The 12th 3R+3C International Symposium

November 18–22, 2024

ACROS Fukuoka, Tenjin, Fukuoka, Japan

Program for Poster presentations

Lobby Area for International Conference Hall (4F)

Cultural Gallery (2F)

Poster session 1	Nov. 19 (Day 2), 17:30–19:30
Poster session 2	Nov. 21 (Day 4), 17:30–19:30

3R+3C International Symposium

Poster Program (2024/10/22 ver.)

Poster session 1 (2024/11/19 17:30-)

P1-01(Session 8-5) **Open Science and Responsible Science Communication**

Hartmut Vodermaier[1]

[1]EMBO Press, The EMBO Journal

P1-02(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]

[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

P1-03(Session 3-2) **Single-molecule analysis of uncharacterised DNA replication initiation sites using Nanopore sequencing technology**

Shin-ichiro Hiraga[1], Alexandra Pyatnitskaya[1], Anna Rogers[2], Sathish Thiyagarajan[2], Conrad Nieduszynski[2], Anne Donaldson[1]

[1]Institute of Medical Sciences, University of Aberdeen, UK, [2]Earlham Institute, Norwich, UK

P1-04(Session 3-3) **R-loop Resolution by ARIP4 Helicase Promotes Androgen-dependent Transcription Induction**

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]

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P1-05(Session 3-4) **DNA replication will not be required for ROS accumulation after chromosome breakages in E. coli.**

Akihiro Kaidow[1],

[1]Dept. Biol., Tokai Univ.

P1-06(Session 3-5) **Visualization of DNA replication errors in living Escherichia coli cells**

Ivan Matic[1]

[1]Institut Cochin, Paris, France

P1-07(Session 3-6) **Top3 drives crossover migration to the meiotic chromosome axis**

Matthew Neale[1,2], Tom Powell[1,2], William H Gittens[1,2]

[1]Genome Damage and Stability Centre, [2]University of Sussex, UK

P1-08(Session 3-7) **Spatial control of the APC/C ensures the rapid degradation of Cyclin B1**

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]

[1]ICR

P1-09(Session 3-8) **Rad54 prevents excessive intergenerational Rad51 aggregation in fission yeast**

Goki Taniguchi[1], May Alexander[1], Hiroshi Iwasaki[1], Hideo Tsubouchi[1]

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P1-10(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]

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P1-11(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]

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P1-12(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]

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P1-13

Temperature sensitive growth of ΔmukB cells were suppressed by the mutations on topoisomerase I or cell wall related genes

Koichiro Akiyama[1], Niki Hironori[1]

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P1-14(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]

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P1-15(Session 16-3)

Substrate accessibility regulation of human TopIIa decatenation by cohesin

Luis Aragon[1], Erin Cutts[1], Sanjana Saravanan[1], Gemma Fisher[1], David Rueda[1]

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P1-16

Nucleoporins cooperate with Polycomb silencers to promote transcriptional repression and repair at DNA double strand breaks

Yubin Bae[1],

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P1-17

Cohesin is involved in the formation of elongating RNA polymerase II complex

Masashige Bando[1], Shoin Tei[1], Atsunori Yoshimura[1], Toyonori Sakata[1], Takashi Sutani[1], Katsuhiko Shirahige[1]

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P1-18

DNA replication profiling using LD-OK-seq in ATR-inactivated cells

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

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P1-19

Roles of Zpr1 in Cellular Proliferation and Genome Maintenance

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P1-20(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]

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P1-21

Identifying the functions of SUMO-modified proteins during meiotic recombination in budding yeast

Regina Bohn [1,2], Aparajintha Connur[1], Zijing Zhang[1], Maithili Patel[1], Nikhil Bhagwat [1,2], Neil Hunter[1,2]

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P1-22(Session 6-3)

Phenotypic sex determines recombination patterning in sex-reversed Rainbow Trout

Cathrine Brekke[1], Tim Martin Knutsen[2]

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P1-23(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]

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P1-24(Session 6-4)

Large-scale conservation of genomic architecture between distant species

Rory Cerbus[2], Kyogo Kawaguchi[1,2,3,4], Ichiro Hiratani[2]

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P1-25(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]

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P1-26(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]

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P1-27

Meiotic Prophase roles of Chl1 in *Saccharomyces cerevisiae*

Hyungseok Choi[1], Keun Pil Kim[1]

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P1-28(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]

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P1-29

Targeting RecFOR to Postreplication Gaps

Camille Henry[1], Gurleen Kaur[2], Megan Cherry[2,3], Sarah Henrikus[2,4], Hope Beyer[1], Elizabeth Wood[1], Sindhu Chitteni-Pattu[1], Antoine van Oijen[2], Andrew Robinson[2], Michael Cox [1]

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P1-30(Session 4-4)

Controlling Genome Topology with Sequences that Trigger Post-replication Gap Formation During Replisome Passage: The E. coli RRS Elements

Michael Cox[1], Phuong Pham[2], Elizabeth Wood[1], Emma Dunbar[1], Myron Goodman[2]

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P1-31

Condensin collaborates with topoisomerases at replication forks to facilitate fork reversal in response to replication stress

Megane Da Mota[2], Axel Delamarre[1], Antoine Barthe[2], Alba Toran-Villarubias[2], Cyril Ribeyre[2], Jessica Jackson[3], Alessandro Vindigni[3], Yea-Lih Lin[2], Philippe Pasero[2], Armelle Lengronne[2]

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P1-32

Identification and functional characterization of a new crossover factor in the mouse

Arnaud De Muyt[1], Laurine Dal toe[1], Céline Adam[2], Mercier Mercier[3], Valérie Borde[2], Thomas Robert[1]

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P1-33(Session 6-5)

Altering DNA replication timing interferes with the precision of epigenome maintenance

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]

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P1-34

Allosteric activation of the SPRTN protease by poly-ubiquitin

Sophie Duerauer[1,2], Hyun Seo Kang[3,4], Christian Wiebeler[5], Yuka Machida[6,7], Dina Sophia Schnapka[1,2], Christian Renz[8], Denitsa Yaneva[1,2], Pedro Weickert[1,2], Helle Ulrich[8], Michael Sattler[3,4], Yuichi Machida[6,7], Nadine Schwierz[5], Julian Stingele[1,2]

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P1-35(Session 6-6)

Exploring mechanisms of self/nonself discrimination at DNA level in fission yeast

Hiro Ebina[1], Shweta Saini[1], Mattia Valentini[1], Haochen Yu[1], Yves Barral[1]

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P1-36

Unbiased genome-wide mapping and characterization of fragile sites in single mammalian cells

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P1-37(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]

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P1-38(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]

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P1-39(Session 6-7)

TTF2 induces mitotic replisome disassembly and MiDAS by coupling the TRAIP E3 ligase to DNA Polymerase Epsilon

Ryo Fujisawa[1], Karim Labib[1]

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P1-40(Session 17-4)

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

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P1-41

Dynamic structures and functions of enzymes working in DNA double-strand break repair

Asako Furukohri[1], Sijia Liu[1], Hiroko Takazaki[1], Misaki Arie[1], Hisashi Tatebe[3], Takayuki Uchihashi[2], Takayuki Kato[1], Akira Shinohara[1]

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P1-42(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]

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P1-43(Session 14-7)

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

William Gittens[1],

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P1-44(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]

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P1-45

Cohesin complex oligomerization maintains end-tethering at DNA double-strand breaks.

Jamie Phipps[1,2], Mathias Toulouze[1,2], Cécile Ducrot[1,2], Rafaël Costa[1,2], Clémentine Brocas[1,2], Thomas Guerin[1,2], Karine Dubrana[1,2]

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P1-46(Session 10-4)

Mutations arising during repair of broken chromosomes in budding yeat

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P1-47

A combinational degron system with AID2 and BromoTag uncovers the relationship between DNA replication and the cell cycle

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P1-48

Cooperation of Cdt2 C-terminal Motifs in Regulating CRL4Cdt2 Dynamics at the DNA Replication Site.

Akiyo Hayashi [1], Tatsuya Bekki[1], Masayuki Kusakabe[2,3], Akiko Ueno[1], Yasushi Shiomi[1], Kaoru Sugasawa[2,3], Hideo Nishitani[1]

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P1-49 **Deciphering the genomic basis of phenotypic variation with TAQing system**

Yuta Hirai[1], Hideyuki Yone[1], Ryunosuke Tahara[1], Kunihiro Ohta[1,2]

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P1-50(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]

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P1-51 **The interaction of histones with the amino-terminal region of Mcm2 is stabilized by FACT but unstabilized by Nap1.**

Kohji Hizume[1],

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P1-52 **Human RAD52 double-ring remodels replication forks restricting fork reversal**

Masayoshi Honda[1], Spies Maria[1]

[1]University of Iowa

P1-53(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]

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P1-54 **Distinctive nuclear zone for RAD51-mediated homologous recombinational DNA repair**

Yasunori Horikoshi[1,2,3], Shima Hiroki[4], Kobayashi Wataru[5,6], Schmid Volker[7], Itabashi Takeshi[8], Iwane Atsuko[8], Sun Jiying[1], Ochiai Hiroshi[9], Kinugasa Yasuha[1], Fukuto Atsuhiko[10], Shi Lin[11], Kurumizaka Hitoshi[5,6], Ikura Tsuyoshi[12], Markaki Yolanda[13,14], Tate Shin-ichi[2,9], Igarashi Kazuhiko[4,15], Cremer Thomas[13], Tashiro Satoshi[1,2,3]

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P1-55(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]

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P1-56(Session 9-3) **Spatial regulation of ribosomal RNA transcription by phase separation and transition**

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

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P1-57(Session 9-4) **Initiation of Meiotic Recombination in Zebrafish Males**

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P1-58(Session 9-5)

FIGNL1 AAA+++ ATPase is essential for removal of RAD51 recombinase from meiotic chromosomes and chromosome condensation in mouse oocytes

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P1-59

Histone methyltransferase NSD2 is involved in the maintenance of chromatin during site-specific double-strand break repair

Koh Iwasaki[1], Kai Shimizu[1], Yoshitaka Kamimura[2], Yasunori Horikoshi[2], Jiying Sun [2], Atsushi Kaneda[3], Satoshi Tashiro[2], Akira Sassa[1], Kiyoe Ura[1]

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P1-60

Analysis of the fission yeast Nrd1 and Pof1 on the accumulation of recombination intermediates

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P1-61(Session 9-6)

Aneuploidy-specific effects on tumor growth and malignant transformation

Minji Jo[1], Oltea Sampetrean[2], Seietsu Rai[1], Tetsuya Negoto[3], Utako Kato[1], Hideyuki Saya[4], Toru Hirota[1]

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P1-62

Chl1 Supports Sister Chromatid Cohesion and Chromosome Morphogenesis during Meiosis

Minkyung Jo[1],

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P1-63

Super-Resolution Microscopy Analysis of RPA, Rad51, and Dmc1 Foci Dynamics during Meiotic Recombination in Saccharomyces cerevisiae

JeongHwan Joo[1],

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P1-64

Towards the understanding of chiasma structure

Yasutaka Kakui[1,2], Sakatsume Jun-ichi[2], Sato Masamitsu[2]

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P1-65

Resilient regulation of Plk1 activity in processing kinetochore-microtubule attachments

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P1-66

Ubiquitin ligase RFWD3 and TLS polymerases contribute to PCNA ubiquitination-dependent DNA damage tolerance in human cells

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P1-67

Smarcad1 and MutSα catalyze unidirectional sliding of a nucleosome away from a mismatch to facilitate eukaryotic DNA mismatch repair on chromatin

Eiichiro Kanatsu[1], Riki Terui[2], Tamiko Minamisawa[3], Yasukazu Daigaku[3], Tatsuro Takahashi[2]

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P1-68(Session 9-7)

The DNA-Tension-Dependent Loop Extrusion Mechanism in Dimeric SMC Complexes

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]

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P1-69(Session 9-8)

Cell cycle regulation of replication initiation by timely binding/dissociation of the DNA bending factor IHF in *Escherichia coli*

Kazutoshi Kasho[1], Ryuji Sakai[1], Kosuke Ito[1], Rion Satomura[1], Mizuki Yoshida[1], Kenya Miyoshi[1], Sho Nakazono[1], Tsutomu Katayama[1]

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P1-70

Replication Stress in Endothelial Cells Orchestrates Attenuation of Cardiomyocyte OXPHOS via Igfbp7 Secretion, Leading to Heart Failure

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P1-71

Promotion of ATP hydrolysis by specific basic patch-dependent multimerization of budding yeast ORC on ssDNA

Hironori Kawakami[1,2], Ryoto Shimada[1], Ayaka Obata[1,3], Yumeho Okazaki[1], Ichiro Horie[1], Hisaaki Shinohara[1], Tsutomu Katayama[2]

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P1-72

Chromosome-dependent aneuploid formation in Spo11-less meiosis

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P1-73

Structural basis for the activation mechanism of DNMT1 in DNA methylation maintenance

Amika Kikuchi[1], Hiroki Onoda[2], Kosuke Yamaguchi[3], Satomi Kori[1], Atsushi Yamagata[4], Atsuya Nishiyama[5], Makoto Nakanishi[5], Pierre-Antoine Defossez[3], Kyohei Arita[1]

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P1-74

Dynamic Chromosomal Distribution of Mismatch Repair Proteins in Embryonic Stem Cells

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P1-75

Development of Cas9-based high throughput platform for cancer drug screening

sohyun Kim[1], Keun Pil Kim[1]

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P1-76

Preparation and evaluation of chromatin regulator, PCGF1-PRC1 complexes

kisuke kobayashi[1,3], Shinsuke Ito[1], Yuri Tomabechi[2], Sayako Kohno[2], Kazushige Katsura[2], Kazuharu Hanada[2], Mikako Shirouzu[2], Haruhiko Koseki[1,3]

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P1-77

TAQing-Driven Recombination for Trait Integration in Yeast

Hiromitsu KONO[1], Hideyuki Yone[1], Kunihiro Ohta[1,2]

[1]Dept. of Biol. Sci., Grad. Sch. of Arts & Sci., Univ. of Tokyo, [2]Universal Biology Institute, Univ. of Tokyo

P1-78 **Effects of DNA substrate structures on lesion excision by nucleotide excision repair in vitro**

Hidetsugu Kozono[1,2], Matsuyama Hiroo [1,2], Tada Haruto[1,2], Kusakabe Masayuki[1,2], Matsumoto Syota[3], Kujirai Tomoya[3], Echigoya Kenta[3], Kurumizaka Hitoshi[3], Sugasawa Kaoru[1,2]

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P1-79 **Uncovering the role of HLTF in fork dynamics during replication stress using single-molecule biophysics**

Ulrike Kuehbacher[1,2], Gheorghe Chistol[1], Karlene Cimprich[1]

[1]Stanford University, [2]University of Copenhagen

P1-80 **High-resolution microscopic analysis of DNA synthesis in meiosis**

JUNSEO LEE[1], Hyung Seok Choi[1], Keun P Kim[1]

[1]Chung-Ang University, Korea

P1-81 **Defining the role of MEN1 in Alternative Lengthening of Telomeres**

Ronnie Ren Jie Low[1], Simon Boulton[1]

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P1-82 **Single-cell ATAC-Seq reveals stage-specific gene regulatory landscape during mouse spermatogenesis**

Tatsuya Hattori[1], Kai Otsuka[1], Tatsuya Nakamura[1], Hinata Chikano[1], Nanami Fukushima[1], Toshiaki Watanabe[2,3], Erika Sasaki[3], Satoshi Namekawa[4], So Maezawa[1]

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P1-83 **Mechanisms for the removal of replication-blocking HMCES- and thiazolidine-DNA adducts in humans**

Yuji Masuda[1,2], Yohei Sugimoto[1,2], Shigenori Iwai[3], Yumi Miyake[4], Rie Kanao[1,2], Chikahide Masutani[1,2]

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P1-84(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]

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Poster session 2 (2024/11/21 17:30-)

P2-01(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]

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P2-02(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]

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P2-03(Session 11-3) **USP37 prevents premature disassembly of stressed replisomes by TRAIP**

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]

[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

P2-04(Session 11-4) **Pluripotent Stem Cells Keep Genome integrity by Maintaining Slow DNA Replication Fork Progression and Abundant Replication Origins**

Kiminori Kurashima[1], Yasunao Kamikawa[1,2], Tomomi Tsubouchi[1]

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P2-05(Session 11-5) **Direct visualization of DNA-bound cohesin in-liquid using high-speed atomic force microscopy**

Yumiko Kurokawa[1,2], Kenichi Umeda[3], Noriyuki Kodera[3], Yasuto Murayama[1,2]

[1]National Institute of Genetics, [2]SOKENDAI, [3]WPI-NanoLSI, Kanazawa University

P2-06(Session 11-6) **Impact of histone modifications on damage recognition process of global genome nucleotide excision repair**

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]

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P2-07(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]

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P2-08(Session 11-7) **Cell Cycle Regulation has Shaped Budding Yeast Replication Origin Structure and Function**

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]

[1]The Francis Crick Institute, [2]University of Copenhagen, [3]Delft University of Technology

P2-09(Session 11-8) **Cryo-EM analyses of UV-damaged recognition protein UV-DDB in nucleosomes during nucleotide excision repair**

Syota Matsumoto[1], Yoshimasa Takizawa[1], Mitsuo Ogasawara[1], Kana Hashimoto[1], Junpei Yamamoto[2], Shigenori Iwai[2], Kaoru Sugasawa[3], Hitoshi Kurumizaka[1]

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P2-10 **Quantitative analysis of the frequency of chromosome loss after a DSB induction**

Seiya Matsuno[1], Hirota Kouji[1], Abe Takuya[2]

[1]Tokyo Metropolitan University, Japan, [2]Tohoku Medical and Pharmaceutical University, Japan

P2-11 **Replication-stress-associated DSBs induced by ionizing radiation risk genomic destabilization and associated clonal evolution**

Yusuke Matsuno[1], Ken-ichi Yoshioka[1]

[1]National Cancer Center Research Institute

P2-12 **Functional analysis of RAD52 in the replication stress response induced by lacO-LacI complexes on a human chromosome**

Kosei Matsushita[1], Koki Narimatsu[1], Kazumasa Yoshida[1], Yasunori Noguchi[1], Miyako Shiraishi[1], Yoko Katsuki[1], Masatoshi Fujita[1]

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P2-13(Session 15-1)

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

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

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P2-14

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

Katsuhiko Minami[1,2], Satoru Ide[1,2], Sachiko Tamura[1], Kazunari Kaizu[3,4], Koichi Higashi[2,5], Atsushi Toyoda[6], Koichi Takahashi[3], Ken Kurokawa[2,5], Kazuhiro Maeshima[1,2]

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P2-15

Investigating the mechanistic basis of G1/S transition

Toshinari Miyauchi[1], Eiko Ozono[1], Jingkun Zeng[1], John Diffley[1]

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P2-16(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]

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P2-17(Session 16-4)

Molecular basis of sister chromatid cohesion studied with purified proteins

YASUTO MURAYAMA[1], Yumiko Kurokawa[1]

[1]National Institute of Genetics

P2-18

Identification of minimal components of DNA-replication coupled symmetric histone recycling

Fritz Nagae[1], Shizuko Endo[2], Yasuto Murayama[2,3], Tsuyoshi Terakawa[1]

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P2-19(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]

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P2-20

Mechanisms regulating Clr4/SUV39H histone methyltransferase activity

Rinko Nakamura[1,2], Yoshimura Yuriko[1], Nakagawa Reiko[3], Nakayama Jun-ichi[1,2]

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P2-21

Structural basis for the recognition of oxidized nucleotides by human MTH1

Teruya Nakamura[1], Yukari Koga-Ogawa[2], Kana Fujimiya[3], Keisuke Hirata[1], Mami Chirifu[1], Masataka Goto[1], Shinji Ikemizu[1], Yusaku Nakabeppu[4], Yuriko Yamagata[1,5]

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P2-22

Chromatin environment and RNA transcription termination regulation in cancer

Chihiro Nakayama[1], Magda Kopczyńska[2], Kinga Kamieniarz-Gdula[2], Takayuki Nojima[1]

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P2-23

Inability of DNA damage response pathways to rescue cells from lethality caused by DNA over-replication

Hong Nguyen Ngoc[1], Aika Okamoto[1], Shiho Ogawa [2,3], Seiji Tanaka[1,2]

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P2-24

Investigation on the induction of re-replication by NEDD8ylation inhibitor, MLN4924 in human cells

Sotaro Hanazaki[1], Chigusa Naka[1], Kusakawa Yuki[1], Akiyo Hayashi[1], Yasushi Shiomi[1], Hideo Nishitani[1]

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P2-25(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]

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P2-26(Session 15-2)

Neddylation inhibition is lethal with FANCJ loss in cancers

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P2-27

PRR14 and PRR14L are responsible for proper chromosome segregation in mitosis

Suzuha Gose[1], Aoi Takami[1], Hiroto Imai[1], Ryota Mochizuki[1], Madison Wong[1], Takamasa Ito[1], Shin-Ya Isobe[1], Chikashi Obuse[1]

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P2-28(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]

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P2-29

Aldehyde-induced DNA-protein crosslinks are resolved by transcription-coupled repair

Yasuyoshi Oka[1], Tomoo Ogi[1]

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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

Yamato Okada[1], Yuki Orihara[1], Daisuke Takahashi[1], Tatsunori Konishi[1], Yukako Oma[1], Masahiko Harata[1], Chihiro Horigome[1]

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P2-31

Elucidating the mechanism of the recruitment of SLX4 in the replication stress response induced by lacO-LacI interaction on a human chromosome

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

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P2-32

The genetic relationship between Polη and Polζ in human TK6 cells

Mone Okuda[1], Fujii Minori[1], Kawasumi Ryotaro[1], Hirota Kouji[1]

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P2-33(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]

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P2-34(Session 15-4) **Competition for resources between replication forks in E. coli**

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

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P2-35(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], GAILLARD Pierre Henri [1,2,3,4,5]

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P2-36(Session 4-5) **Genome replication in asynchronously growing microbial populations**

Simone Pigolotti[1],

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P2-37(Session 20-3) **Proteomic profiling of UV damage repair patches uncovers histone chaperones with central functions in chromatin repair**

Alexandre Plessier[1], Audrey Chansard[1], Eliane Petit[1], Julia Novion Ducassou[2], Yohann Coute[2], Sophie Polo[1]

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P2-38 **Step-wise assembly of the pre-initiation complex**

Thomas Puehringer[1], Emma Couves[1], Berta Canal[2], John Diffley[2], Alessandro Costa[1]

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P2-39(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]

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P2-40 **Nanopore Sequencing of Nucleosomes Assembled at Replication – Nano-SoNAR**

Fernando Rodrigo Rosas Bringas[1], Nishanthi Gangadharan[2], Michael Boemo[2], John Diffley[1]

[1]The Francis Crick Institute, [2]University of Cambridge

P2-41(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

P2-42 **Direct observation of O6-methylguanine-induced futile mismatch repair attempts and subsequent double-strand break formation in *Xenopus* egg extracts.**

Reihi Sakamoto[1], Karin Shigenobu Ueno[1], Tatsuro Takahashi[2]

[1]Guraduate School of System Life Sciences, Kyushu University, [2]Faculty of Science, Kyushu University

P2-43 **Looking for the Cdc45 Dimerization Scaffold via Ultra-Fast Single-Particle Tracking**

Larissa Sambel[1], Gheorghe Chistol[1]

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P2-44(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

P2-45(Session 15-5) **Temperature-Dependent Mechanisms in BacterialGrowth**

Alberto Sassi[1], Simone Pigolotti[1]

[1]Okinawa Institute of Science and Technology

P2-46 **CMG is necessary and sufficient to recruit Mcm10 to promote its helicase activity in the budding yeast Saccharomyces cerevisiae**

Yuna Satake [1], Shiho Ogawa[2,3], Seiji Tanaka[1,2]

[1]Grad. Sch. Eng., Kochi Univ. Tech., [2]Sch. Env. Sci. Eng., Kochi Univ. Tech., [3]Sch. Biol. Env. Sci., Kwansei Univ.

P2-47 **Hi-C Analysis of Structural Variants: Understanding Genomic Rearrangements on 3D Chromosome Structure in Yeast**

Yuki Sen[1], Hiromitsu Kono[1], Kunihiro Ohta[1,2]

[1]Graduate School of Arts and Sciences, University of Tokyo, [2]Universal Biology Institute, University of Tokyo

P2-48 **Linker histone H1 serves as liquid-like “glue” of the chromatin domain**

Masa A Shimazoe[1,2], Satoru Ide[1,2], Sachiko Tamura[1], Kazuhiro Maeshima[1,2]

[1]Genome Dynamics Laboratory, National Institute of Genetics, [2]Graduate Institute for Advanced Studies, SOKENDAI

P2-49 **The depletion of TRAIP results in the retention of PCNA on chromatin during mitosis, leads to inhibiting DNA replication initiation.**

Yasushi Shiomi[1], Hayashi Akiyo [1], Kanemaki Masato[2,3,4], Nishitani Hideo[1]

[1]Graduate School of Science, University of Hyogo, [2]National Institute of Genetics, [3]The Graduate University for Advanced Studies, [4]Department of Biological Science, The University of Tokyo

P2-50 **Analysis of the role of the functionally unknown domain constituting DciA loader in replicative DnaB helicase loading in alpha-proteobacterium *Caulobacter crescentus***

shohei Sato[1], Naoto Itani[1], Keito Watanabe[1], Shogo Ozaki[1], Tsutomu Katayama[1]

[1]Kyushu University

P2-51(Session 14-5) **Diverse actions of Mre11 nuclease during DNA end resection and DNA replication**

Katsunori Sugimoto[1],

[1]Rutgers

P2-52 **An ATR-PrimPol pathway continuously maintains tolerance to chronical heterochromatin-associated replication stress in oncogenic KRAS-driven cancer cells**

IGARASHI Taichi[1,2], Kimiyoshi YANO[2], Lee ZOU[3], Takaaki YASUHARA[1], Bunsyo SHIOTANI[2]

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P2-53(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

P2-54 **Is the cGAS-STING pathway activated in ruptured micronucleus?**

Tohru Takaki[1], Millar Rhona[1,2], Hiley Crispin[2], Boulton Simon[1]

[1]The Francis Crick Institute, [2]UCL Cancer Institute

P2-55 **The involvement of chromatin remodeling factor SMARCAD1 in response to DNA double strand breaks**

Miou Takasu[1,2], Masayuki Kusakabe[1,2], Atsushi Shibata[3], Wataru Sakai[1,2], Kaoru Sugasawa[1,2], Masayuki Yokoi[1,2]

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P2-56(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

P2-57 **ChIP-CryoEM of nucleosome targeting histone variants from cells**

Yoshimasa Takizawa[1], Takuro Shioi[1,2], Suguru Hatazawa[1], Yuki Kobayashi[1], Mitsuo Ogasawara[1], Yasuyuki Ohkawa[3], Hitoshi Kurumizaka[1,2]

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P2-58(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

P2-59(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]

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P2-60 **Molecular mechanism of copy number fluctuation of *CUP1* region in *S. cerevisiae***

TATSUKI TORIYAMA[1], Kazuki Ikezawa[2], Shiho Ogawa[2,3], Seiji Tanaka[1,2]

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P2-61 **Mechanism of immune signalling factor sequestration on chromatin by the adenovirus core protein VII**

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P2-62 **Mechanism of DnaB helicase loading to *oriC* via the low affinity interaction with initiator protein DnaA for bidirectional replication initiation**

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P2-63 **Metabolic stress-induced long ncRNA transcription governs the formation of meiotic DNA breaks in the fission yeast**

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P2-64

Amido-bridged nucleic acid-modified antisense oligonucleotide targeting MCM8 as a cancer-specific chemosensitizer for platinum compounds

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P2-65(Session 14-6)

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

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P2-66

Analysis of age-related repetitive sequence instability driven by epigenetic changes

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P2-67(Session 18-1)

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

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P2-68(Session 12-5)

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

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P2-69(Session 18-2)

CDCA7 is an evolutionarily conserved hemimethylated DNA sensor in eukaryotes

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P2-70(Session 18-3)

Mechanisms of nucleosome uncoiling at the replication fork

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P2-71(Session 18-4)

Pro-DSB components drive intermolecular chromosome condensation in distinct island regions during meiotic prophase

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P2-72

Recurrent transcriptional pausing and restart at centromeres causes gross chromosomal rearrangements through R-loop formation

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P2-73(Session 18-5)

Non-canonical functions of UHRF1 maintain DNA methylation homeostasis in cancer cells.

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P2-74

Roles of reverse gyrase in maintaining the genome architecture of hyperthermophiles

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P2-75

Functional analysis of BRCA2 in hematopoiesis

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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

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P2-77(Session 18-6)

Development of photoactivatable endonuclease for meiotic recombination

Hideyuki Yone[1], Yuri Kawashima[2], Hayato Hirai[1], Hiromitsu Kono[1], Kunihiro Ohta[1,3]

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P2-78

BRF2, a component of Type III TFIIIB, mediates redox stress response and genome integrity via regulation of gene expression

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P2-79(Session 18-7)

Mechanisms in chromosome origin unwinding promoted by bacterial initiator DnaA protein and a ubiquitous nucleoid-associated protein HU.

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P2-80

Spatial organization of supercoil dynamics during DNA replication

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P2-81

Werner helicase and MutLα endonuclease control the fidelity of single-strand annealing

Kawasoe Yoshitaka[1], Satomi Oda[2], Aya Sakazume[3], Ryoko Hisamochi[3], Taisei Miyata[3], Tatsuro Takahashi[1]

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P2-82

Single-molecular Condensin I and Topoisomerase IIα compact DNA

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P2-83(Session 18-8) **The RIF1-PP1 complex shapes DNA replication initiation zones to establish the replication timing program**

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