

The 3rd Annual Meeting for Whole-Organism Science Society
Joint Meeting with
The 12th Annual Meeting of Structural-Biological Whole Cell Project

The 3rd Annual Meeting for Whole-Organism Science Society

Joint Meeting with

**The 12th Annual Meeting of
Structural-Biological Whole Cell Project**

September 21 (Sat) - 22 (Sun), 2013

Engineering Science International Bldg. (Sigma Hall)
School/Graduate School of Engineering Science,
TOYONAKA campus, Osaka University, Toyonaka, Osaka, Japan

<http://www.thermus.org/>

The 3rd Annual Meeting for Whole-Organism Science Society
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The 12th Annual Meeting of Structural-Biological Whole Cell Project

PROGRAM

Saturday, September 21

13:00 – 13:10 **Introduction**
Seiki Kuramitsu

13:10 – 16:00 **<Symposium> Model Organisms (1)** Abstract No.
Multicellular Organisms

Chair persons: Tomoko Yamakawa and Ryoji Masui
13:10 – 13:50 ***Oikopleura dioica* ホヤ**
A new model organism in developmental genetics: 【1】
The appendicularian, *Oikopleura dioica*
発生遺伝学の新しいモデル生物、ワカレオタマボヤの紹介と研究の現状
°Takeshi A. Onuma, Kanae Kishi, Tatsuya Omotezako, and Hiroki Nishida
(Dept. of Biol. Sci., Grad. Sch. of Sci., Osaka Univ.)

13:50 – 14:30 ***Caenorhabditis elegans* 線虫** 【2】
A neuronal algorithm for spatial navigation in the nematode *C. elegans*.
°Kotaro Kimura
(Dept. of Biol. Sci., Grad. Sch. of Sci., Osaka Univ.)

Chair persons: Kotaro Kimura and Kazumi Nishijima
14:30 – 15:30 ***Drosophila melanogaster* ショウジョウバエ** 【3】
Studies on mechanisms of development using *Drosophila* genetics
ショウジョウバエの遺伝学を用いた発生機構の研究
°Kenji Matsuno
(Dept. of Biol. Sci., Grad. Sch. of Sci., Osaka Univ.)

**Identification of genetic modifiers that interact with pecanex,
encoding a component of Notch signaling in *Drosophila*** 【4】
Notch シグナル伝達系構成因子、Pecanex と遺伝的に相互作用する調節遺伝子の
網羅的探索
°Tomoko Yamakawa¹, Yu Atsumi², Shiori Kubo¹, and Kenji Matsuno¹
(¹Dept. of Biol. Sci., Grad. Sch. of Sci., Osaka Univ.; ²Dept. of Biol. Sci./Tec.,
Tokyo Univ. of Sci.)

**Quantification of mechanical force driving the left-right asymmetric of
the gut in *Drosophila*** 【5】
ショウジョウバエ胚消化管の左右非対称製を生み出す機械的な力の定量化
°Mai Adachi¹, Naotaka Nakazawa^{1,2}, Reo Maeda², Shukei Sugita³, Takeo Matsumoto³,
and Kenji Matsuno¹
(¹Dept. of Biol. Sci., Grad. Sch. of Sci., Osaka Univ.; ²Dept. of Biol. Sci / Tec.;
Tokyo Univ. of Sci., ³Dept. of Mech. Eng., Nagoya Inst. of Tech.)

15:30 – 16:00 **Model Organisms: Resources**

**Large amount genetic resources in the Gene Engineering Division,
RIKEN BioResource Center**

◦Takehiko 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)

【10】

16:00 – 16:15 **Break, Taking Photographs of Members**

16:15 – 17:30 **Oral Presentation**

Abstract No.

Chair persons: Tomoko Yamakawa and Yuya Nishida

***Drosophila melanogaster* ショウジョウバエ**

**Identification of genetic modifiers that interact with pecanex,
encoding a Notch signaling component in *Drosophila***

◦Shiori Kubo¹, Tomoko Yamakawa¹, Yu Atsumi², and Kenji Matsuno¹
(¹Dept. of Biol. Sci., Grad. Sch. of Sci., Osaka Univ.;
²Dept. of Biol. Sci., Grad. Sch. of Sci./Tec., Tokyo Univ. of Science.)

【6】

***Drosophila melanogaster* ショウジョウバエ**

**Roles of the embryonic midline as a global cue for the formation of cell polarity in
*Drosophila***

細胞極性の形成中心としてのショウジョウバエ胚正中線の機能
◦Alice Tsuboi¹, Reo Maeda², Ryo Hatori^{1,2}, Takeshi Sasamura¹, and Kenji Matsuno¹
(¹Dept. of Biol. Sci., Grad. Sch. of Sci., Osaka Univ.;
²Dept. of Biol. Sci., Grad. Sch. of Sci./Tec., Tokyo Univ. of Science.)

【7】

***Drosophila melanogaster* ショウジョウバエ**

The role of glycan modifications of Notch receptor in *Drosophila* Notchsignali

ショウジョウバエ Notch シグナルにおける Notch 受容体の糖鎖修飾の機能
◦Kenjiro Matsumoto, Akira Ishio, Takeshi Sasamura, Tomoko Yamakawa,
and Kenji Matsuno
(Dept. Biol. Sci., Grad. Sch. Sci., Osaka Univ.)

【8】

***Drosophila melanogaster* ショウジョウバエ**

**Disruption of *Drosophila melanogaster* lipid metabolism genes causes tissue overgrowth
associated with altered developmental signaling**

ショウジョウバエ脂質合成酵素の欠損はシグナル伝達系の制御に異常をきたし、
細胞の過増殖を引き起こす
◦Takeshi Sasamura¹, Kenji Matsuno¹, and Mark E. Fortini²
(¹Dept. Biol. Sci., Grad. Sch. Sci., Osaka Univ.; ²Thomas Jefferson Univ.)

【9】

Imaging: By Calculation 計算機科学によるイメージング

Difference of Hydrogen-Bond Strengths Makes Functional Difference in Rhodopsin

ロドプシンの機能に違いを生み出す水素結合強度の違い
◦Keisuke Saito^{1,2}, Hideki Kandori³, and Hiroshi Ishikita¹
(¹Osaka Univ., ²JST PRESTO; ³Nagoya Inst. of Tech.)

【15】

Imaging: By Calculation 計算機科学によるイメージング

Linear response approach to QM/MM boundary problem

【17】

QM/MM 境界問題に対する線形応答関数アプローチ

◦Shusuke Yamanaka¹, Kazuto Nakata², Yasutaka Kitagawa¹, Takashi Kawakami¹,
Kizashi Yamaguchi², Mitsutaka Okumura¹, and Haruki Nakamura¹
(¹Osaka Univ.; ²NEC Corp.)

***Thermus thermophilus HB8* 高度好熱菌**

【20】

Purification and characterization of *Thermus thermophilus* UvrD

◦Yukari Iikura, Takehiko Shibata, and Tsutomu Mikawa
(Cell. Mol. Biol. RIKEN)

***Thermus thermophilus HB8* 高度好熱菌**

【21】

Functional analysis of RadA/Sms, a bacterial RecA paralog involved in homologous recombination

DNA 相同組換えに関する RecA パラログ蛋白質 RadA/Sms の機能解析

◦Masao Inoue¹, Yuki Fujii², Kenji Fukui¹, Noriko Nakagawa¹, Ryoji Masui¹,
and Seiki Kuramitsu^{1,2}
(¹Dept. Biol. Sci., Grad. Sch. Sci., Osaka Univ.; ²Grad. Sch. Frontier Biosci., Osaka Univ.)

***Thermus thermophilus HB8* 高度好熱菌**

【22】

Archaeal-type nuclease/helicase, NurA/HerA,

are involved in decreased tolerance to UV irradiation in *Thermus thermophilus HB8*.

Thermus thermophilus HB8 由来アーキア型ヌクレアーゼ・ヘリカーゼ NurA/ HerA
は紫外線耐性の低下をもたらす。

◦Yuki Fujii¹, Masao Inoue², Kenji Fukui², Ryoji Masui², and Seiki Kuramitsu^{1,2}

(¹Grad. Sch. Frontier Biosci., Osaka Univ.; ²Dept. Bio. Sci., Grad. Sch. Sci., Osaka Univ.)

***Thermus thermophilus HB8* 高度好熱菌**

【23】

Thermostable DNA repair protein suppresses errors in PCR

◦Kenji Fukui, Ryoji Masui, and Seiki Kuramitsu

(Dept. Biol. Sci., Grad. Sch. Sci., Osaka Univ.)

***Thermus thermophilus HB8* 高度好熱菌**

【27】

Mechanism for hyper-sensitivity to lysine analogue of *Thermus thermophilus* HB27

高度好熱菌 *Thermus thermophilus* HB27 のリジンアナログ超感受性機構の解析

Yuko Kanemaru¹, Fumihito Hasebe¹, [◦]Takeo Tomita¹,
Tomohisa Kuzuyama¹, and Makoto Nishiyama^{1,2}

(¹Biotechnology Research Center, The University of Tokyo; ²RIKEN SPring-8 Center)

***Sulfolobus acidocaldarius* 好熱性古細菌**

【28】

Analysis of transcriptional regulation mechanism of amino acid biosynthetic genes in thermoacidophilic archaeon *Sulfolobus acidocaldarius*

超好熱・好酸性古細菌 *Sulfolobus acidocaldarius* におけるアミノ酸合成酵素の
転写調節機構の解析

◦Nagisa Akiyama, Takeo Tomita, Tomohisa Kuzuyama, and Makoto Nishiyama
(Biotechnology Research Center, The Univ. of Tokyo)

***Thermus thermophilus HB8* 高度好熱菌**

【30】

Structural and functional analyses of formylglycinamide ribonucleotide amidotransferase

ホルミルグリシンアミドリボヌクレオチドアミドトランスクレオチダーゼの構造機能解析

◦Yuzo Watanabe¹, Gen-ichi Sampei², and Gota Kawai¹

(¹Chiba Inst. Tech.; ²Univ. Electro-Commun.)

Thermus thermophilus HB8 高度好熱菌

Crystal structures of MqnD, a menaquinone biosynthetic enzyme from *Thermus thermophilus*, complexed with the product, 1,4-dihydroxy-6-naphthoate, and its analogs [31]

°Ryoichi Arai¹, Kyoko Matsuo¹ and Tohru Dairi²

(¹Fac. of Tex. Sci. & Tech., Shinshu Univ.; ²Grad. Sch. of Eng., Hokkaido Univ.)

Thermus thermophilus HB8 高度好熱菌

Purification and structural analysis of PilQ in the *Thermus thermophilus* [32]

Thermus thermophilus 由来線毛関連タンパク質 PilQ の精製および構造解析

°Ayumi Sasaki¹, Hiroki Kasai¹, Masatada Tamakoshi², and Ayumi Koike-Takeshita¹

(¹Dept. Appl. Biosci., Grad. Sch. Eng., Kanagawa Inst. of Tech.; ²Tokyo Univ. Pharm. and Life Sci.)

Thermus thermophilus HB8 高度好熱菌

Analyses of interacting proteins with PilF and PilT from *Thermus thermophilus*. [33]

高度好熱性細菌 *Thermus thermophilus* 由来 線毛関連タンパク質 PilF, PilT 相互作用タンパク質の解析

°Takuto Yasuda¹, Masatada Tamakoshi², and Ayumi Koike-Takeshita¹

(¹Dept. Appl. Biosci., Grad. Sch. Eng., Kanagawa Inst. of Tech.; ²Tokyo Univ. Pharm. and Life Sci.)

Thermus thermophilus HB8 高度好熱菌

Whole-cell research of *Thermus thermophilus* HB8:

[37]

Proteome-wide analysis of protein acetylation

高度好熱菌丸ごと一匹解析：蛋白質アセチル化の網羅的解析

°Hiroki Okanishi, Kwang Kim, Ryoji Masui, and Seiki Kuramitsu
(Dept. Biol. Sci., Grad. Sch. Sci., Osaka Univ.)

Thermus thermophilus HB8 高度好熱菌

Whole-cell research of *Thermus thermophilus* HB8: Protein phosphorylation [38]

高度好熱菌丸ごと一匹解析：タンパク質のリン酸化修飾

°Yota Iio¹, Yoshio Takahata², Masao Inoue¹, Kim Kwang¹, Kenji Fukui¹, Yoshihiro Agari³, Akeo Shinkai³, Ryoji Masui¹ and Seiki Kuramitsu^{1,2}

(¹Dept. Biol. Sci., Grad. Sch. Sci., Osaka Univ.; ²Grad. Sch. Frontier Biosci., Osaka Univ.;
³RIKEN SPring-8 Center)

Thermus thermophilus HB8 高度好熱菌

Biochemical and genetic analyses of a functionally unknown protein from *Thermus thermophilus* HB8 [39]

高度好熱菌 *Thermus thermophilus* HB8 由来機能未知タンパク質の生化学的・遺伝学的解析

°Takero Miyagawa¹, Yota Iio², Ryoji Masui² and Seiki Kuramitsu^{1,2}

(¹Grad. Sch. Frontier Biosci., Osaka Univ; ²Dept. Biol. Sci., Grad. Sch. Sci., Osaka Univ.)

Thermus thermophilus HB8 高度好熱菌

[40]

Whole-Cell Research of *Thermus thermophilus* HB8: Role of RNases

°Hiromasa Ohyama¹, Yoshihiro Agari², Kenji Fukui², Noriko Nakagawa¹, Akeo Shinkai², Seiki Kuramitsu¹, and Ryoji Masui¹

(¹Dept. Biol. Sci., Grad. Sch. Sci., Osaka Univ. ²RIKEN SPring-8 Center, Harima Inst.)

Thermus thermophilus HB8 高度好熱菌

**The Depth Analysis of *Thermus thermophilus* Exonuclease I
by Real-time Activity Measurement**

[41]

リアルタイムの活性測定による高度好熱菌由来エキソヌクレアーゼの詳細な解析

°Tomofumi Sakai¹, Atsuhiro Shimada², Kim Kwang², Ryoji Masui², and Seiki Kuramitsu^{1,2}

(¹Grad. Sch. Frontier Biosci., Osaka Univ.; ²Grad. Sch. Sci. Bio., Osaka Univ.)

Thermus thermophilus HB8 高度好熱菌

**Insights of functional DNA binding of the bacterial histone-like protein HU
in *Thermus thermophilus* HB8**

[42]

°Yoshiyuki Tochizawa¹, Yuya Nishida¹, Yosuke Toyotake¹, Hiroki Okanishi²,

Kwang Kim², Ryoji Masui², and Seiki Kuramitsu^{1,2}

(¹Grad. Sch. Frontier Biosci., Osaka Univ.; ²Dept. Biol. Sci., Grad. Sch. Sci., Osaka Univ.)

Thermus thermophilus HB8 高度好熱菌

Nucleoid-associated protein HU may act on RNA

[43]

核様体構成タンパク質である HU が RNA と働く可能性について

°Yuya Nishida¹, Noriko Nakagawa², Ryoji Masui², and Seiki Kuramitsu^{1,2}

(¹Grad. Sch. Frontier Biosci., Osaka Univ.; ² Dept. Biol. Sci., Grad. Sch. Sci., Osaka Univ.)

17:30 – 18:15 **Poster Discussion (odd number)**

18:15 – 19:00 **Poster Discussion (even number)**

19:00 – 21:00 **Banquet** (BBQ style with local Minoh Beer (<http://www.minoh-beer.jp/>))

Sunday, September 22

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

9:00 – 12:20 **<Symposium> Model Organisms (2) and Intracellular Network/Modeling** Abstract No.

Chair Persons: Gen-ichi Sampei and Akira Nakamura

9:00 – 9:40 ***Thermus thermophilus* HB8 高度好熱菌**
Genes and enzymes involved in biosyntheses of unusual polyamines in *Thermus thermophilus* HB8 【11】
°Tairo Oshima¹, Toshiyuki Moriya¹, and Shinnosuke Fujiwara²
(¹Inst. Environ. Microbiol., Kyowa-kako Co.; ²Technol. Kwasei Gakuin Univ.)

9:40 – 10:20 ***Escherichia coli* 大腸菌**
Towards complete understanding of the physiological network system of *E. coli* 【12】
大腸菌全細胞機能ネットワーク解明に向けて
°Hirotada Mori

10:20 – 11:00 ***Escherichia coli* 大腸菌**
Towards whole genome-scale modeling of *E. coli* 【13】
大腸菌全ゲノムモデリングプロジェクトの構想
°Koichi Takahashi
(Laboratory for Biochemical Simulation, Computer Biology Research Core,
RIKEN Quantitative Biology Center)

11:00 – 11:10 **Model Organism モデル生物**
Systems metabolic engineering –Toward rational design of microbial cell factories 【45】
システムズ代謝工学にむけた代謝解析技術の開発
°Fumio Matsuda, Katsunori Yoshikawa, Yoshihiro Toya, and Shimizu Hiroshi
(Department of Bioinformatic Engineering, Osaka University)

11:10 – 11:50 **Chair Persons: Noritake Yasuoka and Seiki Kuramitsu**
Model Organisms モデル生物 【14】
X 線結晶構造解析では見えにくい「H⁺」から蛋白質の光反応を見る
°Hiroshi Ishikita
(Dept. Biol. Sci., Grad. Sch. Sci., Osaka Univ.)

11:50 – 12:30 **Model Organisms モデル生物** 【16】
DFT studies on importance of hydrogen bonds in active sites
Yasutaka Kitagawa, Hiroyuki Nakano, Yuka Iwasaki, Natsumi Yasuda,
Takashi Kawakami, Shusuke Yamanaka, and Mitsutaka Okumura
(Dept. Chem., Grad. Sch. Sci., Osaka Univ.)

12:30 – 13:30 **Lunch Break**

13:30 – 14:00 **Poster Discussion**

14:00 – 14:15 General Assembly (学会総会)

14:15 – 17:10 <Symposium> Model Organisms (3)

Abstract No.

Chair Persons: Kei Yura and Ryoji Masui

14:15 – 14:35 Model Organisms: Data bases

To open up and explore Structural Life Science Data Cloud (SLS_DC)

[46]

構造生命科学データクラウドの未来を拓く・序章

Hideaki Sugawara

(National Institute of Genetics)

14:35 – 15:20 *Thermus thermophilus* HB8 高度好熱菌

Regulatory mechanism of DNA recombinational repair in bacteria

[18]

バクテリアにおけるDNA組換え修復の制御機構

Tsutomu Mikawa *et al.*

(Cellular & Molecular Biology Unit, RIKEN)

C-terminal acidic region of *Thermus thermophilus* RecA play a role in dissociation from DNA

[19]

◦ Takeshi Shinohara^{1,2}, Takehiko Shibata^{1,2}, and Tsutomu Mikawa²

(¹Grad. Sch. Nanobiosci., Yokohama City Univ.; ²Cell. & Mol. Biol.Unit, RIKEN)

15:20 – 15:40 *T. thermophilus* and the Other Model Organisms 高度好熱菌を含むモデル生物

Hiroyuki Hori Lab., Ehime University

Thermus thermophilus HB8 高度好熱菌

Does D20 formation by eubacterial dihydrouridine synthase require the other modified nucleotides for its modification in tRNA ?

[24]

真正細菌ジヒドロウリジン合成酵素のD20形成は

tRNA上の他の修飾ヌクレオチドを必要とするのか？

◦ H. Kusuba¹, T. Yoshida¹, E. Iwasaki¹, T. Awai¹,

A. Hirata¹, C. Tomikawa¹, R. Yamagami¹, and H. Hori^{1,2}

(¹Grad. Sch. Sci. and Eng., Ehime Univ.; ²VBL, Ehime Univ.)

Saccharomyces cerevisiae 出芽酵母

Eukaryotic tRNA (m²G10) methyltransferase (Trm11-Trm112) recognizes the whole structure of tRNA

[25]

Yeast tRNA (m2G10) methyltransferase (Trm11-Trm112) 基質認識機構構造の解明

◦ Shiro Ohmori¹, Yu Nishida¹, Kazuki Okada¹, Akira Hirata¹, and Hiroyuki Hori^{1,2}

(¹Department of Materials Science and Biotechnology, Graduate School of Science and Engineering, Ehime University; ²VBL, Ehime University)

Thermus thermophilus 高度好熱菌

Establishment of the large-scale purification method of tRNA using solid phase DNA probe

[26]

固相化DNAプローブ法を用いた好熱菌tRNAの大量精製法の確立

◦ Ai Kazayama¹, Ryota Yamagami¹, Takashi Yokogawa², and Hiroyuki Hori^{1,3}

(¹Grad. Sch. Sci. and Eng., Ehime Univ.; ²Grad. Sch. Eng., Gifu Univ., ³VBL, Ehime Univ.)

- 15:40 – 16:10 ***T. thermophilus* and the Other Model Organisms 高度好熱菌を含むモデル生物** [29]
Molecular evolution of the enzymes in the purine biosynthetic pathway
プリンヌクレオチド生合成系酵素群の分子進化
°Gota Kawai¹, Yuzo Watanabe¹, and Gen-ichi Sampei²
(¹Chiba Inst. Tech.; ²Univ. Electro-Commun.)
- Chair persons: Tairo Oshima and Kenji Matsuno
- 16:10 – 16:40 ***Thermus thermophilus* HB8 高度好熱菌** [35]
Beyond structural genomics of *Thermus thermophilus* HB8:
Post-translational modification
°Ryoji Masui¹, Kwang Kim¹, Yoshio Takahata², Hiroki Okanishi¹, Masao Inoue¹,
Yota Iio¹, Takero Miyagawa², Noriko Nakagawa¹, Akeo Shinki³,
and Seiki Kuramitsu^{1,2}
(¹Dept. Biol. Sci., Grad. Sch. Sci. Osaka Univ.; ²Grad. Sch. Frontier Biosci., Osaka
Univ.; ³RIKEN Spring-8 Center)
- Proteome analysis of RNase knock-out mutants by AMT technique** [36]
°Kwang Kim¹, Hiromasa Ohyama¹, Hiroki Okanishi¹, Tomofumi Sakai²,
Ryoji Masui¹, and Seiki Kuramitsu^{1,2}
(¹Dept. Biol. Sci., Grad. Sch. Sci., Osaka Univ.; ²Grad. Sch. Frontier Biosciences,
Osaka Univ.)
- 16:40 – 17:10 ***Thermus thermophilus* HB8 高度好熱菌** [44]
Prediction of DNA-binding sites on transcription factors
and their target DNA sequences
Ayumi Numazawa¹ and °Kei Yura^{1,2}
(¹Department of Life Sciences, Graduate School of Humanities and Sciences,
Ochanomizu University; ²Center for Informational Biology, Ochanomizu University)
- 17:10 – 17:20 **Award Ceremony**
Tairo Oshima (President)

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ABSTRACTS

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Photographs



The 1st Annual meeting



The 2nd Annual meeting

2003.8.2



The 3rd Annual meeting



The 4th Annual meeting



The 5th Annual meeting

The 3rd Annual Meeting for Whole-Organism Science Society
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The 12th Annual Meeting of Structural-Biological Whole Cell Project



The 6th Annual meeting



The 7th Annual meeting



The 8th Annual meeting



The 9th Annual meeting



The 10th Annual meeting



The 11th Annual meeting

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MAP

