

**The 2nd Annual Meeting for
Whole-Organism Science Society**
Joint Meeting with
**The 11th Annual Meeting of
Structural-Biological Whole Cell Project**



September 28 (Fri) - 29 (Sat), 2012
Public Relations Center

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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 *Drosophila* serine palmitoyl transferase and acetyl-coA carboxylase cause tissue overgrowth associated with altered Notch and Wnt signaling** [1]
○Takeshi Sasamura¹, Kenji Matsuno¹, Mark E. Fortini²
(¹Osaka Univ., ²Thomas Jefferson Univ.)
- 14:00 – 14:30 ***Halocynthia roretzi*, 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 *E.coli* genes in long-term stationary phase - Application of new single gene deletion library with bar code tag -** [6]
○Hirotsada Mori¹, Yuta Otsuka¹ and Barry L. Wanner²
(¹Grad. Sch. of Biol. Sci., Nara Inst. of Sci. and Technol.,
²Dep. 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 Ago¹, Go Ueno¹, Kunio Hirata¹, Takaaki, Hikima¹, Hironori Murakami¹, Eiki Yamashita², and Masaki Yamamoto¹
(¹RIKEN SPring-8 Center, ²Osaka Univ.)
- 17:00 – 17:30 **Achieved protein micro-crystallography at the micro-focus beamline BL32XU** [9]
○Kunio Hirata¹, Yoshiaki Kawano¹, Koichi Hashimoto¹, Go Ueno¹, Kazuya Hasegawa^{1,2}, Hideo Okumura², Takashi Kumasaka^{1,2}, and Masaki Yamamoto¹
(¹RIKEN/SPring-8 Center, ²JASRI/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}, Kenjiroo 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 - [6]

Hirotsada 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-Trm112) [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 Ohyama¹, 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 ³RIKEN SPring-8 Center, Harima Inst.)

- Nucleotide binding extremely stabilizes a protein kinase from *Thermus thermophilus* HB8** [24]
 ○Takeo 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, Atsuhiko 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]
 ○Atsuhiko 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, Atsuhiko 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 TTHA0118 from *Thermus thermophilus* HB8** [41]
 ○Yuri Uemura¹, Taisuke Wakamatsu¹, Atsuhiko 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. thermophilus* 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 (¹RIKEN Spring-8 Center, Harima Inst., ²Dep. Biol. Sci., Grad. Sch. Sci., Osaka Univ.)
- Crystal structure of PurC from *Sulfolobus tokodaii*** [50]
 ○Ryosuke Umabayashi¹, 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.)

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 *Thermus thermophilus* HB8** [20]
○Ryoji Masui^{1,2} and Seiki Kuramitsu^{1,2}
(¹Grad. Sch. Sci., Osaka Univ., ²RIKEN 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 *Paracoccus* 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 *Thermococcus kodakarensis*, TK0280** [29]
○Takeo Tomita¹, Yin Lu Lu¹, Kento Takahashi¹, Haruyuki Atomi², Tomohisa Kuzuyama¹, Makoto Nishiyama^{1,3}
(¹Biotechnology Research Center, The University of Tokyo, ²Grad. Sch. of Eng., Kyoto Univ., ³RIKEN SPring-8 Center)
- 13:30 – 13:45 **Type IV pilus structural protein of *Thermus thermophilus* HB8 and HB27** [32]
○Masatada Tamakoshi^{1,2}, Hibiki Itoga¹, Satoshi Akanuma¹, Akihiko Yamagishi¹
(¹Dept. Mol. Biol., Tokyo Univ. of Pharm. Life Sci., ²RIKEN SPring-8 Center, Harima Institute)
- 13:45– 14:00 **A comparative study on homologous recombination mediators from *T. thermophilus*** [34]
○Takeshi Shinohara^{1,2}, Tatsuhiko Inoue³, Ryouji Masui³, Seiki Kuramitsu³, Takehiko Shibata^{1,2}, Tsutomu Mikawa²
(¹Grad. Sch. Nanobiosci., Yokohama City Univ., ²RIKEN Adv. Sci. Inst., ³Department 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 *T. thermophilus* 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 *Thermus thermophilus* 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 *T. thermophilus* 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 Bessho¹, Yasumasa Joti², Takashi Kimura³, Aya Kitamura¹, Akemi Shibuya¹, Masami Ueta⁴, Akira Wada⁴, Shoji Takeuchi⁵, Toshifumi Sakaguchi⁶, Tamakoshi Masatada⁷, Shota Nitahara⁷, Toshiyuki Moriya⁸, Tairo Oshima⁸, Yoshinori Nishino³
(¹RIKEN Spring-8 Center., ²XFEL division, JASRI, ³RIES, Hokkaido Univ., ⁴Yoshida Biol. Lab. ⁵Tokyo Univ., ⁶Pref. Univ. Hiroshima, ⁷Tokyo Univ. of Pharm. and Life Sci., ⁸Kyowa-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 Kanagawa², Gota Kawai^{2,4}
(¹Univ. Electro-Commun., ²RIKEN SPring-8 Center, ³SPring8/JASRI, ⁴Chiba 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)

The 1st Annual Meeting



The 2nd Annual Meeting



The 3rd Annual Meeting



The 4th Annual Meeting



The 5th Annual Meeting



The 6th Annual Meeting



The 7th Annual Meeting



The 8th Annual Meeting



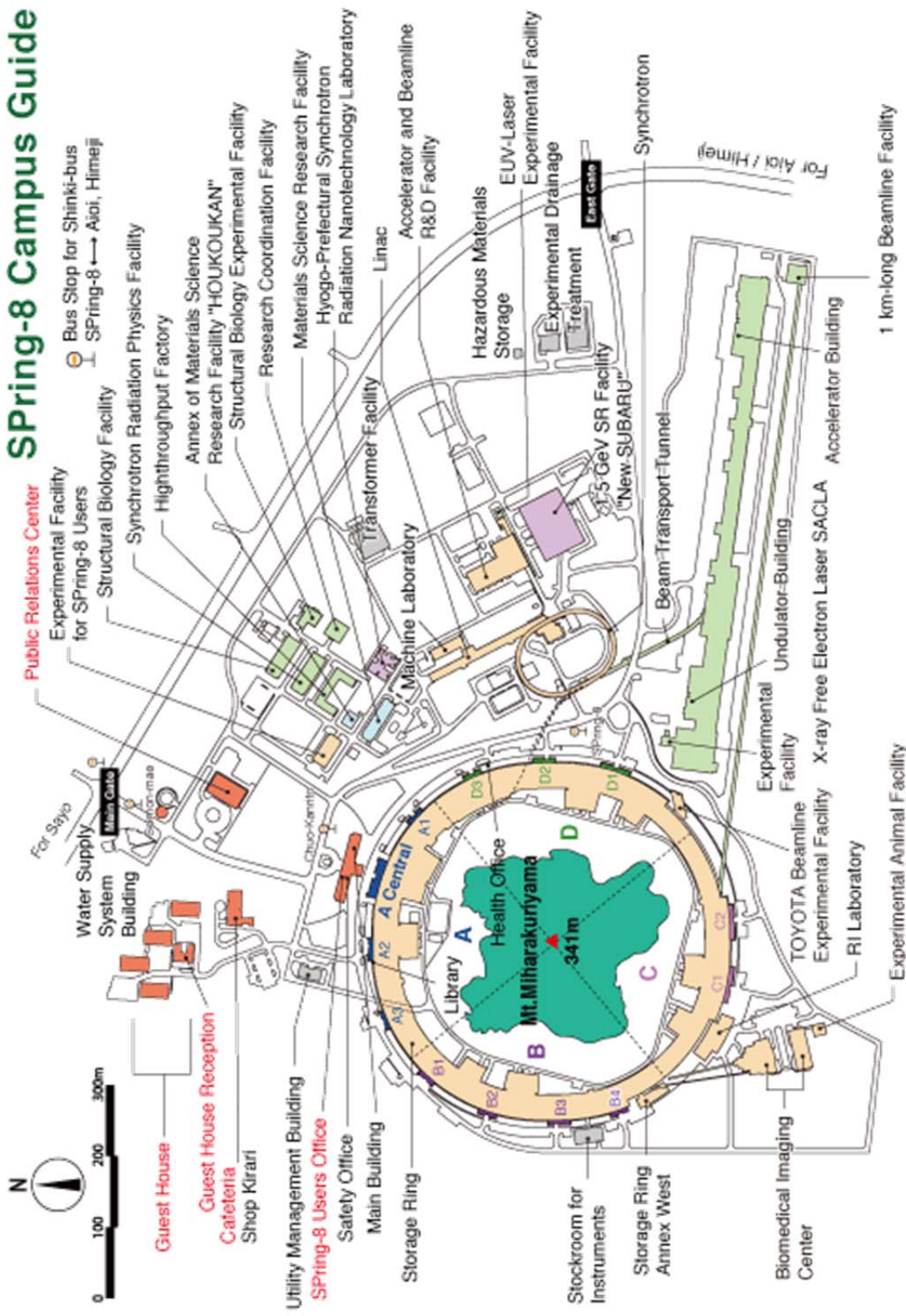
The 9th Annual Meeting



The 10th Annual Meeting



SPRING-8 Campus Guide



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