bermejo[2]

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| | [1]Cancer Molecular and Cellular Biology Institute (USAL-CSIC), [2]Margarita Salas Center for Biological Research (CIB-CSIC), [3]Research Center for Epigenetic Disease, University of Tokyo |
| 17:50-17:55 | Session 3-2<br>**Single-molecule analysis of uncharacterised DNA replication initiation sites using Nanopore sequencing technology**<br>Shin-ichiro Hiraga[1], Alexandra Pyatnitskaya[1], Anna Rogers[2], Sathish Thiyagarajan[2], Conrad Nieduszynski[2], Anne Donaldson[1]<br>[1]Institute of Medical Sciences, University of Aberdeen, UK, [2]Earlham Institute, Norwich, UK |
| 17:55-18:00 | Session 3-3<br>**R-loop Resolution by ARIP4 Helicase Promotes Androgen-dependent Transcription Induction**<br>Raissa Regina Ng[1], Zhongyang Lin[2], Yanmin Zhang[1], Shih Chieh Ti[1], Asif Javed[1], Jason Wing Hon Wong[1], Qingming Fang[3], Justin Wai Chung Leung[4], Alex Hin Ning Tang[5], Michael Shing Yan Huen[1]<br>[1]The University of Hong Kong |
| 18:00-18:05 | Session 3-4<br>**DNA replication will not be required for ROS accumulation after chromosome breakages in E. coli.**<br>Akihiro Kaidow[1]<br>[1]Dept. Biol., Tokai Univ. |
| 18:05-18:10 | Session 3-5<br>**Visualization of DNA replication errors in living Escherichia coli cells**<br>Ivan Matic[1]<br>[1]Institut Cochin, Paris, France |
| 18:10-18:15 | Session 3-6<br>**Top3 drives crossover migration to the meiotic chromosome axis**<br>Matthew Neale[1,2], Tom Powell[1,2], William H Gittens[1,2]<br>[1]Genome Damage and Stability Centre, [2]University of Sussex, UK |
| 18:15-18:20 | Session 3-7<br>**Spatial control of the APC/C ensures the rapid degradation of Cyclin B1**<br>Luca Cirillo[1], Rose Young[1], Sapthaswaran Veerapathiran[1], Annalisa Roberti[1], Catherine Coates[1], Reyhan Muhammad[1], Theodoros Roumeliotis[1], Jyoti Choudhary[1], Claudio Alfieri[1], Jonathon Pines[1]<br>[1]ICR |
| 18:20-18:25 | Session 3-8<br>**Rad54 prevents excessive intergenerational Rad51 aggregation in fission yeast**<br>Goki Taniguchi[1], May Alexander[1], Hiroshi Iwasaki[1], Hideo Tsubouchi[1]<br>[1]Tokyo Institute of Technology |
| 18:25-18:30 | Session 3-9 |

**Pre-RC forming proteins commonly have G-quadruplex binding activity in the intrinsically disordered regions**

Shou Waga[1], Minami Takano[1], Chisa Nishio[1], Kana Hosono[1], Yuna Akiniwa[1], Chiho Shioda[1]

[1]Dpt. of Chem. and Biol. Sci., Japan Women's University

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19:00-21:00 Reception (The Lively Fukuoka Hakata, Banquet Rooms 1F&2F)

# Day 2 (19 Nov. 2024)

## 8:30-10:10 Session 4 (Chairs: Shogo Ozaki & Suckjoon Jun)

08:30-08:50 Session 4-1

**Specific mechanisms of the initiation complexes for bidirectional loading of DnaB helicases and a novel role for the DNA-bending nucleoid protein IHF in replication cycle regulation**

Tsutomu Katayama[1], Shogo Ozaki[1], Kazutoshi Kasho[1], Hironori Kawakami[1,2]

[1]Kyushu Univ., Grad. Sch. of Pharm. Sci., Depart. of Mol. Biol., [2](Present) Sanyo-Onoda City Univ., Fac. of Pharm. Sci.

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08:50-09:10 Session 4-2

**Dispensability of extrinsic DnaA regulators in Escherichia coli cell-cycle control**

Thias Oberg Boesen[1,3], Godefroid Charbon[2,3], Haochen Fu[1,3], Cara Jensen[1], Michael Sandler[1], Suckjoon Jun[1], Anders Løbner-Olesen[2]

[1]University of California San Diego, [2]University of Copenhagen, [3]These authors contributed equally to this work.

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09:10-09:30 Session 4-3

**Profiling a single-stranded DNA region within predicted G-quadruplexes in the E. coli and B. subtilis genome**

Yano Koichi [1], Akiyama Koichiro[1,2], Muraoka Masafumi[2], Hironori Niki[2]

[1]Rikkyo University, [2] National Institute of Genetics

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Withdrawal

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09:30-09:40 Session 4-5

**Genome replication in asynchronously growing microbial populations**

Simone Pigolotti[1]

[1]Okinawa Institute of Science and Technology

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09:40-09:50 Session 4-6

**Molecular mechanism of bacterial cytokinesis position control by the Min system helping stable chromosome maintenance**

Michiyo Mizuuchi[1], Min Li[1], Jagat Budhathoki[1], William Carlquist[1], Kiyoshi Mizuuchi[1]

[1]National Institutes of Health USA

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09:50-10:00 Session 4-7

**Cytidine deaminases promote DNA replication stress resistance in pancreatic cancer cells**

Tajinder Ubhi[1], Olga Zaslaver[1], Andrew Quaile[1], Dennis Plenker[2], Nhu-An Pham[3], Angela Bekesi[4], Jason Moffat[1], Steven Gallinger[3], Beata Vertessy[4], David Tuveson[2], Hannes Rost[1], Grant Brown[1]

[1]University of Toronto, [2]Cold Spring Harbor Laboratory, [3]Princess Margaret Cancer Centre, [4]BME Budapest University of Technology and Economics, [5]Ontario Institute for Cancer Research

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| 10:00-10:30 | Coffee break |

## 10:30-11:40 Session 5 (Chairs: Yasukazu Daigaku & Evi Soutoglou)

10:30-10:50 Session 5-1

**Cryo-EM structures and functions of the RAD51 paralog complexes**

Stephen West[1]

[1]The Francis Crick Institute

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10:50-11:00 Session 5-2

**RAD51 paralogs travel with the replicative helicase to facilitate lesion bypass**

Adeola Fagunloye[1], Alessio De Magis[2], Jordan Little[3], Isabel Contreras[1], Braulio Bonilla[4], Nathan Clark[3], Katrin Paeschke[2], Kara Bernstein[1]

[1]University of Pennsylvania School of Medicine, [2]University Hospital Bonn, [3]University of Utah, [4]University of Pittsburgh School of Medicine

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11:00-11:20 Session 5-3

**How 3D genome organization guides homology-directed DNA repair**

Federico Teloni[1], Zsuzsanna Takacs[1], Christoph C. H. Langer[1], Inès Prlesi[1], Thomas Steinacker[1], Wen Tan[2], Jan-Michael Peters[2], Daniel Gerlich[1]

[1]IMBA, Vienna BioCenter, [2]IMP, Vienna BioCenter

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11:20-11:30 Session 5-4

**Visualizing homology search during DNA double-strand break repair in yeast**

Aoi Makita[1], Suzuka Hoshino[2], Masahiko Harata[1,2], Chihiro Horigome[1,2]

[1]Tohoku University, Graduate School of Agricultural Science, [2]Tohoku University, Faculty of Agriculture

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11:30-11:40 Session 5-5

**ATM and 53BP1 regulate alternative end joining-mediated V(D)J recombination**

Jinglong Wang[1], Cheyenne Sadeghi[1], Long Le[1], Marie Le Bouteiller[1], Richard Frock[1]

[1]Stanford University

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## 11:40-12:01 Session 6 (3-min Short talks)

11:40-11:43 Session 6-1

**DPPA3 Disrupts UHRF1 Chromatin Localization by Targeting the SRA Domain**

Atsuya Nishiyama[2], Tanimoto Shota[2], Chiba Yoshie[2], Sugimura Keita[2], Ota Ayana[2], Arita Kyohei[1], Makoto Nakanishi[2]

[1]Yokohama City University, [2]The University of Tokyo

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11:43-11:46 Session 6-2

**Contribution of translesion synthesis for mutagenesis via a novel food-induced formamidopyrimidine-derivative**

Jun-ichi Akagi[1], Masayuki Yokoi[2], Yumi Miyake[3], Tsuyoshi Shirai[4], Tomohiro Baba[5], Kohei Matsushita[1], Fumio Hanaoka[2,6], Kaoru Sugasawa[2], Shigenori Iwai[5], Kumiko Ogawa[1]

[1]Div. of Pathology, Natl. Inst. of Health Sciences, [2]Biosignal Res. Ctr., Kobe Univ., [3]Forefront Res. Ctr., Grad. Sch. of Sci., Osaka Univ., [4]Dept. of Bioscience, Nagahama Inst. of Bio-Sci. and Tech., [5]Grad. Sch. of Eng. Sci., Osaka Univ., [6]Natl. Inst. of Genetics

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| 11:46-11:49 | Session 6-3<br>**Phenotypic sex determines recombination patterning in sex-reversed Rainbow Trout**<br>Cathrine Brekke[1], Tim Martin Knutsen[2]<br>[1]Faculty of Bioscience, Norwegian University of Life Sciences, [2]Aquagen, Ås, Norway |
| 11:49-11:52 | Session 6-4<br>**Large-scale conservation of genomic architecture between distant species**<br>Rory Cerbus[2], Kyogo Kawaguchi[1,2,3,4], Ichiro Hiratani[2]<br>[1]RIKEN Cluster for Pioneering Research, [2]RIKEN Center for Biosystems Dynamics Research (BDR), [3]Institute for Physics of Intelligence, The University of Tokyo, [4]Universal Biology Institute, The University of Tokyo |
| 11:52-11:55 | Session 6-5<br>**Altering DNA replication timing interferes with the precision of epigenome maintenance**<br>Qian Du[1,2], Nazaret Reveron-Gomez[1,3], Alva Biran[1], Nicolas Alcaraz[1], Jonathan Humbert[1], Kyle N. Klein[4,5], Peiyao A. Zhao[4,5], Masato Kanemaki[6,7], David M. Gilbert[4,5], Anja Groth[1,3]<br>[1]NNF Center for Protein Research,University of Copenhagen,Denmark, [2]Garvan Institute of Medical Research, UNSW Sydney, Australia, [3]Biotech Research and Innovation Centre, University of Copenhagen, [4]Department of Biological Science, Florida State University, USA, [5]San Diego Biomedical Research Institute, La Jolla, CA, USA, [6]National Institute of Genetics, ROIS, Mishima, Japan, [7]Graduate Institute for Advanced Studies, SOKENDAI,Shizuoka,Japan |
| 11:55-11:58 | Session 6-6<br>**Exploring mechanisms of self/nonself discrimination at DNA level in fission yeast**<br>Hiro Ebina[1], Shweta Saini[1], Mattia Valentini[1], Haochen Yu[1], Yves Barral[1]<br>[1]Institute of Biochemistry, ETH Zürich, Switzerland |
| 11:58-12:01 | Session 6-7<br>**TTF2 induces mitotic replisome disassembly and MiDAS by coupling the TRAIP E3 ligase to DNA Polymerase Epsilon**<br>Ryo Fujisawa[1], Karim Labib[1]<br>[1]MRC-PPU, University of Dundee, U.K. |

## 12:01-12:06 Photo shooting

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| 12:06-14:00 | Lunch |

## 14:00-15:30 Session 7 (Chairs: Rie Kanao & Stephen West)

14:00-14:20 Session 7-1

**STK19 positions TFIIH for cell-free transcription-coupled DNA repair**

Tycho E.T. Mevissen[1], Maximilian Kümmecke[1], Ernst Schmid[1], Lucas Farnung[1], Johannes Walter[1]

[1]Harvard Medical School

14:20-14:40 Session 7-2

**The Agile Dance of XP Proteins in Nucleotide Excision Repair**

Wei Yang[3], Jinseok Kim[3], Li Eric CL[3], Fumio Hanaoka[1], Kaoru Sugasawa[2]

[1]National Institute of Genetics, Shizuoka, [2]Kobe University, [3]National Institutes of Health, USA

14:40-15:00 Session 7-3

**Chromatin dynamics regulating DNA damage recognition for nucleotide excision repair**

Kaoru Sugasawa[1,2]

[1]Biosignal Research Center, Kobe University, [2]Graduate School of Science, Kobe University

15:00-15:20 Session 7-4

**A mechanism that facilitates DNA mismatch repair during chromatin replication**

Tatsuro Takahashi[1], Eiichiro Kanatsu[2], Reihi Sakamoto[2], Riki Terui[1], Karin Shigenobu-Ueno[2], Yasukazu Daigaku[3], Tamiko Minamisawa[3]

[1]Faculty of Science, Kyushu University, [2]Graduate School of Systems Life Sciences, Kyushu University, [3]Cancer Institute, Japanese Foundation for Cancer Research

15:20-15:30 Session 7-5

**Stabilization of mononucleotide microsatellites by DNA mismatch repair and DNA polymerase proofreading in human cells**

Shinya Oda[1], Seijiro Shioi[1], Kyoko Hidaka[2], Ryosuke Fujikane[3], Masumi Hidaka[3], Yoshimichi Nakatsu[1]

[1]Cancer Genet Lab, Clin Res Inst, NHO Kyushu Cancer Ctr, [2]Ctr Fund Edu, Univ Kitakyushu, [3]Dpt Physiol Sci Mol Biol, Fukuoka Dent Coll

15:30-15:50 Coffee break

## 15:50-17:00 Session 8 (Chairs: Yasuyoshi Oka & Wei Yang)

15:50-16:10 Session 8-1

**DNA damage tolerance mechanisms in humans**

Chikahide Masutani[1,2], Rie Kanao[1,2], Rika Kusumoto-Matsuo[1,3,4], Yuji Masuda[1,2]

[1]Dept. Genome Dynamics, Res. Inst. Environ. Med., Nagoya Univ., [2]Dept. Mol. Phamaco-Biol., Nagoya Univ. Grad. Sch. Med., [3]Res. Fellow, JSPS, [4]Present address: Adv. Cancer Trans. Res. Inst., Showa Univ.

16:10-16:30 Session 8-2

**DNA repair and longevity: from bats to whales**

Vera Gorbunova [1], Andrei Seluanov[1]

[1] University of Rochester

16:30-16:40 Session 8-3

**Focal amplification of a super-enhancer with the accumulation of non-coding RNAs in breast cancer**

Noriko Saitoh[1], Maierdan Palihati[1], Hiroaki Tachiwana[1], Yuichi Ichikawa[1]

[1]The Cancer Institute of JFCR

16:40-16:50 Session 8-4

**NELF promotes transcription termination and cell cycle**

Chihiro Nakayama[1], Qi Fang[1], Yasukazu Daigaku[2], Yuki Aoi[3], Hiroshi Kimura[4], Ali Shilatifard[3], Michael Tellier[5], TAKAYUKI NOJIMA[1]

[1]Medical Institute of Bioregulation, Kyushu University, [2]Cancer Institute, Japanese Foundation for Cancer Research, [3]Feinberg School of Medicine, Northwestern University, [4]Cell Biology Centre, Tokyo Institute of Technology, [5]University of Leicester

16:50-17:00 Session 8-5

**Open Science and Responsible Science Communication**

Hartmut Vodermaier[1]

[1]EMBO Press, The EMBO Journal

## 17:00-17:24 Session 9 (3-min Short talks)

17:00-17:03 Session 9-1

**Principles of chromosome organisation for meiotic recombination**

Mathilde Biot[2], Atilla Toth[1], Christine Brun[2], Leon Guichard[2], Bernard de Massy[2], Corinne GREY[2]

[1]Faculty of Medecine, TU Dresden, Germany, [2]IGH, CNRS University of Montpellier, France

17:03-17:06 Session 9-2

**Multiple mechanisms driving genomic instability in BRCA1-deficient cancer cells**

LiYao Huang[1], Ashleigh King[1], Jean Metson[1], Raquel Cuella Martin[2], J Ross Chapman[1]

[1]MRC, WIMM, University of Oxford, [2]Department of Human Genetics, McGill University

17:06-17:09 Session 9-3

**Spatial regulation of ribosomal RNA transcription by phase separation and transition**

Satoru Ide[1,2], Yasuto Murayama[2], Kazuhiro Maeshima[2]

[1]Tokyo Metropolitan Institute of Medical Science, [2]National Institute of Genetics

17:09-17:12 Session 9-4

**Initiation of Meiotic Recombination in Zebrafish Males**

Yukiko Imai[1], Clement Julie [2]

[1]Model Fish Genetics Lab, National Institute of Genetics, Japan, [2]IHPE, Univ. Perpignan-CNRS-IFREMER-Montpellier Univ., France

17:12-17:15 Session 9-5

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| | **FIGNL1 AAA+++ ATPase is essential for removal of RAD51 recombinase from meiotic chromosomes and chromosome condensation in mouse oocytes**<br>Masaru Ito[1], Shou Soeda[1], Akira Shinohara[1]<br>[1]Institute for Protein Research, Osaka University |
| 17:15-17:18 | Session 9-6<br>**Aneuploidy-specific effects on tumor growth and malignant transformation**<br>Minji Jo[1], Oltea Sampetrean[2], Seietsu Rai[1], Tetsuya Negoto[3], Utako Kato[1], Hideyuki Saya[4], Toru Hirota[1]<br>[1]Japanese Foundation for Cancer Research, [2]Keio University, [3]Kurume University, [4]Fujita Health University |
| 17:18-17:21 | Session 9-7<br>**The DNA-Tension-Dependent Loop Extrusion Mechanism in Dimeric SMC Complexes**<br>Takaharu Kanno[1,4], Biswajit Pradahan[2], Pinto Adrian[5], Tetiker Damla[2], Baaske Martin[2], Cutt Erin[6], Chatzicharlampous Constantinos[3], Schüler Herwig[3], Deep Amar[7], Corbett Kevin[7], Aragon Luis[6], Virnau Peter[5], Björkegren Camilla[1], Kim Eugene[2]<br>[1]Karolinska Institutet, Sweden, [2]Max Planck Institute of Biophysics, Germany, [3]Lund University, Sweden, [4]The University of Tokyo, Japan, [5]Johannes Gutenberg University Mainz, Germany, [6]MRC London Institute of Medical Sciences (LMS), UK, [7]University of California, USA |
| 17:21-17:24 | Session 9-8<br>**Cell cycle regulation of replication initiation by timely binding/dissociation of the DNA bending factor IHF in *Escherichia coli***<br>Kazutoshi Kasho[1], Ryuji Sakai[1], Kosuke Ito[1], Rion Satomura[1], Mizuki Yoshida[1], Kenya Miyoshi[1], Sho Nakazono[1], Tsutomu Katayama[1]<br>[1]Kyushu University, Japan |

## 17:30-19:30 Poster Session 1

Odd numbers: 17:30-18:30, Even numbers 18:30-19:30

Place A (2F, cultural gallery): P1-01~68

Place B (4F, foyer): P1-69~84

# Day 3 (20 Nov. 2024)

## 8:30-9:40 Session 10 (Chairs: Mariko Sasaki & Scott Keeney)

08:30-08:50 Session 10-1

**BRCA1 promotes DNA resection by Exonuclease 1 and BLM/WRN-DNA2**

Satona Ohno[1], Ichiro Amitani[1], Naofumi Handa[1], Taeho Kim[1], Stephen Kowalczykowski[1]

[1] Department of Microbiology & Molecular Genetics, Department of Molecular & Cellular Biology, University of California, Davis, CA 95616, USA

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08:50-09:10 Session 10-2

**The Synaptic Role of the Swit-Sfr1 Heterodimer in Rad51-Driven Strand Exchange during Homologous Recombination**

Hiroshi Iwasaki[1]

[1]Cell Biology Center, Science Tokyo

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09:10-09:30 Session 10-3

**Molecular mechanism of DNA end resection and repair pathway choice in DNA double-strand break repair**

Miki Shinohara[1,2], Tomoki Tamai[1], Giordano Reginato[3], Ryusei Ojiri[1], Sasada Kenta[1], Valérie Borde [4], Petr Cejka[3], Katsunori Sugimoto[5]

[1]Grad. Schl. of Agri., Kindai University, [2]ATRI, Kindai University, [3]Università della Svizzera italiana (USI), [4]Institut Curie, [5]The State University of New Jersey

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09:30-09:40 Session 10-4

**Mutations arising during repair of broken chromosomes in budding yeat**

James Haber[1,2], Neal Sugawara[1], Simona Dalin [3], Sophie Webster[3], Rameen Beroukhim[3]

[1]Department of Biology, Brandeis University Waltham MA USA, [2]Tokyo Institute of Technology, Tokyo Japan, [3]Dana Farber Cancer Institute, Boston, USA

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## 9:40-10:04 Session 11 (3-min Short talks)

09:40-09:43 Session 11-1

**The mechanisms of the recruitment of SLX4-XPF nuclease complex in the response to replication stress induced by lacO-LacI interaction**

Yoko Katsuki[1], Takuma Okano[1], Soki Haruta[1], Tomoki Matsumura[1], Yasunori Noguchi[1], Miyako Shiraishi[1], Kazumasa Yoshida[1], Masatoshi Fujita[1]

[1]Grad. Sch. Pharm. Sci., Kyushu Univ.

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09:43-09:46 Session 11-2

**CTF18 promotes cellular tolerance against chain-terminating nucleoside analogs (CTNAs) in cooperation with polymerase epsilon's exonuclease activity**

Mubasshir Washif[1], Tasnim Ahmad[1], Md Bayejid Hosen[1], Md Ratul Rahman[1], Tomoya Taniguchi[1], Hiromori Okubo[1], Kouji Hirota[1], Ryotaro Kawasumi[1]

[1]Tokyo Metropolitan University

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09:46-09:49 Session 11-3

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|---|---|
| | **USP37 prevents premature disassembly of stressed replisomes by TRAIP**<br>Olga Kochenova[1,2,6], Giuseppina D'Alessandro[3,6], Domenic Pilger*[4], Ernst Schmid*[1], Sean Richards[3], Marcos Rios Garcia[5], Satpal Jhujh[5], Andrea Voigt[3], Christopher Carnie[3], R. Alex Wu[1], Nadia Gueorguieva[3], Grant Stewart[5], Johannes Walter#[1,2], Stephen Jackson#[3]<br>[1]Harvard Medical School, [2]Howard Hughes Medical Institute, [3]Cancer Research UK Cambridge Institute, [4]University of Cambridge, [5]University of Birmingham, [6]Equal contribution, *Equal contribution, #Equal contribution |
| 09:49-09:52 | Session 11-4<br>**Pluripotent Stem Cells Keep Genome integrity by Maintaining Slow DNA Replication Fork Progression and Abundant Replication Origins**<br>Kiminori Kurashima[1], Yasunao Kamikawa[1,2], Tomomi Tsubouchi[1]<br>[1]Lab. of Stem Cell Biol., Natl. Inst. for Basic Biol., Japan, [2]Present adress: Hiroshima Univ., Japan |
| 09:52-09:55 | Session 11-5<br>**Direct visualization of DNA-bound cohesin in-liquid using high-speed atomic force microscopy**<br>Yumiko Kurokawa[1,2], Kenichi Umeda[3], Noriyuki Kodera[3], Yasuto Murayama[1,2]<br>[1]National Institute of Genetics, [2]SOKENDAI, [3]WPI-NanoLSI, Kanazawa University |
| 09:55-09:58 | Session 11-6<br>**Impact of histone modifications on damage recognition process of global genome nucleotide excision repair**<br>Masayuki Kusakabe[1,2], Mizuki Watada[1,2], Takumi Maeda[1,2], Erina Kakumu[1,2], Kanae Fujiwara[1,2], Mizuki Otobe[1,2], Wataru Sakai[1,2], Masayuki Yokoi[1,2], Kaoru Sugasawa[1,2]<br>[1]Biosignal Research Center, Kobe University, [2]Graduate School of Science, Kobe University |
| 09:58-10:01 | Session 11-7<br>**Cell Cycle Regulation has Shaped Budding Yeast Replication Origin Structure and Function**<br>Chew Theng Lim[1], Thomas Miller[1,2], Kang Wei Tan[1], Saurabh Talele[3], Anne Early[1], Philip East[1], Humberto Sanchez[3], Nynke Dekker[3], Alessandro Costa[1], John Diffley[1]<br>[1]The Francis Crick Institute, [2]University of Copenhagen, [3]Delft University of Technology |
| 10:01-10:04 | Session 11-8<br>**Cryo-EM analyses of UV-damaged recognition protein UV-DDB in nucleosomes during nucleotide excision repair**<br>Syota Matsumoto[1], Yoshimasa Takizawa[1], Mitsuo Ogasawara[1], Kana Hashimoto[1], Junpei Yamamoto[2], Shigenori Iwai[2], Kaoru Sugasawa[3], Hitoshi Kurumizaka[1]<br>[1]Institute for Quantitative Biosciences, The University of Tokyo, [2]Graduate School of Engineering Science, Osaka University, [3]Biosignal Research Center, Kobe University |
| 10:04-10:24 | Coffee break |

## 10:24-12:04 Session 12 (Chairs: Takuro Nakagawa & Stephen Kowalczykowski)

10:24-10:44 Session 12-1

**Building a meiotic DNA breaking machine**

Zhi Zheng[2,3], Lyuqin Zheng[2], Kaixian Liu[2], You Yu[2], Juncheng Wang[2], Meret Arter[2], David Ontoso[1,2], Soonjoung Kim[2], Dinshaw Patel[2,3], Scott Keeney [1,2,3]

[1]Howard Hughes Medical Institute, [2]Memorial Sloan Kettering Cancer Center, [3]Gerstner Sloan Kettering Graduate School

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10:44-11:04 Session 12-2

**Do artificial DSBs successfully induce meiotic recombination and chromosome segregation?**

Kunihiro Ohta[1]

[1]Dept. of Life Sciences, Univ. of Tokyo

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11:04-11:24 Session 12-3

**Regulation of DNA synthesis during double-strand break repair**

Valerie Borde[1,2,3,4], Sophie Loeillet[1,2,3,4], Yulia Gryaznova[1,2,3,4], Hrishi Dhondge[1,2,3,4], Chunlong Chen[1,2,3,4]

[1]Institut Curie, [2]PSL University, [3]CNRS, [4]Dynamics of Genetic Information

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11:24-11:34 Session 12-4

**NCADP2 SMC-condensin subunit: a new regulator of meiotic prophase I chromosome assembly in the mouse.**

Laurine Dal Toe[1], Boubou Diagouraga[1], Julien Cau[1], Estelle Grosjean[1], Audrey Bost [1], Thomas ROBERT[1]

[1]CNRS, Montpellier, France

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11:34-11:44 Session 12-5

**Identification of budding yeast proteins that antagonize the mismatch repair system to promote hybrid fertility**

Ting-Fang Wang[1]

[1]Institute of Molecular Biology, Academia Sinica, Taipei, Taiwan

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11:44-11:54 Session 12-6

**Hop2-Mnd1 as a Gatekeeper of DNA Sequence Fidelity in Dmc1-Mediated Recombination**

Jo-Ching Peng[1], Hao-Yen Chang[1,3], Yuting Liang Sun[3], Mara Prentiss[4], Hung-Wen Li[3], Peter Chi[1,2]

[1]IBS, National Taiwan University,Taiwan, [2]Institute of Biological Chemistry, Academia Sinica, Taiwan, [3]Department of Chemistry, National Taiwan University, Taiwan, [4]Department of Physics, Harvard University, USA

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11:54-12:04 Session 12-7

**Mediator-Recombinase Interaction and RPA Binding Dynamics Modulate Recombinase Nucleoprotein Assembly**

Hung-Wen Li[1], Chin-Dian Wei Wei[1], Hao-Yen Chang[1,2], Asako Furukohri[3], Akira Shinohara[3], Peter Chi[2,4]

[1]Dept. of Chemistry, National Taiwan University, Taiwan, [2]Biochemical Sciences, National Taiwan University, Taiwan, [3]Institute for Protein Research, Osaka University, Japan, [4]Institute of Biological Chemistry, Academia Sinica, Taiwan

12:25- Excursion
- The optional bus tour only for the registered participants (Registration is now closed)
- Gathering at ACROS Fukuoka, 1F, South entrance [Park side]

19:00-21:00 Banquet (Nishitetsu Grand Hotel, 2F, Banquet Room)

# Day 4 (21 Nov. 2024)

## 8:30-10:10 Session 13 (Chairs: Yasuto Murayama & Johannes Walter)

08:30-08:40 Session 13-1

**RAD5$^{OE}$-INDUCED REPLICATION STRESS PROMOTES MITOTIC RECOMBINATION, LOSS OF HETEROZYGOSITY AND ANEUPLOIDY IN *SACCHAROMYCES CEREVISAE***

Rodney Rothstein[1,2], Eric E. Bryant[3], Dirk Remus[4], Ivana Sunjevaric[1], Alain Nicolas[5], Robert J.D. Reid[1]

[1]Columbia University, Dept Genetics & Development, NY, USA, [2]Columbia University, Dept Systems Biology, NY, USA, [3]Columbia University, Dept Biology, NY, USA, [4]Memorial Sloane Kettering Cancer Center, New York, USA, [5]Institute for Research on Cancer and Aging, CNRS, Nice, FRANCE

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08:40-08:50 Session 13-2

**Fission yeast Cnp1/CENP-A causes gross chromosomal rearrangements at centromeres**

Takuro Nakagawa[1,2], Shinnosuke Tomita[1,2], Ziyi Pan[1,2]

[1]Dept of Biol Sci, Grad Sch of Sci, Osaka University, [2]Forefront Res Center, Grad Sch of Sci, Osaka University

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08:50-09:10 Session 13-3

**Genome organization in DNA repair pathway choice and mutagenesis**

Sylvain Audibert[1], Diana Rubio[1], Ophelie Martin[1], Karen Meaburn[1], Raquel Carreira Rodriguez[1], Evi Soutoglou[1]

Sussex University

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09:10-09:30 Session 13-4

**A role of BRCA2 in maintenance of hematopoietic stem cells**

Kosuke Yamazaki[2], Tomohiro Iguchi[2], Midori Yamaguchi[1], Aimi Sano[2], Kazuto Takayasu[2], Yusa Kosuke[3], Kanemaki Masato[4], Ichiro Taniuchi[5], Hisao Masai[2], Hiroyuki Sasanuma[2]

[1]Center for Basic Tech. Res., TMiMS, [2]Genome Dynamics, TMiMS, [3]Lab. of Stem Cell Genetics, Kyoto University, [4]Lab. of Molecular Cell Engineering, NIG, [5]Lab. for Transcriptional Regulation, RIKEN

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09:30-09:50 Session 13-5

**The Smc5/6 complex, DNA supercoiling and topoisomerases.**

Camilla Bjorkegren[1], Kristian Jeppsson[1], Takaharu Kanno[1], Biswajit Pradhan[2], Eugene Kim[2], Toyonori Sakata[3], Katsuhiko Shirahige[3]

[1]Karolinska Institutet, Sweden, [2]Max Planck Institute of Biophysics, Frankfurt am Main, Germany, [3]IQB, The University of Tokyo, Japan

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09:50-10:10 Session 13-6

**Molecular mechanisms that regulate SLX4-XPF-ATR-RAD52 axis-mediated DNA damage response to replication stress induced by nucleoprotein obstacles**

Masatoshi Fujita[1], Yoko Katsuki[1], Takuma Okano[1], Kosei Matsushita[1]

[1]Graduate School of Pharmaceutical Sciences, Kyushu University

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| 10:10-10:30 | Coffee break |

## 10:30-11:40 Session 14 (Chairs: Ichiro Hiratani & Camilla Bjorkegren)

10:30-10:40 Session 14-1

**SLX4/FANCP: Playing with nucleases, helicases and beyond**

Pierre Marie DEHÉ[1,2,3,4,5], Stéphanie GON[1,2,3,4,5], Isao KURAOKA[6], Romane MARANO[1,2,3,4,5], Manon RICQUEBOURG[1,2,3,4,5], Sarah SCAGLIONE[1,2,3,4,5], Arato TAKEDACHI[6], Pierre Henri GAILLARD[1,2,3,4,5]

[1]Cancer Research Centre Marseille (CRCM), France, [2]U1068 Inserm, Marseille, France, [3]UMR7258 CNRS, Marseille France, [4]Institut Paoli-Calmettes, Marseille, France, [5]Aix Marseille University, Marseille, France, [6]Department of Chemistry, Faculty of Science, Fukuoka University

10:40-10:50 Session 14-2

**When Base Excision Repair goes wrong: chromosome fragmentation upon TORC2 inhibition depends on nuclear actin-dependent remodeler activity**

Susan M Gasser[1,2], Kenji Shimada[3], Verena Hurst[3], C.D. Tarashev[3], C.B. Gerhold[3], Masahiko Harata[3], Barbara van Loon[4]

[1]ISREC Foundation, [2]University of Lausanne, [3]Friedrich Miescher Institute for biomedical Research, [4]Norwegian Technical University

10:50-11:00 Session 14-3

**Trajectory and uniqueness of mutational signatures in yeast mutators**

Sophie Loeillet[1], Ana Houel[1], Patricia Legoix[2], Sylvain BAULANDE[2], Kowalczykowski Stephen C.[3], Arturo LONDONO-VALLEJO[1], NICOLAS Alain[1,2,4]

[1]Institut Curie, CNRS UMR3244 Paris France, [2]Institut Curie, ICGEX, Paris France, [3]University California Davis, USA, [4]IRCAN CNRS, Nice, France

11:00-11:10 Session 14-4

**Human endonuclease ANKLE1 processes chromatin bridges by cleaving mechanically stressed DNA**

Ying Wai Chan[1], Huadong Jiang[1], Fei He[1,2], Artem Efremov[2]

[1]The University of Hong Kong, [2]Shenzhen Bay Laboratory

11:10-11:20 Session 14-5

**Diverse actions of Mre11 nuclease during DNA end resection and DNA replication**

Katsunori Sugimoto[1]

[1]Rutgers

11:20-11:30 Session 14-6

**Fission yeast histone deacetylase Clr6 is repaired for the growth of cells with circular chromosomes**

Masaru Ueno[1], Hiroto Tamura[1], Kaito Nakamura[1], Gento Takagi[1]

[1]Hiroshima University

11:30-11:40 Session 14-7

**Disruption of chromatin induces Topoisomerase 2 activity at sites of transcriptional stress**

William Gittens[1]

[1]Genome Damage and Stability Centre, University of Sussex, UK

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11:40-12:04 Session 15 (3-min Short talks)

11:40-11:43 Session 15-1

**Human AAA+ ATPase FIGNL1 suppresses RAD51-mediated ultra-fine bridge formation**

Kenichiro Matsuzaki[1], Miki Shinohara[1,2]

[1]Grad. Sch. Agri., Kindai Univ., [2]ATIRI, Kindai Univ.

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11:43-11:46 Session 15-2

**Neddylation inhibition is lethal with FANCJ loss in cancers**

Aki Nunomiya[1], Nanda Kumar Jegadesan[1,2], Dana Branzei[1,3]

[1]DNA repair Lab, IFOM ETS, [2]Johnson & Johnson Innovative Medicine, [3]Istituto di Genetica Molecolare, IGM-CNR

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11:46-11:49 Session 15-3

**Molecular characterization of the single-stranded DNA binding activity of the initiation complex constructed at the eubacterial replication origin**

Shogo Ozaki[1], Yasutaka Wakasugi[1], Chuyuan Lu[1], Ryusei Yoshida[1], Ayaka Kubaru[1], Nanato Kiyohara[1], Tsutomu Katayama [1]

[1]Kyushu University

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11:49-11:52 Session 15-4

**Competition for resources between replication forks in E. coli**

Florian Pflug[1], Bhat Deepak[2], Pigolotti Simone[1]

[1]Okinawa Institute of Science and Technology (OIST), [2]Vellore Institute of Technology (VIT)

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11:52-11:55 Session 15-5

**Temperature-Dependent Mechanisms in Bacterial Growth**

Alberto Sassi[1], Simone Pigolotti[1]

[1]Okinawa Institute of Science and Technology

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11:55-11:58 Session 15-6

**Macromolecular clustering drives mitotic chromosome assembly**

Motoko Takahashi[1], Chang Liu[1], Toru Hirota[1]

[1]Japanese Foundation for Cancer Research (JFCR), Cancer Institute

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11:58-12:01 Session 15-7

**Fluorescence-based analysis for DNA damage response in living cell**

Arato Takedachi[1], Gakuto Fukushima[1], Yoshihiro Fujimura[1], Ayano Baba[1], Kousuke Matsuo[1], Haruto Kojima[1], Rui Oda[1], Hayato Nishino[1], Isao Kuraoka[1]

[1]Fukuoka University

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12:01-12:04 Session 15-8

**Resection of DNA double-strand breaks activates MRN- and 9–1–1-dependent ATR checkpoint and end-processing pathways in *Xenopus* egg extracts**

Kensuke Tatsukawa[1], Reihi Sakamoto[2], Tatsuro Takahashi[1], Eiji Ohashi[1,3]

[1]Faculty of Science, Kyushu University, [2]Graduate School of System Life Sciences, Kyushu University, [3]Nagahama Institute of Bio-Science and Technology

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12:04-14:00 Lunch

## 14:00-15:30 Session 16 (Chairs: Yoshitaka Kawasoe & Cristina Cardoso)

14:00-14:20 Session 16-1

**STAG1-cohesin-specific contribution in building higher-order chromatin structure**

Ryota Sakata[1], Yoshimi Kinoshita[1], Ana Losada[2], Tomoko Nishiyama[1]

[1]Graduate School of Science, Kyoto University, [2] Chromosome Dynamics Group, Molecular Oncology Programme, CNIO

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14:20-14:40 Session 16-2

**Life without Loop Extrusion?**

Thomas Guérin[1,2], Christopher Barrington[1], Georgii Pobegalov[1], Maxim Molodtsov[1], Frank Uhlmann[1]

[1]The Francis Crick Institute, London, [2]Université Paris-Saclay, CEA, Fontenay-aux-Roses

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Withdrawal

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14:40-14:50 Session 16-4

**Molecular basis of sister chromatid cohesion studied with purified proteins**

YASUTO MURAYAMA[1], Yumiko Kurokawa[1]

[1]National Institute of Genetics

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14:50-15:00 Session 16-5

**Impact of the genomic DNA-to-cytoplasmic ratio in mouse preimplantation development**

Tao Pan[2], Natsumi Taira[1], Koya Shimabukuro[2], Takaya Totsuka[1], Tomo Kondo[1], Miho Ohsugi[1,2]

[1]Dept of Biol Sci, Grad Sch of Sci, The Univ of Tokyo, [2]Dept of Life Sci, Grad Sch of Arts and Sci, The Univ of Tokyo

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15:00-15:20 Session 16-6

**Embryonic genome instability upon somatic DNA replication timing program emergence**

Ichiro Hiratani[1], Saori Takahashi[1], Hirohisa Kyogoku[1,2], Takuya Hayakawa[3], Hisashi Miura[1], Asami Oji[1], Yoshiko Kondo[1], Shin-ichiro Takebayashi[3], Tomoya Kitajima[1]

[1]RIKEN Center for Biosystems Dynamics Research, Kobe, Japan, [2]Graduate School of Agricultural Science, Kobe Univ, Kobe, Japan, [3]Graduate School of Bioresources, Mie Univ, Tsu, Japan

15:20-15:50 Coffee break

## 15:50-17:00 Session 17 (Chairs: Esashi Fumiko & Frank Uhlmann)

15:50-16:10 Session 17-1

**rDNA instability and cellular senescence**

Takehiko Kobayashi[1]

[1]Univ. of Tokyo, IQB

16:10-16:30 Session 17-2

**Toward a deep understanding of mitotic chromosome assembly**

Tatsuya Hirano[1]

[1]Chromosome Dynamics Laboratory, RIKEN

16:30-16:50 Session 17-3

**The ancient unsolved problem of mitotic chromosome formation**

William Earnshaw[1], Kumiko Samejima[1], Fernanda Cisneros-Soberanis[1], Moonmoon Deb[1], Johan Gibcus[2], Leonid Mirny[3], Job Dekker[2], Anton Goloborodko[4]

[1]University of Edinburgh, [2]University of Massachusetts Chan Medical School, [3]Massachusetts Institute of Technology, [4]Institute of Molecular Biotechnology; Vienna

16:50-17:00 Session 17-4

**Context-dependent kinetochore phosphorylation by Aurora B through microtubule-mediated substrate masking**

Hironori Funabiki[1], Yiming Niu[1], Hideaki Konishi[1]

[1]The Rockefeller University

## 17:00-17:24 Session 18 (3-min Short talks)

17:00-17:03 Session 18-1

**STK19 facilitates the clearance of lesion-stalled RNAPII during transcription-coupled DNA repair**

Diana van den Heuvel[2,9], Marta Rodríguez-Martínez[1,9], Paula J. van der Meer[2,9], Nicolas Nieto Moreno[3], Jiyoung Park[4], Hyun-Suk Kim[4], Janne J.M. van Schie[2], Annelotte P. Wondergem[2], Areetha D'Souza[4], George Yakoub[2], Anna E. Herlihy[1], Krushanka Kashyap[3], Thierry Boissière[1,3], Jane Walker[1], Richard Mitter[1], Katja Apelt[2], Klaas de Lint[6], Idil Kirdök[6], Mats Ljungman[7], Rob M.F. Wolthuis[6], Patrick Cramer[8], Orlando D. Schärer[4,5], Goran Kokic[8,10], Jesper Q. Svejstrup[1,3,10], Martijn S. Luijsterburg[2,10]

[1]The Francis Crick Institute, UK, [2]Leiden University Medical Center, NL, [3]University of Copenhagen, DK, [4]Institute for Basic Science, Ulsan, Republic of Korea, [5]Ulsan National Institute of Science & Technology, Rep. of Korea, [6]Cancer Center Amsterdam, Amsterdam University Medical Center, NL, [7]University of Michigan, Ann Arbor, MI,

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| | USA, [8]Max Planck Institute for Multidisciplinary Sciences, DE, [9]Equal contribution, [10]Corresponding authors |
| 17:03-17:06 | Session 18-2<br>**CDCA7 is an evolutionarily conserved hemimethylated DNA sensor in eukaryotes**<br>Isabel Wassing[3,4], Atsuya Nishiyama[2,4], Reia Shikimachi[1], Qingyuan Jia[3], Amika Kikuchi[1], Moeri Hiruta[1], Keita Sugimura[2], Xin Hong[2], Yoshie Chiba[2], Junhui Peng[3], Chris Jenness[3], Makoto Nakanishi[2], Li Zhao[3], Kyohei Arita[1], Hironori Funabiki[3],<br>[1]Yokohama City University, [2]The University of Tokyo, [3]Rockefeller University, [4]equal contribution |
| 17:06-17:09 | Session 18-3<br>**Mechanisms of nucleosome uncoiling at the replication fork**<br>Oliver Willhoft[1], Milos Cvetkovic[1], Daniel Felfoldi[1], Alessandro Costa[1]<br>[1]The Francis Crick Institute |
| 17:09-17:12 | Session 18-4<br>**Pro-DSB components drive intermolecular chromosome condensation in distinct island regions during meiotic prophase**<br>Ellie M. Wright[1], George G. B. Brown[1], Matthew J. Neale[1]<br>[1]Genome Damage and Stability Centre, University of Sussex, BN1 NRQ, Falmer, UK |
| 17:12-17:15 | Session 18-5<br>**Non-canonical functions of UHRF1 maintain DNA methylation homeostasis in cancer cells.**<br>Kosuke Yamaguchi[1,2], Xiaoying Chen[2], Brianna Rodgers[2], Fumihito Miura[3], Pavel Bashtrykov[4], Frédéric Bonhomme[5], Catalina Salinas-Luypaert[6], Deis Haxholli[7], Nicole Gutekunst[4], Bihter Özdemir Aygenli[8], Laure Ferry[2], Olivier Kirsh[2], Marthe Laisné[2], Andrea Scelfo[6], Enes Ugur[7], Paola B. Arimondo[5], Heinrich Leonhardt[7], Masato T. Kanemaki[1], Till Bartke[8], Daniele Fachinetti[6], Albert Jeltsch[4], Takashi Ito[3], Pierre-Antoine Defossez[2]<br>[1]National Institute of Genetics, [2]Université Paris Cité, UMR7216, [3]Kyushu University Graduate School of Medical Sciences, [4]Institute of Biochemistry and Technical Biochemistry, [5]Institut Pasteur, UMR3523, [6]Institut Curie, UMR144, [7]Ludwig-Maximilians-Universität München, [8]Institute of Functional Epigenetics |
| 17:15-17:18 | Session 18-6<br>**Development of photoactivatable endonuclease for meiotic recombination**<br>Hideyuki Yone[1], Yuri Kawashima[2], Hayato Hirai[1], Hiromitsu Kono[1], Kunihiro Ohta[1,3]<br>[1]Grad. Sch. of Arts & Sci., Univ. of Tokyo, [2]Res. Inst. Rad. Biol. & Med., Hiroshima Univ., [3]Universal Biology Institute, Univ. of Tokyo |
| 17:18-17:21 | Session 18-7<br>**Mechanisms in chromosome origin unwinding promoted by bacterial initiator DnaA protein and a ubiquitous nucleoid-associated protein HU.**<br>Ryusei Yoshida[1], Shogo Ozaki[1], Hironori Kawakami[1], Tsutomu Katayama[1]<br>[1]Graduate School of Pharmaceutical Sciences, Kyushu University |
| 17:21-17:24 | Session 18-8 |

**The RIF1-PP1 complex shapes DNA replication initiation zones to establish the replication timing program**

XIAOXUAN ZHU[1], Atabek Bektash[1,2], Yuki Hatoyama[1,2], Sachiko Sakamoto[1], Chun-Long Chen[3], Yasukazu Daigaku[4], Masato Kanemaki[1,2,5]

[1]National Institute of Genetics, [2]SOKENDAI, [3]Institut Curie, [4]Cancer Institute for JFCR, [5]The University of Tokyo

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17:30-19:30 Poster session 2

Odd numbers: 17:30-18:30, Even numbers 18:30-19:30

Place A (2F, cultural gallery): P2-01~68

Place B (4F, foyer): P2-69~83

# Day 5 (22 Nov. 2024)

## 8:30-10:00 Session 19 (Chairs: Tomoko Nishiyama & William Earnshaw)

08:30-08:50 Session 19-1

**Replication-dependent histone (Repli-Histo) labeling specifically visualizes physical properties of euchromatin/heterochromatin in living human cells.**

Kazuhiro Maeshima[1,2], Minami Katsuhiko[1,2], Satoru Ide[1,2], Sachiko Tamura[1]

[1]National Institute of Genetics, [2]SOKENDAI

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08:50-09:10 Session 19-2

**Regulation of sex chromosome replication**

Cristina Cardoso[1]

[1]Technical University of Darmstadt, Germany

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09:10-09:30 Session 19-3

**DNA Replication and Chromatin Organization in Early Zebrafish Embryos**

Hiroshi Kimura[1,2], Yuko Sato[2]

[1]Cell Biology Ctr, Inst Integr Res, Institute of Science Tokyo, [2]Cell Biology Ctr, Inst Innov Res, Tokyo Institute of Technology

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09:30-09:50 Session 19-4

**How cells enrich Aurora B activity at centromeres in mitosis**

Toru Hirota[1]

[1]Japanese Foundation for Cancer Research (JFCR), Cancer Institute

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09:50-10:00 Session 19-5

**Contextual Roles of BRCA2 and PALB2 in Safeguarding Centromere Integrity**

Emily Graham[1], Lucia Rampazzo[1], Chin Wei Brian Leung[1], Jacob Wall[1], Emoke Zsanett Gerocz[1], Mikhail Liskovykh[3], 311, Masato T. Kanemaki[4], Hiroshi Masumoto[2], Vladimir Larionov[3], Natalay Kouprina[3], Fumiko Esashi[1]

[1]University of Oxford, UK, [2]Kazusa DNA Research Institute, Japan, [3]National Cancer Institute, National Institutes of Health, US, [4]National Institute of Genetics, Japan

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10:00-10:20 Coffee break

## 10:20-11:50 Session 20 (Chairs: Satoru Ide & Valérie Borde)

10:20-10:40 Session 20-1

**Evolution of chromosome ends**

Junko Kanoh[1]

[1]Graduate School of Arts and Sciences, the University of Tokyo

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10:40-11:00 Session 20-2

**Structural studies for understanding chromatin function in genome regulation**

Hitoshi Kurumizaka[1]

[1]Institute for Quantitative Biosciences, The University of Tokyo

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| 11:00-11:10 | Session 20-3<br>**Proteomic profiling of UV damage repair patches uncovers histone chaperones with central functions in chromatin repair**<br>Alexandre Plessier[1], Audrey Chansard[1], Eliane Petit[1], Julia Novion Ducassou[2], Yohann Coute[2], Sophie Polo[1]<br>[1]CNRS/Université Paris Cité, Paris, France, [2]CNRS/CEA/University Grenoble Alpes, Grenoble, France |
| 11:10-11:30 | Session 20-4<br>**Transcription elongation is regulated by Cohesin**<br>KATSUHIKO SHIRAHIGE[1,2], Shoin Tei[1], Toyonari Sakata[1,2], Atsunori Yoshimura[1], Takashi Sutani[1], Masashige Bando[1]<br>[1]Institute For Quantitative Biosciences, The University of Tokyo, [2]Department of Cell and Molecular Biology, Karolinska Institutet |
| 11:30-11:50 | Session 20-5<br>**Endogenous aldehyde-induced DNA damage is resolved by transcription-coupled repair, leading to hematopoietic abnormalities and aging phenotypes in mice**<br>Yasuyoshi Oka[1], Yuka Nakazawa[1], Mayuko Shimada[1], Tomoo Ogi[1,2,3,4]<br>[1]Res. Inst. of Environmental Medicine (RIeM), Nagoya University, [2]Dept. of Human Genetics and Molecular Biology, Nagoya University, [3]COMIT Center for One Medicine, Nagoya University, [4]Institute for Glyco-core Research (iGCORE), Nagoya University |

## 11:50-12:00 Closing remarks

# Poster Sessions

## Poster Session 1 (Day 2)
## Odd numbers: 17:30-18:30, Even numbers 18:30-19:30
## Place A (2F, cultural gallery): P1-01~68
## Place B (4F, foyer): P1-69~84

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| P1-01<br>(Session 08-5) | **Open Science and Responsible Science Communication**<br>Hartmut Vodermaier (The EMBO Journal) |
| P1-02<br>(Session 03-1) | **Strand asymmetry of DNA damage tolerance mechanisms**<br>Rodrigo Bermejo (CIB-CSIC) |
| P1-03<br>(Session 03-2) | **Single-molecule analysis of uncharacterised DNA replication initiation sites using Nanopore sequencing technology**<br>Shin-ichiro Hiraga (Univ. of Aberdeen) |
| P1-04<br>(Session 03-3) | **R-loop Resolution by ARIP4 Helicase Promotes Androgen-dependent Transcription Induction**<br>Michael Huen (HKU) |
| P1-05<br>(Session 03-4) | **DNA replication will not be required for ROS accumulation after chromosome breakages in E. coli.**<br>Akihiro Kaidow (Tokai Univ.) |
| P1-06<br>(Session 03-5) | **Visualization of DNA replication errors in living Escherichia coli cells**<br>Ivan Matic (Institut Cochin) |
| P1-07<br>(Session 03-6) | **Top3 drives crossover migration to the meiotic chromosome axis**<br>Matt Neale (University of Sussex) |
| P1-08<br>(Session 03-7) | **Spatial control of the APC/C ensures the rapid degradation of Cyclin B1**<br>Jon Pines (ICR) |
| P1-09<br>(Session 03-8) | **Rad54 prevents excessive intergenerational Rad51 aggregation in fission yeast**<br>Hideo Tsubouchi (Tokyo Inst. Tech.) |
| P1-10<br>(Session 03-9) | **Pre-RC forming proteins commonly have G-quadruplex binding activity in the intrinsically disordered regions**<br>Shou Waga (Japan Women's Univ.) |
| P1-11<br>(Session 06-1) | **DPPA3 Disrupts UHRF1 Chromatin Localization by Targeting the SRA Domain**<br>Atsuya Nishiyama (Univ. of Tokyo) |
| P1-12<br>(Session 06-2) | **Contribution of translesion synthesis for mutagenesis via a novel food-induced formamidopyrimidine-derivative**<br>Akagi Jun-ichi (NIHS/MHLW) |
| P1-13 | **Temperature sensitive growth of ΔmukB cells were suppressed by the mutations on topoisomerase I or cell wall related genes**<br>Koichiro Akiyama (NIG) |
| P1-14 | **Trajectory and uniqueness of mutational signatures in yeast mutators** |

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| (Session 14-3) | NICOLAS Alain (IRCAN, NIce France) |
| ~~P1-15~~<br>~~(Session 16-3)~~ | **Withdrawal** |
| P1-16 | **Nucleoporins cooperate with Polycomb silencers to promote transcriptional repression and repair at DNA double strand breaks**<br>Yubin Bae (DGIST) |
| P1-17 | **Cohesin is involved in the formation of elongating RNA polymerase II complex**<br>Bando, Masashige (Bando, Masashige) |
| P1-18 | **DNA replication profiling using LD-OK-seq in ATR-inactivated cells**<br>Atabek Bektash (NIG) |
| P1-19 | **Roles of Zpr1 in Cellular Proliferation and Genome Maintenance**<br>Szabolcs Bene (IFOM ETS, Italy) |
| P1-20<br>(Session 05-2) | **RAD51 paralogs travel with the replicative helicase to facilitate lesion bypass**<br>Kara Bernstein (Univ. Pennsylvania) |
| P1-21 | **Identifying the functions of SUMO-modified proteins during meiotic recombination in budding yeast**<br>Regina Bohn (UC Davis) |
| P1-22<br>(Session 06-3) | **Phenotypic sex determines recombination patterning in sex-reversed Rainbow Trout**<br>Cathrine Brekke (NMBU) |
| P1-23<br>(Session 04-7) | **Cytidine deaminases promote DNA replication stress resistance in pancreatic cancer cells**<br>Grant Brown (University of Toronto) |
| P1-24<br>(Session 06-4) | **Large-scale conservation of genomic architecture between distant species**<br>Rory T. Cerbus (RIKEN BDR) |
| P1-25<br>(Session 14-4) | **Human endonuclease ANKLE1 processes chromatin bridges by cleaving mechanically stressed DNA**<br>Gary YW Chan (University Hong Kong) |
| P1-26<br>(Session 12-6) | **Hop2-Mnd1 as a Gatekeeper of DNA Sequence Fidelity in Dmc1-Mediated Recombination**<br>Peter Chi (NTU) |
| P1-27 | **Meiotic Prophase roles of Chl1 in *Saccharomyces cerevisiae***<br>Hyungseok Choi (Chung-Ang Univ.) |
| P1-28<br>(Session 02-6) | **When DNA becomes its own enemy: Reconstitution of DNA-induced replication stalling**<br>Gideon Coster (ICR, London UK) |
| ~~P1-29~~ | Withdrawal |
| ~~P1-30~~<br>~~(Session 04-4)~~ | Withdrawal |
| P1-31 | **Condensin collaborates with topoisomerases at replication forks to facilitate fork reversal in response to replication stress** |

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| | Megane Da Mota (UMR9002 CNRS) |
| P1-32 | **Identification and functional characterization of a new crossover factor in the mouse**<br>Arnaud De Muyt (CBS) |
| P1-33<br>(Session 06-5) | **Altering DNA replication timing interferes with the precision of epigenome maintenance**<br>Qian Du (NNF CPR, KU, Denmark) |
| P1-34 | **Allosteric activation of the SPRTN protease by poly-ubiquitin**<br>Sophie Dürauer (LMU München) |
| P1-35<br>(Session 06-6) | **Exploring mechanisms of self/nonself discrimination at DNA level in fission yeast**<br>Hiro Ebina (ETH Zürich) |
| P1-36 | **Unbiased genome-wide mapping and characterization of fragile sites in single mammalian cells**<br>Jothivanan (RIKEN BDR) |
| P1-37<br>(Session 19-5) | **Contextual Roles of BRCA2 and PALB2 in Safeguarding Centromere Integrity**<br>Fumiko Esashi (University of Oxford) |
| P1-38<br>(Session 05-5) | **ATM and 53BP1 regulate alternative end joining-mediated V(D)J recombination**<br>Richard Frock (Stanford University) |
| P1-39<br>(Session 06-7) | **TTF2 induces mitotic replisome disassembly and MiDAS by coupling the TRAIP E3 ligase to DNA Polymerase Epsilon**<br>Ryo Fujisawa (MRC-PPU, Dundee) |
| P1-40<br>(Session 17-4) | **Context-dependent kinetochore phosphorylation by Aurora B through microtubule-mediated substrate masking**<br>Hiro Funabiki (Rockefeller Univ) |
| P1-41 | **Dynamic structures and functions of enzymes working in DNA double-strand break repair**<br>Asako Furukohri (IPR, Osaka univ.) |
| P1-42<br>(Session 14-2) | **When Base Excision Repair goes wrong: chromosome fragmentation upon TORC2 inhibition depends on nuclear actin-dependent remodeler activity**<br>Susan M Gasser (ISREC Foundation, University of Lausanne) |
| P1-43<br>(Session 14-7) | **Disruption of chromatin induces Topoisomerase 2 activity at sites of transcriptional stress**<br>Will Gittens (Uni. of Sussex, UK) |
| P1-44<br>(Session 09-1) | **Principles of chromosome organisation for meiotic recombination**<br>Corinne Grey (IGH CNRS Montpellier) |
| P1-45 | **Cohesin complex oligomerization maintains end-tethering at DNA double-strand breaks.**<br>Thomas Guérin (CEA Paris Saclay) |
| P1-46<br>(Session 10-4) | **Mutations arising during repair of broken chromosomes in budding yeat**<br>Jim Haber (Brandeis University) |

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| P1-47 | **A combinational degron system with AID2 and BromoTag uncovers the relationship between DNA replication and the cell cycle**<br>Yuki Hatoyama (NIG) |
| P1-48 | **Cooperation of Cdt2 C-terminal Motifs in Regulating CRL4Cdt2 Dynamics at the DNA Replication Site.**<br>Akiyo Hayashi (Univ. of Hyogo) |
| P1-49 | **Deciphering the genomic basis of phenotypic variation with TAQing system**<br>Yuta Hirai (Univ. of Tokyo) |
| P1-50<br>(Session 16-6) | **Embryonic genome instability upon somatic DNA replication timing program emergence**<br>Ichiro Hiratani (RIKEN BDR) |
| P1-51 | **The interaction of histones with the amino-terminal region of Mcm2 is stabilized by FACT but unstabilized by Nap1.**<br>Kohji HIZUME (Saitama Med. Univ.) |
| P1-52 | **Human RAD52 double-ring remodels replication forks restricting fork reversal**<br>Masa Honda (University of Iowa) |
| P1-53<br>(Session 05-4) | **Visualizing homology search during DNA double-strand break repair in yeast**<br>Chihiro HORIGOME (Tohoku University) |
| P1-54 | **Distinctive nuclear zone for RAD51-mediated homologous recombinational DNA repair**<br>Yasunori HORIKOSHI (Hiroshima University) |
| P1-55<br>(Session 09-2) | **Multiple mechanisms driving genomic instability in BRCA1-deficient cancer cells**<br>Li-Yao Huang (WIMM. Oxford) |
| P1-56<br>(Session 09-3) | **Spatial regulation of ribosomal RNA transcription by phase separation and transition**<br>Satoru Ide (TMIMS) |
| P1-57<br>(Session 09-4) | **Initiation of Meiotic Recombination in Zebrafish Males**<br>Yukiko Imai (NIG) |
| P1-58<br>(Session 09-5) | **FIGNL1 AAA+++ ATPase is essential for removal of RAD51 recombinase from meiotic chromosomes and chromosome condensation in mouse oocytes**<br>Masaru Ito (Osaka University) |
| P1-59 | **Histone methyltransferase NSD2 is involved in the maintenance of chromatin during site-specific double-strand break repair**<br>Koh Iwasaki (Chiba University) |
| P1-60 | **Analysis of the fission yeast Nrd1 and Pof1 on the accumulation of recombination intermediates**<br>JIANG BEIBEI (Hiroshima University) |
| P1-61<br>(Session 09-6) | **Aneuploidy-specific effects on tumor growth and malignant transformation**<br>Minji Jo (Cancer Inst., JFCR) |
| P1-62 | **Chl1 Supports Sister Chromatid Cohesion and Chromosome Morphogenesis during Meiosis** |

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| | Min Kyung Jo (Chung-Ang University) |
| P1-63 | **Super-Resolution Microscopy Analysis of RPA, Rad51, and Dmc1 Foci Dynamics during Meiotic Recombination in Saccharomyces cerevisiae**<br>Jeong Hwan Joo (Chung-Ang University) |
| P1-64 | **Towards the understanding of chiasma structure**<br>Yasutaka Kakui (WIAS, Waseda univ.) |
| P1-65 | **Resilient regulation of Plk1 activity in processing kinetochore-microtubule attachments**<br>Nana Kamakura (JFCR, Cancer Inst.) |
| P1-66 | **Ubiquitin ligase RFWD3 and TLS polymerases contribute to PCNA ubiquitination-dependent DNA damage tolerance in human cells**<br>Rie Kanao (Nagoya University) |
| P1-67 | **Smarcad1 and MutSα catalyze unidirectional sliding of a nucleosome away from a mismatch to facilitate eukaryotic DNA mismatch repair on chromatin**<br>KANATSU, Eiichiro (Kyushu University) |
| P1-68<br>(Session 09-7) | **The DNA-Tension-Dependent Loop Extrusion Mechanism in Dimeric SMC Complexes**<br>Takaharu Kanno (Karolinska Institute) |
| P1-69<br>(Session 09-8) | **Cell cycle regulation of replication initiation by timely binding/dissociation of the DNA bending factor IHF in *Escherichia coli***<br>Kazutoshi Kasho (Kyushu University ) |
| P1-70 | **Replication Stress in Endothelial Cells Orchestrates Attenuation of Cardiomyocyte OXPHOS via Igfbp7 Secretion, Leading to Heart Failure**<br>Manami Katoh (University of Tokyo) |
| P1-71 | **Promotion of ATP hydrolysis by specific basic patch-dependent multimerization of budding yeast ORC on ssDNA**<br>Hironori Kawakami<br>(Sanyo-Onoda City Uni) |
| P1-72 | **Chromosome-dependent aneuploid formation in Spo11-less meiosis**<br>Yuri Kawashima (Hiroshima University) |
| P1-73 | **Structural basis for the activation mechanism of DNMT1 in DNA methylation maintenance**<br>Amika Kikuchi (Yokohama City Univ.) |
| P1-74 | **Dynamic Chromosomal Distribution of Mismatch Repair Proteins in Embryonic Stem Cells**<br>Hyoseung Kim (Chung-Ang University) |
| P1-75 | **Development of Cas9-based high throughput platform for cancer drug screening**<br>Sohyun Kim (Chung-Ang university) |
| P1-76 | **Preparation and evaluation of chromatin regulator, PCGF1-PRC1 complexes**<br>Kisuke Kobayashi (RIKEN IMS) |
| P1-77 | **TAQing-Driven Recombination for Trait Integration in Yeast** |

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| | Hiromitsu Kono (The Univ. of Tokyo) |
| P1-78 | **Effects of DNA substrate structures on lesion excision by nucleotide excision repair in vitro**<br>Hidetsugu Kozono (Kobe University) |
| P1-79 | **Uncovering the role of HLTF in fork dynamics during replication stress using single-molecule biophysics**<br>Ulrike Kühbacher (Stanford University) |
| P1-80 | **High-resolution microscopic analysis of DNA synthesis in meiosis**<br>JUNSEO LEE (Chung-Ang University) |
| P1-81 | **Defining the role of MEN1 in Alternative Lengthening of Telomeres**<br>Ronnie Low (Francis Crick Ins) |
| P1-82 | **Single-cell ATAC-Seq reveals stage-specific gene regulatory landscape during mouse spermatogenesis**<br>So Maezawa (Tokyo Univ. of Sci.) |
| P1-83 | **Mechanisms for the removal of replication-blocking HMCES- and thiazolidine-DNA adducts in humans**<br>Masuda Yuji (RIEM, Nagoya Univ.) |
| P1-84<br>(Session 08-3) | **Focal amplification of a super-enhancer with the accumulation of non-coding RNAs in breast cancer**<br>Noriko Saitoh (Cancer Inst JFCR) |

## Poster Session 2 (Day 4)
## Odd numbers: 17:30-18:30, Even numbers 18:30-19:30
## Place A (2F, cultural gallery): P2-01~68
## Place B (4F, foyer): P2-69~83

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| P2-01<br>(Session 11-1) | **The mechanisms of the recruitment of SLX4-XPF nuclease complex in the response to replication stress induced by lacO-LacI interaction**<br>Yoko Katsuki (Kyushu University) |
| P2-02<br>(Session 11-2) | **CTF18 promotes cellular tolerance against chain-terminating nucleoside analogs (CTNAs) in cooperation with polymerase epsilon's exonuclease activity**<br>Ryotaro Kawasumi (Tokyo Metropolitan University) |
| P2-03<br>(Session 11-3) | **USP37 prevents premature disassembly of stressed replisomes by TRAIP**<br>Olga Kochenova (HMS/HHMI) |
| P2-04<br>(Session 11-4) | **Pluripotent Stem Cells Keep Genome integrity by Maintaining Slow DNA Replication Fork Progression and Abundant Replication Origins**<br>Kurashima Kiminori (NIBB) |
| P2-05<br>(Session 11-5) | **Direct visualization of DNA-bound cohesin in-liquid using high-speed atomic force microscopy**<br>Yumiko KUROKAWA (Nat. Inst. of Genet.) |
| P2-06<br>(Session 11-6) | **Impact of histone modifications on damage recognition process of global genome nucleotide excision repair**<br>Masayuki Kusakabe (Kobe University) |
| P2-07<br>(Session 12-7) | **Mediator-Recombinase Interaction and RPA Binding Dynamics Modulate Recombinase Nucleoprotein Assembly**<br>Hung-Wen Li (National Taiwan Univ) |
| P2-08<br>(Session 11-7) | **Cell Cycle Regulation has Shaped Budding Yeast Replication Origin Structure and Function**<br>Chew Theng Lim (Francis Crick Inst.) |
| P2-09<br>(Session 11-8) | **Cryo-EM analyses of UV-damaged recognition protein UV-DDB in nucleosomes during nucleotide excision repair**<br>Syota Matsumoto (The Univ. of Tokyo) |
| P2-10 | **Quantitative analysis of the frequency of chromosome loss after a DSB induction**<br>Matsuno Seiya (TMU) |
| P2-11 | **Replication-stress-associated DSBs induced by ionizing radiation risk genomic destabilization and associated clonal evolution**<br>Yusuke Matsuno (NCCRI) |
| P2-12 | **Functional analysis of RAD52 in the replication stress response induced by lacO-LacI complexes on a human chromosome**<br>Matsushita Kosei (Kyushu University) |
| P2-13<br>(Session 15-1) | **Human AAA+ ATPase FIGNL1 suppresses RAD51-mediated ultra-fine bridge formation**<br>Kenichiro Matsuzaki (Kindai University) |

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| P2-14 | **Replication-dependent histone (Repli-Histo) labeling specifically visualizes the physical properties of euchromatin/heterochromatin in living human cells**<br>Katsuhiko Minami (NIG) |
| P2-15 | **Investigating the mechanistic basis of G1/S transition**<br>Toshinari Miyauchi (Francis Crick Inst.) |
| P2-16<br>(Session 04-6) | **Molecular mechanism of bacterial cytokinesis position control by the Min system helping stable chromosome maintenance**<br>Kiyoshi Mizuuchi (LMB, NIDDK, NIH) |
| P2-17<br>(Session 16-4) | **Molecular basis of sister chromatid cohesion studied with purified proteins**<br>YASUTO MURAYAMA (NIG) |
| P2-18 | **Identification of minimal components of DNA-replication coupled symmetric histone recycling**<br>Fritz Nagae (Kyoto University) |
| P2-19<br>(Session 13-2) | **Fission yeast Cnp1/CENP-A causes gross chromosomal rearrangements at centromeres**<br>Takuro Nakagawa (Osaka University) |
| P2-20 | **Mechanisms regulating Clr4/SUV39H histone methyltransferase activity**<br>Rinko Nakamura (NIBB) |
| P2-21 | **Structural basis for the recognition of oxidized nucleotides by human MTH1**<br>Teruya Nakamura (Kumamoto University) |
| P2-22 | **Chromatin environment and RNA transcription termination regulation in cancer**<br>Chihiro Nakayama (Kyushu University) |
| P2-23 | **Inability of DNA damage response pathways to rescue cells from lethality caused by DNA over-replication**<br>Nguyen Ngoc Hong (Kochi Univ. of Tech.) |
| P2-24 | **Investigation on the induction of re-replication by NEDD8ylation inhibitor, MLN4924 in human cells**<br>Hideo NISHITANI (University of Hyogo) |
| P2-25<br>(Session 08-4) | **NELF promotes transcription termination and cell cycle**<br>Taka Nojima (Kyushu University) |
| P2-26<br>(Session 15-2) | **Neddylation inhibition is lethal with FANCJ loss in cancers**<br>Aki Nunomiya (IFOM) |
| P2-27 | **PRR14 and PRR14L are responsible for proper chromosome segregation in mitosis**<br>Chikashi Obuse (Osaka University) |
| P2-28<br>(Session 07-5) | **Stabilization of mononucleotide microsatellites by DNA mismatch repair and DNA polymerase proofreading in human cells**<br>Shinya Oda (Kyushu Cancer Center) |
| P2-29 | **Aldehyde-induced DNA-protein crosslinks are resolved by transcription-coupled repair**<br>Yasuyoshi Oka (Nagoya University) |

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| P2-30 | **Nuclear pore association plays a crucial role in the establishment of SUMO E3 ligase Mms21-mediated DNA damage-induced cohesion**<br>Yamato Okada (Tohoku University) |
| P2-31 | **Elucidating the mechanism of the recruitment of SLX4 in the replication stress response induced by lacO-LacI interaction on a human chromosome**<br>Takuma Okano (Kyushu University) |
| P2-32 | **The genetic relationship between Polη and Polζ in human TK6 cells**<br>Okuda Mone (TMU) |
| P2-33<br>(Session 15-3) | **Molecular characterization of the single-stranded DNA binding activity of the initiation complex constructed at the eubacterial replication origin**<br>Shogo Ozaki (Kyushu University) |
| P2-34<br>(Session 15-4) | **Competition for resources between replication forks in E. coli**<br>Florian Pflug (OIST) |
| P2-35<br>(Session 14-1) | **SLX4/FANCP: Playing with nucleases, helicases and beyond**<br>PH GAILLARD (CRCM, France) |
| P2-36<br>(Session 04-5) | **Genome replication in asynchronously growing microbial populations**<br>Simone Pigolotti (OIST) |
| P2-37<br>(Session 20-3) | **Proteomic profiling of UV damage repair patches uncovers histone chaperones with central functions in chromatin repair**<br>Sophie Polo (CNRS Paris France) |
| P2-38 | **Step-wise assembly of the pre-initiation complex**<br>Thomas Puehringer (Crick Institute) |
| P2-39<br>(Session 12-4) | **NCADP2 SMC-condensin subunit: a new regulator of meiotic prophase I chromosome assembly in the mouse.**<br>Thomas ROBERT (CBS, CNRS) |
| P2-40 | **Nanopore Sequencing of Nucleosomes Assembled at Replication – Nano-SoNAR**<br>Fernando R. Bringas (The Crick Institute) |
| P2-41<br>(Session 13-1) | **RAD5$^{OE}$-INDUCED REPLICATION STRESS PROMOTES MITOTIC RECOMBINATION, LOSS OF HETEROZYGOSITY AND ANEUPLOIDY IN *SACCHAROMYCES CEREVISAE***<br>Rodney Rothstein (Columbia Univ Med) |
| P2-42 | **Direct observation of O6-methylguanine-induced futile mismatch repair attempts and subsequent double-strand break formation in *Xenopus* egg extracts.**<br>Reihi Sakamoto (Kyushu University) |
| P2-43 | **Looking for the Cdc45 Dimerization Scaffold via Ultra-Fast Single-Particle Tracking**<br>Larissa Sambel (Stanford University) |
| P2-44<br>(Session 02-5) | **The structure-specific nuclease Rad27/FEN-1 maintains the stability of the ribosomal RNA gene locus.**<br>Mariko Sasaki (NIG) |
| P2-45 | **Temperature-Dependent Mechanisms in Bacterial Growth** |

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| (Session 15-5) | Alberto Sassi (OIST) |
| P2-46 | **CMG is necessary and sufficient to recruit Mcm10 to promote its helicase activity in the budding yeast Saccharomyces cerevisiae**<br>Yuna Satake (Kochi Univ. of Tech.) |
| P2-47 | **Hi-C Analysis of Structural Variants: Understanding Genomic Rearrangements on 3D Chromosome Structure in Yeast**<br>Yuki Sen (Univ. of Tokyo) |
| P2-48 | **Linker histone H1 serves as liquid-like "glue" of the chromatin domain**<br>Masa A. Shimazoe (NIG / SOKENDAI) |
| P2-49 | **The depletion of TRAIP results in the retention of PCNA on chromatin during mitosis, leads to inhibiting DNA replication initiation.**<br>Yasushi Shiomi (Univ. of Hyogo) |
| P2-50 | **Analysis of the role of the functionally unknown domain constituting DciA loader in replicative DnaB helicase loading in alpha-proteobacterium *Caulobacter crescentus***<br>Shohei Sato (Kyushu University) |
| P2-51<br>(Session 14-5) | **Diverse actions of Mre11 nuclease during DNA end resection and DNA replication**<br>Katsunori Sugimoto (Rutgers) |
| P2-52 | **An ATR-PrimPol pathway continuously maintains tolerance to chronical heterochromatin-associated replication stress in oncogenic KRAS-driven cancer cells**<br>Taichi Igarashi (Kyoto University) |
| P2-53<br>(Session 15-6) | **Macromolecular clustering drives mitotic chromosome assembly**<br>Motoko Takahashi (The Cancer Inst.JFCR) |
| P2-54 | **Is the cGAS-STING pathway activated in ruptured micronucleus?**<br>Tohru Takaki (Francis Crick) |
| P2-55 | **The involvement of chromatin remodeling factor SMARCAD1 in response to DNA double strand breaks**<br>Miou Takasu (Kobe university) |
| P2-56<br>(Session 15-7) | **Fluorescence-based analysis for DNA damage response in living cell**<br>Arato Takedachi (Fukuoka University) |
| P2-57 | **ChIP-CryoEM of nucleosome targeting histone variants from cells**<br>Yoshimasa Takizawa (University of Tokyo) |
| P2-58<br>(Session 02-4) | **Identification of atypical replication origin in the metallothionein-encoding repeats in the budding yeast Saccharomyces cerevisiae**<br>Seiji Tanaka (Kochi Univ. of Tech.) |
| P2-59<br>(Session 15-8) | **Resection of DNA double-strand breaks activates MRN- and 9–1–1-dependent ATR checkpoint and end-processing pathways in *Xenopus* egg extracts**<br>Kensuke Tatsukawa (Kyushu University) |
| P2-60 | **Molecular mechanism of copy number fluctuation of *CUP1* region in *S. cerevisiae***<br>Tatsuki Toriyama (Kochi Univ. of Tech.) |

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| P2-61 | **Mechanism of immune signalling factor sequestration on chromatin by the adenovirus core protein VII**<br>Kotaro Tsukada (University of Tokyo) |
| P2-62 | **Mechanism of DnaB helicase loading to *oriC* via the low affinity interaction with initiator protein DnaA for bidirectional replication initiation**<br>Takumi, Tsuruda (Kyushu University) |
| P2-63 | **Metabolic stress-induced long ncRNA transcription governs the formation of meiotic DNA breaks in the fission yeast**<br>Tsuruta Yusuke (TMU) |
| P2-64 | **Amido-bridged nucleic acid-modified antisense oligonucleotide targeting MCM8 as a cancer-specific chemosensitizer for platinum compounds**<br>Yuki Uchibori (Kyushu University) |
| P2-65<br>(Session 14-6) | **Fission yeast histone deacetylase Clr6 is repaired for the growth of cells with circular chromosomes**<br>Masaru Ueno (Hiroshima University) |
| P2-66 | **Analysis of age-related repetitive sequence instability driven by epigenetic changes**<br>Yuta Uneme (Univ. of Tokyo) |
| P2-67<br>(Session 18-1) | **STK19 facilitates the clearance of lesion-stalled RNAPII during transcription-coupled DNA repair**<br>Diana van den Heuvel (Diana van den Heuvel) |
| P2-68<br>(Session 12-5) | **Identification of budding yeast proteins that antagonize the mismatch repair system to promote hybrid fertility**<br>Ting-Fang Wang (IMB, Academia Sinica) |
| P2-69<br>(Session 18-2) | **CDCA7 is an evolutionarily conserved hemimethylated DNA sensor in eukaryotes**<br>Isabel Wassing (Rockefeller Uni) |
| P2-70<br>(Session 18-3) | **Mechanisms of nucleosome uncoiling at the replication fork**<br>Oliver Willhoft (Francis Crick Inst) |
| P2-71<br>(Session 18-4) | **Pro-DSB components drive intermolecular chromosome condensation in distinct island regions during meiotic prophase**<br>Ellie Wright (University of Sussex) |
| P2-72 | **Recurrent transcriptional pausing and restart at centromeres causes gross chromosomal rearrangements through R-loop formation**<br>Ran XU (Osaka University) |
| P2-73<br>(Session 18-5) | **Non-canonical functions of UHRF1 maintain DNA methylation homeostasis in cancer cells.**<br>Kosuke Yamaguchi (NIG, Kanemaki-Lab) |
| P2-74 | **Roles of reverse gyrase in maintaining the genome architecture of hyperthermophiles**<br>Kodai Yamaura (Kyoto university) |
| P2-75 | **Functional analysis of BRCA2 in hematopoiesis**<br>Kosuke YAMAZAKI (TMiMS) |

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| P2-76 | **Impacts of heavy water on DNA double-strand break repairs and cellular transcription, potentially via quantum-level mechanisms underlying kinetic isotope effects**<br>Takeshi Yasuda (QST) |
| P2-77<br>(Session 18-6) | **Development of photoactivatable endonuclease for meiotic recombination**<br>Hideyuki Yone (Univ. of Tokyo) |
| P2-78 | **BRF2, a component of Type III TFIIIB, mediates redox stress response and genome integrity via regulation of gene expression**<br>Seobin Yoon (Chung-ang University) |
| P2-79<br>(Session 18-7) | **Mechanisms in chromosome origin unwinding promoted by bacterial initiator DnaA protein and a ubiquitous nucleoid-associated protein HU.**<br>Ryusei Yoshida (Kyushu University) |
| P2-80 | **Spatial organization of supercoil dynamics during DNA replication**<br>Yoshiharu Kusano (JFCR) |
| P2-81 | **Werner helicase and MutLα endonuclease control the fidelity of single-strand annealing**<br>Yoshitaka Kawasoe (Kyushu University) |
| P2-82 | **Single-molecular Condensin I and Topoisomerase IIα compact DNA**<br>Tsubota Yuko (Kyoto Univ.) |
| P2-83<br>(Session 18-8) | **The RIF1-PP1 complex shapes DNA replication initiation zones to establish the replication timing program**<br>XIAOXUAN ZHU (NIG, Japan) |