

The 2nd Annual Meeting for Whole-Organism Science Society

Joint Meeting with The 11th Annual Meeting of Structural-Biological Whole Cell Project

Program

Friday, September 28

<Symposium> Model Organisms (1)

Abstract No.

Chair Persons: Gota Kawai and Seiki Kuramitsu

13:30 – 14:00	Disruption of <i>Drosophila</i> serine palmitoyl transferase and acetyl-coA carboxylase cause tissue overgrowth associated with altered Notch and Wnt signaling	【1】
	○ Takeshi Sasamura ¹ , Kenji Matsuno ¹ , Mark E. Fortini ² (¹ Osaka Univ., ² Thomas Jefferson Univ.)	
14:00 – 14:30	<i>Halocynthia roretzi</i>, a Japanese ascidian species, as a model animal for the study of chordate embryogenesis	【4】
	○ Gaku Kumano, Naohito Takatori, Hiroki Nishida (Dep. of Biol. Sci., Grad. Sch. of Sci., Osaka Univ.)	
14:30 – 15:00	Reverse proteomics in fission yeast	【5】
	○ Akihisa Matsuyama, Minoru Yoshida (Chem. Genet. Lab., RIKEN Adv. Sci. Instit.)	
15:00 – 15:30	Functional profiling of the <i>E.coli</i> genes in long-term stationary phase - Application of new single gene deletion library with bar code tag -	【6】
	○ Hirotada Mori ¹ , Yuta Otsuka ¹ and Barry L. Wanner ² (¹ Grad. Sch. of Biol. Sci., Nara Inst. of Sci. and Technol., ² Dep. of Biol. Sci., Purdue Univ.)	
15:30 – 16:00	Coffee Break, Taking Photographs of All Members	

<Symposium> Imagings of SACLA and SPring-8

Abstract No.

Chair Persons: Masaki Yamamoto and Noritake Yasuoka

16:00 – 16:30	Molecular imaging of whole cells with coherent X-rays	【7】
	Changyong Song (RIKEN SPring-8 Center)	
16:30 – 17:00	Protein crystallography free from radiation damage at SACLA	【8】
	○ Hideo Ago ¹ , Go Ueno ¹ , Kunio Hirata ¹ , Takaaki, Hikima ¹ , Hironori Murakami ¹ , Eiki Yamashita ² , and Masaki Yamamoto ¹ (¹ RIKEN SPring-8 Center, ² Osaka Univ.)	
17:00 – 17:30	Achieved protein micro-crystallography at the micro-focus beamline BL32XU	【9】
	○ Kunio Hirata ¹ , Yoshiaki Kawano ¹ , Koichi Hashimoto ¹ , Go Ueno ¹ , Kazuya Hasegawa ^{1,2} , Hideo Okumura ² , Takashi Kumasaka ^{1,2} , and Masaki Yamamoto ¹ (¹ RIKEN/SPring-8 Center, ² JASRI/SPring-8)	

17:30 – 18:00 **SAXS & MD simulation to investigate protein flexibility in solution** 【10】

○Mamoru Sato¹, Mitsunori Ikeguchi¹, Tomotaka Oroguchi²

(¹Yokohama City Univ., ²Keio Univ.)

18:00 – 19:30 **Seminar Banquet (in Cafeteria)**

19:30 – 21:15 **Oral Presentation**

Chair Persons: Keiko Sakamoto, Hitoshi Iino, and Kenji Fukui

Quantification of mechanical force driving the left-handed twisting of the gut epithelial tube in *Drosophila* 【2】

○Naotaka Nakazawa^{1,3}, Reo Maeda¹, Shukei Sugita², Takeo Matsumoto², and Kenji Matsuno³

(¹Dept. Biol. Sci./Tec., Tokyo Univ. Sci., ²Dept. Mech. Eng., Nagoya Inst. Tech.,

³Dept. Biol. Sci., Osaka Univ.)

Control of cell number mediated by a *Drosophila* RhoGEF, Pebble, is required for left-right asymmetric development of the embryonic hindgut 【3】

○Mitsutoshi Nakamura^{1,2}, Kenjiro Matsumoto^{1,2}, Yuta Iwamoto^{1,2}, Takeshi Muguruma¹,

Naotaka Nakazawa^{1,2}, Ryo Hatori^{1,2}, Kiichiro Taniguchi¹, Reo Maeda¹, and Kenji Matsuno²

(¹Dep. Biol. Sci. and Technol., Tokyo Univ. Sci., ²Dep. Biol. Sci., Grad. Sch. of Sci., Osaka Univ.)

Functional profiling of the *E. coli* genes in long-term stationary phase

- Application of new single gene deletion library with bar code tag -

○Hirotada Mori¹, ○Yuta Otsuka¹ and Barry L. Wanner² (¹Grad. Sch. Biol. Sci., Nara Inst. Sci. and

Technol., ²Dep. Biol. Sci., Purdue University)

Substrate tRNA recognition mechanism of tRNA (m⁵U54) methyltransferase (TrmFO) based on biochemical analysis 【13】

○Ryota Yamagami¹, Koki Yamashita¹, Hiroshi Nishimasu², Chikako Iwashita¹, Akira Hirata¹,

Osamu Nureki², and Hiroyuki Hori^{1,3} (¹Dept. Materials Sci. Biotechnol., Grad. Sch. of

Sci. and Eng., Ehime Univ., ²Dept. of Basic Biophysic. and Biochem. Grad. Sch. of Sci., Univ. of Tokyo, ³VBL, Ehime Univ.)

Substrate tRNA recognition mechanism of eubacterial tRNA (m¹A58) methyltransferase (TrmI) from *Thermus thermophilus* 【14】

○Hiroyuki Takuma¹, Masayuki Minoji¹, Natumi Ushio¹, Chie Tomikawa¹, Akira Hirata¹,

Chikako Iwashita¹, Ochi Anna¹, and Hiroyuki Hori^{1,2} (¹Dept. of Materials Sci. and Biotechnol.,

Grad. Sch. of Sci. and Eng., Ehime Univ., ²VBL, Ehime Univ.)

Functional analysis of Yeast tRNA (m²G10) methyltransferase (Trm11-Trm12) 【15】

○Yu Nishida, Kazuki Okada, Akira Hirata, and Hiroyuki Hori (Dept. of Materials Sci. and

Biotechnol., Grad. Sch. of Sci. and Eng., Ehime Univ.)

Whole-cell research of *Thermus thermophilus* HB8: N-terminomics using MS/MS database 【21】

○Kwang Kim¹, Hiroki Okanishi¹, Kiyoshi Yamazaki², Teruo Yasunaga², Yoshitaka Bessho³, Ryoji

Masui^{1,3}, and Seiki Kuramitsu^{1,3} (¹Dept. Biol. Sci., Grad. Sch. Sci., Osaka Univ., ²Dept. of Genome

Informatics, Research Institute for Microbial Diseases, Osaka Univ, and ³RIKEN SPring-8 Center, Harima Institute.)

Whole-cell research of *Thermus thermophilus* HB8: role of RNases 【22】

○Hiromasa Ohya¹, Yoshihiro Agari², Kenji Fukui², Noriko Nakagawa^{1,2}, Akeo Shinkai²,

Seiki Kuramitsu^{1,2}, and Ryoji Masui^{1,2} (¹Dept. Biol. Sci., Grad. Sch. Sci., Osaka Univ.,

²RIKEN SPring-8 Center, Harima Inst.)

Whole cell research of *Thermus thermophilus* HB8: protein phosphorylation 【23】

○Yota Iio¹, Yoshio Takahata², Masao Inoue¹, Kwang Kim¹, Kenji Fukui³, Yoshihiro Agari³,

Akeo Shinkai³, Ryoji Masui^{1,3} and Seiki Kuramitsu^{1,2,3} (¹Dept. Biol. Sci., Grad. Sch. Sci.,

Osaka Univ., ²Grad. Sch. Frontier Biosci., Osaka Univ., and ³ RIKEN SPring-8 Center,

Harima Inst.)

- Nucleotide binding extremely stabilizes a protein kinase from *Thermus thermophilus* HB8** 【24】
 ○Takero Miyagawa¹, Ryoji Masui^{2,3} and Seiki Kuramitsu^{1,2,3} (¹Grad. Sch. Frontier Biosci., Osaka Univ., ²Grad. Sch. Sci., Osaka Univ., and ³RIKEN SPring-8 Center, Harima Inst.)
- Whole-cell research of *Thermus thermophilus* HB8: protein acetylation** 【25】
 ○Hiroki Okanishi¹, Kwang Kim¹, Ryoji Masui^{1,2}, and Seiki Kuramitsu^{1,2} (¹Dept. Biol. Sci., Grad. Sch. Sci., Osaka Univ.; ²RIKEN SPring-8 Center)
- RIKEN SPring-8 Center Protein Crystallography Database** 【27】
 ○Naoki Kunishima¹, Michihiro Sugahara¹, Tomoyuki Tanaka¹, Hisashi Naitow¹, Yoshihiro Agari¹, Akeo Shinkai¹, Seiki Kuramitsu¹, Koro Nishikata², Tetsuro Toyoda², Yukuhiko Asada¹ (¹RIKEN SPring-8 Center, ²RIKEN Bioinformatics and Systems Engineering Division)
- Functional analysis of TTC1871 LysR-type transcriptional regulator** 【30】
 ○Matsushita Hajime¹, Takeo Tomita¹, Tomohisa Kuzuyama¹, Makoto Nishiyama^{1,2}
 (¹Biotechnology Research Center, The University of Tokyo, ²RIKEN SPring-8 center)
- Analysis of structure-function relationships of homoisocitrate dehydrogenase homologs from *Sulfolobus acidocaldarius*** 【31】
 ○Kento Takahashi¹, Takeo Tomita¹, Tomohisa Kuzuyama¹, Makoto Nishiyama^{1,2}
 (¹Biotechnology Research Center, The University of Tokyo, ²RIKEN Spring-8)
- Analyses of interacting proteins with PilF and PilT from *Thermus thermophilus*** 【33】
 ○Takuto Yasuda¹, Ayumi koike¹ (¹Dept. Appl. Biosci., Grad. Sch. Eng., Kanagawa Inst. of Tech.)
- Developing a new disulfide formation assay using superfolder GFP** 【19】
 ○Yuma Mori, Takashi Tamura, Akio Ebihara, Seiki Kuramitsu, and Kenji Inagaki (Dept of Bioscience, Grad. Sch. Nat. Sci. & Tech., Okayama Univ.)
- Regulatory mechanism for endonuclease activity of the DNA mismatch repair endonuclease MutL** 【35】
 ○Kenji Fukui¹, Hitoshi Iino¹, Tatsuya Yamamoto², Kwang Kim³, Atsuhiro Shimada³, Seiki Kuramitsu^{1,3} (¹RIKEN Harima Inst., ²Keio Univ., ³Osaka Univ.)
- Small-angle X-ray scattering analysis of the DNA mismatch repair endonuclease** 【36】
 ○Hitoshi Iino¹, Takaaki Hikima¹, Seiki Kuramitsu^{1,2}, and Kenji Fukui¹ (¹RIKEN SPring-8 Center, ²Grad. Sch. of Sci. Osaka Univ.)
- MutS stimulates the endonuclease activity of MutL in an ATP hydrolysis-dependent manner** 【37】
 ○Atsuhiro Shimada¹, Ryoji Masui^{1,2}, Seiki Kuramitsu^{1,2}, and Kenji Fukui² (¹Grad. Sch. of Sci. Osaka Univ., ²RIKEN SPring-8 Center, Harima Inst.)
- Kinetic analysis of interactions between MutS and MutL involved in DNA mismatch repair** 【38】
 ○Yoshito Hata¹, Atsuhiro Shimada¹, Ryoji Masui^{1,2}, Kenji Fukui², and Seiki Kuramitsu^{1,2} (¹Dept. Biol. Sci., Grad. Sch. Sci., Osaka Univ., ²RIKEN SPring-8 Center, Harima Inst.)
- Molecular functional analysis of RadA/Sms protein, a bacterial RecA paralog** 【39】
 ○Masao Inoue¹, Kenji Fukui², Noriko Nakagawa^{1,2}, Ryoji Masui^{1,2}, and Seiki Kuramitsu^{1,2}
 (¹Dept. Biol. Sci., Grad. Sch. Sci., Osaka Univ., ²RIKEN SPring-8 Center, Harima Inst.)
- Genetic analysis of putative nucleases and helicases involved in double-strand break repair in *Thermus thermophilus* HB8** 【40】
 ○Yuki Fujii¹, Masao Inoue², Kenji Fukui³, Ryoji Masui^{2,3}, and Seiki Kuramitsu^{1,2,3} (¹Grad. Sch. Frontier Biosci., Osaka Univ., ²Grad. Sch. Sci., Osaka Univ., and ³RIKEN SPring-8 Center, Harima Inst.)
- Analysis of unique catalytic mechanism of exonuclease TTNA0118 from *Thermus thermophilus* HB8** 【41】
 ○Yuri Uemura¹, Taisuke Wakamatsu¹, Atsuhiro Shimada², Ryoji Masui^{2,3} and Seiki Kuramitsu^{1,2,3}
 (¹Grad. Sch. Frontier Biosci., Osaka Univ., ²Grad. Sch. Sci., Osaka Univ., ³RIKEN SPring-8 Center, Harima Inst.)
- Nucleoid-associated histone-like protein HU may act on RNA** 【42】
 ○Yuya Nishida¹, Noriko Nakagawa^{2,3}, Ryoji Masui^{2,3} and Seiki Kuramitsu^{1,2,3} (¹Grad. Sch. Frontier Biosci., Osaka Univ., ²RIKEN SPring-8 Center, Harima Inst., ³Grad. Sch. Sci., Osaka Univ.)

Identification of various types of post-translational modifications of the bacterial histone-like protein HU in *Thermus thermophilus* HB8

【43】

○Yoshiyuki Tochizawa¹, Yuya Nishida¹, Kwang Kim², Ryoji Masui^{2,3}, and Seiki Kuramitsu^{1,2,3}
(¹Grad. Sch. Frontier Biosci., Osaka Univ., ²Grad. Sch. Sci., Osaka Univ., and ³RIKEN SPring-8 Center, Harima Inst.)

Structural analysis of the heterodimer structure of the *T. thermophiles* tRNA modification enzymes, MnmE/MnmG using SAXS

【48】

○Aya Kitamura¹, Takaaki Hikima¹, Masaki Yamamoto¹, Kayoko Matsumoto¹, Toshi Arima¹, Kwang Kim², Seiki Kuramitsu^{1,2}, Yoshitaka Bessho¹ (RIKEN Spring-8 Center, Harima Inst., ²Dep. Biol. Sci., Grad. Sch. Sci., Osaka Univ.)

Crystal structure of PurC from *Sulfolobus tokodaii*

【50】

○Ryosuke Umebayashi¹, Mayumi Kanagawa², Seiki Baba^{2,3}, Gota Kawai^{2,4}, and Gen-ichi Sampei^{1,2}
(¹Univ. Electro-Commun., ²RIKEN SPring-8 Center, ³SPring-8/JASRI, ⁴Chiba Inst. Tech.)

Crystal structure of PurU from *Thermus thermophilus* HB8

【51】

○Yuki Yanagida¹, Naoki Ogata¹, Mayumi Kusano², Mayumi Kanagawa³, Yumiko Inoue³, Seiki Baba^{3,4}, Gota Kawai^{2,3}, and Gen-ichi Sampei^{1,3} (¹Univ. Electro-Commun., ²Chiba Inst. Tech., ³RIKEN SPring-8 Center, ⁴SPring-8/JASRI)

Reaction mechanisms of the two related enzymes, PurN and PurU

【52】

Mayumi Kusano¹, Toshiaki Shimasaki¹, Gen-ichi Sampei^{2,3} and ○Gota Kawai^{1,3} (¹Chiba Inst. Tech., ²Univ. Electro-Commun., ³RIKEN SPring-8 Center)

Nucleoside salvage pathway in *Thermus thermophilus* HB8

【53】

○Fumiaki Tomoike¹, Noriko Nakagawa^{2,3}, Seiki Kuramitsu^{1,2,3}, and Ryoji Masui^{2,3} (¹Grad. Sch. Frontier Biosci., Osaka Univ., ²Grad. Sch. Sci., Osaka Univ., ³RIKEN SPring-8 Center.)

Mn-catalase as a primary scavenger of intracellular hydrogen peroxide in *Thermus thermophilus*

【54】

○Akio Ebihara^{1,2}, Miho Manzoku¹, Kenji Fukui¹, Seiki Kuramitsu^{1,3} (¹RIKEN SPring-8 Center, ²Gifu Univ., ³Osaka Univ.)

Whole-cell research of *Thermus thermophilus* HB8: metabolism via whole-cell proteomics

【55】

○Kwang Kim¹, Hiroki Okanishi¹, Ryoji Masui^{1,2}, and Seiki Kuramitsu^{1,2} (¹Dept. Biol. Sci., Grad. Sch. Sci., Osaka Univ., and ²RIKEN SPring-8 Center, Harima Inst.)

21:15 – 22:00 **Poster Discussion and Mixer**

Saturday, September 29

8:30 – 9:00 **Morning Poster Discussion**

<Symposium> Model Organisms (2) : Thermophiles etc.

Abstract No.

Chair Persons: Hiroyuki Hori and Ken Hirotsu

9:00 – 9:10 **Visiting Yellowstone National Park, the place of discovery of thermophiles** 【11】

Hiroyuki Hori

(Ehime Univ.)

9:10 – 9:30 **Adaptation of *Thermus thermophilus* to environmental temperature via tRNA modification enzymes-modified nucleotides network in tRNA** 【12】

Chie Tomikawa¹, Kazuo Ishida¹, Takashi Kunibayashi¹, Anna Ochi¹, Tamotsu Kanai², Akira Hirata¹, Chikako Iwashita¹, and ○Hiroyuki Hori^{1,3}

(¹Grad. Sch. of Sci. and Eng., Ehime Univ., ²Grad. Sch. of Eng., Kyoto Univ., ³VBL, Ehime Univ.)

9:30 – 10:00 **Studies on molecular recognition by tylosin-resistance methyltransferase enzyme** 【16】

Satoko Yoshizawa

(Centre de Génétique Moléculaire UPR 3404, CNRS, Université Paris-Sud)

10:00 – 10:30 **Functions of Genes Involved in Polyamine Biosynthesis in *Thermus thermophilus*** 【17】

○Tairo Oshima¹, Toshiyuki Moriya¹, Yumiko Takeda², Toshihiro Ohta², Yuka Niiya³, Toshiro Iwaki³, and Masami Ishida³

(¹Inst of Envir. Microbiol., Kyowa-kako Co., ²The Dep. of Envir. Genomics, Tokyo Univ. of Pharm. and Life Sci., ³The Grad. Sch. of Marine and Technol., Tokyo Univ. of Marine Sci. and Technol.)

10:30 – 11:00 **A trial to predict DNA-binding residues and their target sequences of transcription factors** 【18】

Ayumi Numazawa, ○Kei Yura (Ochanomizu Univ.)

11:00 – 11:30 **Poster Discussion**

11:30 – 12:15 **Lunch Break**

12:15 – 12:30 **General Assembly (学会総会)**

<Symposium> Model Organisms (3) : Extreme Thermophiles etc. Abstract No.

Chair Persons: Tairo Oshima and Takashi Tamura

12:30 – 12:45	Curation of genome annotation of <i>Thermus thermophilus</i> HB8	【20】
	○Ryoji Masui ^{1,2} and Seiki Kuramitsu ^{1,2} (¹ Grad. Sch. Sci., Osaka Univ., ² RIKEN SPring-8 Center)	
12:45 – 13:00	Thermophiles resources, fission yeast resources and other genetic materials at RIKEN BioResource Center	【26】
	○Takehide Murata, Masato Okubo, Shotaro Kishikawa, Yukari Kujime, Chitose Kurihara, Megumi Sakayori, Koji Nakade, Satoko Masuzaki, Takahito Yamasaki, and Yuichi Obata (Gene Engineering Division, RIKEN BioResource Center)	
13:00 – 13:15	An L-glucose catabolic pathway in <i>Paracoccus</i> sp. 43P	【28】
	Tetsu Shimizu, Naoki Takaya, and ○Akira Nakamura (Faculty of Life Environ. Sci., University of Tsukuba)	
13:15 – 13:30	Substrate recognition mechanism of a homolog of homoisocitrate dehydrogenase from <i>Thermococcus kodakarensis</i>, TK0280	【29】
	○Takeo Tomita ¹ , Yin Lu Lu ¹ , Kento Takahashi ¹ , Haruyuki Atomii ² , Tomohisa Kuzuyama ¹ , Makoto Nishiyama ^{1,3} (¹ Biotechnology Research Center, The University of Tokyo, ² Grad. Sch. of Eng., Kyoto Univ., ³ RIKEN SPring-8 Center)	
13:30 – 13:45	Type IV pilus structural protein of <i>Thermus thermophilus</i> HB8 and HB27	【32】
	○Masatada Tamakoshi ^{1,2} , Hibiki Itoga ¹ , Satoshi Akanuma ¹ , Akihiko Yamagishi ¹ (¹ Dept. Mol. Biol., Tokyo Univ. of Pharm. Life Sci., ² RIKEN SPring-8 Center, Harima Institute)	
13:45 – 14:00	A comparative study on homologous recombination mediators from <i>T. thermophilus</i>	【34】
	○Takeshi Shinohara ^{1,2} , Tatsuhiko Inoue ³ , Ryouji Masui ³ , Seiki Kuramitsu ³ , Takehiko Shibata ^{1,2} , Tsutomu Mikawa ² (¹ Grad. Sch. Nanobiosci., Yokohama City Univ., ² RIKEN Adv. Sci. Inst., ³ Department of Biological Sciences, Graduate School of Science, Osaka University)	
14:00 – 14:15	Coffee Break	
	Chair Persons: Yoshinori Koyama and Tsutomu Mikawa	
14:15 – 14:30	Functional identification of transcriptional regulators from <i>T. thermophilus</i> HB8	【44】
	Akeo Shinkai (RIKEN SPring-8 Center, Harima Inst.)	
14:30 – 14:45	Structural and functional analysis of TetR family transcriptional regulator PfmR from <i>Thermus thermophilus</i> HB8	【45】
	○Yoshihiro Agari, Keiko Sakamoto, Akeo Shinkai (RIKEN SPring-8 Center, Harima Inst.)	
14:45 – 15:00	Structural and functional analysis of TetR family transcriptional regulator TTHA0167 from <i>T. thermophilus</i> HB8	【46】
	○Keiko Sakamoto, Yoshihiro Agari, Akeo Shinkai (RIKEN SPring-8 Center, Harima Inst.)	

15:00 – 15:15	Research and development of bio-molecular imaging technology at SPring-8/SACLA	【47】
	○Yoshitaka Bessho ¹ , Yasumasa Joti ² , Takashi Kimura ³ , Aya Kitamura ¹ , Akemi Shibuya ¹ , Masami Ueta ⁴ , Akira Wada ⁴ , Shoji Takeuchi ⁵ , Toshifumi Sakaguchi ⁶ , Tamakoshi Masatada ⁷ , Shota Nitahara ⁷ , Toshiyuki Moriya ⁸ , Tairo Oshima ⁸ , Yoshinori Nishino ³	
	(¹ RIKEN Spring-8 Center, ² XFEL division, JASRI, ³ RIES, Hokkaido Univ., ⁴ Yoshida Biol. Lab. ⁵ Tokyo Univ., ⁶ Pref. Univ. Hiroshima, ⁷ Tokyo Univ. of Pharm. and Life Sci., ⁸ Kyowa-kako Co. Ltd.)	
15:15 – 15:30	Origin and evolution of the enzymes in the purine biosynthetic pathway: an analysis in view of protein structures	【49】
	○Gen-ichi Sampei ^{1,2} , Seiki Baba ^{2,3} , Mayumi Kanagawa ² , Gota Kawai ^{2,4}	
	(¹ Univ. Electro-Commun., ² RIKEN SPring-8 Center, ³ SPring8/JASRI, ⁴ Chiba Inst. Tech.)	
15:30 – 15:45	Example of genome-based identification of novel enzymatic activity and metabolic pathway	【56】
	Yutaka Kawarabayashi (Lab. for Func. Genomics of Extremophiles, Kyushu Univ.)	
15:45 – 16:00	Award Ceremony	
	Tairo Oshima (President)	