The 1st Annual Meeting for Whole-Organism Science Society
Joint Meeting with
The 10th Annual Meeting of Structural-Biological Whole Cell Project of *Thermus thermophilus* HB8

Program

Friday, August 19

13:30 – 14:00 **General Assembly**
Seiki Kuramitsu

Session 1 **Chairpersons: Keiko Sakamoto and Kenji Fukui**

14:00 – 15:30 **Short Presentation (1)**
Abstract No.:【1】-【29】

15:30 – 15:45 **Coffee Break**

Session 2 **Chairpersons: Hitoshi Iino and Yuri Uemura**

15:45 – 17:00 **Short Presentation (2)**
Abstract No.:【30】-【64】

17:00 – 17:30 **Check in**

17:30 – 19:00 **Seminar Banquet (in Cafeteria)**

19:00 – 19:45 **Poster Session (1)** **odd numbers**
19:45 – 20:30 **Poster Session (2)** **even numbers**

20:30 – 22:00 **Free Discussion (with posters, stars, and beer)**

Saturday, August 20

Session 3 **System Biology** Abstract No.

Chairpersons: Takeo Tomita and Akira Nakamura

9:00 – 9:30 **Characteristic distribution pattern of chaperonin substrates on the metabolic network** 【18】
Kazuhiro Takemoto (PRESTO, JST; U. Tokyo)

9:30 – 10:00 **TthA0610/1422; A protein-folding system in periplasmic space in *Thermus thermophilus* HB8** 【19】
○Takashi Tamura, Takamasa Yoshida, Yuma Mori, Akio Ebihara, Seiki Kuramitsu, and Kenji Inagaki (Dept of Bioscience, Grad. Sch. Nat. Sci. & Tech., Okayama Univ.)

10:00 – 10:30 **Isolation and genomic analysis of a *Myoviridae* bacteriophage fMN1 of the extreme thermophile *Thermus thermophilus*** 【20】

○Masatada Tamakoshi[1,2], Takayuki Izumi[1], Motoki Sugisawa[1], Kenshiro Oshima[3], Toh Hidehiro[4], Kaoru Mitsuoka[5], Masahira Hattori[3], and Akihiko Yamagishi[1] ([1]Dept. Mol. Biol., Tokyo Univ. of Pharm. Life Sci., [2]RIKEN SPring-8 Center, Harima Institute, [3]Grad. Sch. of Frontier Sci., Univ. of Tokyo, [4]Med. Inst. of Bioregulation., Kyushu Univ., [5]Biomed. Information Res. Center (BIRC), Nat. Inst. of Advanced Industrial Sci. and Tech. (AIST))

Chairpersons: Yasuo Suda and Akihiro Okamoto

10:30 – 11:00 **Structural analysis of membrane proteins involved in iron uptake** 【22】
○Hiroshi Sugimoto, Youichi Naoe, and Yoshitsugu Shiro (Biometal Science Laboratory, RIKEN Spring-8 Center)

11:00 – 11:30 **Crystal structure of the catalytic domain of multidomain PHB depolymerase** 【23】
Tamao Hisano (RIKEN SPring-8 Center)

11:30 – 12:00 **Taking Photographs of All Members**

12:00 – 13:00 **Lunch Break**

Session 4 Imagings

Abstract No.

Chairpersons: Masaki Yamamoto and Naoki Kunishima

13:00 – 13:30 **Protein micro-crystallography at the micro focus beamline BL32XU at SPring-8** 【24】
○Kunio Hirata[1], Yoshiaki Kawano[1], Koichi Hashimoto[1], Go Ueno[1], Takaaki Hikima1, Hironori Murakami1, Nobutaka Shimizu1,2, Kazuya Hasegawa2, Takashi Kumasaka[2], and Masaki Yamamoto[1] ([1]SR Life Science Instrumentation Unit, RIKEN SPring-8 Center, [2]Structural Biology Group, SPring8/JASRI.)

13:30 – 14:00 **Remote access to SPring-8 structural biology beamlines** 【25】
○Go Ueno[1], Kazuya Hasegawa[2], Takaaki Hikima[1], Hironori Murakami[1], Yukito Furukawa[2], Takashi Kumasaka[1,2], and Masaki Yamamoto[1] ([1]RIKEN SPring-8 Center, [2]SPring-8/JASRI)

14:00 – 14:30 **Research and development of RNA/RNP bio-molecular imaging technology at SPring-8/SACLA** 【26】
○Yoshitaka Bessho[1], Yasumasa Joti[2], Takashi Kimura[3], Aya Kitamura[1], Shoji Takeuchi[4], Yoshinori Nishino[3] ([1]RIKEN Spring-8 Center., [2]XFEL division, JASRI, [3]RIES, Hokkaido Univ., [4]Tokyo Univ.)

14:30 – 15:00 **Simulation study to examine the possibility of high-resolution biomolecular imaging with SACLA** 【27】
Yasumasa Joti (XFEL Division, JASRI)

15:00 – 15:30 **Structure analysis of biological macromolecules** 【28】
Koji Yonekura (RIKEN SPring-8 Center)

15:30 – 16:00 **Coffee Break**

Session 5 System Biology : Central-Dogma Related

Abstract No.

Chairpersons: Tsutomu Mikawa and Masao Inoue

16:00 – 16:30 **DNA repair system of *Thermus thermophilus* HB8** 【30】
Ryoji Masui ([1]Dept. Biol. Sci., Grad. Sch. Sci., Osaka Univ., [2]RIKEN SPring-8 Center, Harima Inst.)

16:30 – 17:00 **Reconstitution of homologous recombination *in vitro* by *T. thermophilus* proteins** 【37】
○Jin Inoue[1, 2], Takehiko Shibata[1, 2], and Tsutomu Mikawa[1, 2] ([1]RIKEN Adv. Sci. Inst., [2]Grad. School of Nanobioscience, Yokohama City Univ.)

17:00 – 17:30 **Study of transcriptional regulatory system of *T. thermophilus* HB8: Structure and function of two TetR family proteins** 【42】
○Akeo Shinkai, Yoshihiro Agari, and Keiko Sakamoto (RIKEN SPring-8 Center, Harima Inst.)

17:30 – 18:30 **Supper Break**

Session 6 Model Organism and Metabolic Systems

Abstract No.

Chairpersons: Kazumi Nishijima and Gen-ichi Sampei

18:30 – 19:00 **Arabidopsis transcriptome and epigenome analysis in abiotic stress responses** 【2】
Akihiro Matsui[1], Jong-Myong Kim[1], Taiko Kim To[1], Kentaro Nakaminami[1], Junko Ishida[1], Taeko Morosawa[1], Maho Tanaka[1], Shuhei Kobayashi[1,2], Chau Thi Cam Nguyen[1,2], Kazuo Shinozaki[3], Tetsuro Toyoda[4], and ○Motoaki Seki[1,2] ([1]RIKEN Plant Science Center, Plant Genomic Network Research Team, [2]Kihara Institute for Biological Research, Yokohama City University, [3]RIKEN Plant Science Center, Gene Discovery Research Group, [4]RIKEN BASE)

19:00 – 19:30 **Dissecting enzyme mechanisms in the purine nucleotides biosynthetic pathway** 【50】
○Gota Kawai[1,2], Mayumi Kusano[1], Seiki Baba[2,3], Mayumi Kanagawa[2], and Gen-ichi Sampei[2,4] ([1]Chiba Inst. Tech., [2]RIKEN SPring-8 Center, [3]SPring8/JASRI, [4]Univ. Electro-Commun.)

19:30 – 20:00 **Metabolic pathway for sym-homospermidine production in *Thermus thermophilus*** 【55】
Tairo Oshima (Institute of Environmental Microbiology, Kyowa-kako)

20:00 – 20:30 **Poster Session (3) (poster No. 1-35)**
20:30 – 21:00 **Poster Session (4) (poster No. 36-End)**

21:00 – 22:30 **Free Discussion (with posters, stars, and beer)**

Sunday, August 21

Session 7 Model Organism and Functional Discovery

		Abstract No.
	Chairpersons: Motoaki Seki and Akio Ebihara	
9:00 – 9:30	**Towards complete understanding of cellular systems** Hirotada Mori (Graduate School of Biological Sciences, Nara Institute of Science and Technology)	【3】
9:30 – 10:00	***In vivo, in vitro*, and X-ray crystallographic analyses suggested the involvement of an uncharacterized TIM barrel protein in a protection against oxidative stress** Shuhei Nakane[1], Taisuke Wakamatsu[2], Ryoji Masui[1,3], Seiki Kuramitsu[1,3], and ○Kenji Fukui[3] ([1]Grad. Sch. Sci., Osaka Univ., [2]Grad. Sch. Frontier Biosci., Osaka Univ., [3]RIKEN SPring-8 Center.)	【60】
10:00 – 10:30	**Prediction of protein function utilizing its structural information** Kei Yura (Center Info. Biol., Ochanomizu Univ.)	【61】
10:30 – 10:45	**Coffee Break**	
	Chairpersons: Tairo Oshima and Hiroyuki Hori	
10:45 – 10:55	**Progress in the plasmid construction for protein production and gene disruption of *T. thermophilus* HB8** Seiki Kuramitsu[1,2] ([1]Grad. Sch. Sci., Osaka Univ., [2]RIKEN SPring-8 Center.)	【4-13】
10:55 – 11:05	**Transcriptome analysis and dataset of DNA microarray** Yoshihiro Agari (RIKEN SPring-8 Center.)	【4-13】
11:05 – 11:15	**Whole-cell proteome analysis of *T. thermophilus* HB8 by accurate mass and time tag technique** ○Kwang Kim[1], Hiroki Okanishi[1], Yoshio Tatahata[2], Ryoji Masui[1,3], and Seiki Kuramistu[1,2,3] ([1]Dept. Biol. Sci., Grad. Sch. Sci., Osaka Univ., [2]Grad. Sch. Frontier Biosciences, Osaka Univ., [3]RIKEN SPring-8 Center, Harima Institute.)	【14】
11:15 – 11:45	**Thermophiles resources and other precious genetic materials at RIKEN BioResource Center** ○Shotaro Kishikawa[1], Takahito Yamasaki[1], Yukari Kujime[1], Megumi Sakayori[1], Masato Okubo[1], Chitose Kurihara[1], Koji Nakade[1], Takehide Urata[1], and Yuichi Obata[1] ([1]Gene Engineering Division, RIKEN BioResource Center)	【1】
11:45 – 12:10	**Discussion**	
12:10 – 12:15	**Closing remarks** Seiki Kuramitsu	

1. **Thermophiles resources and other precious genetic materials at RIKEN BioResource Center**

   ○Shotaro Kishikawa[1], Takahito Yamasaki[1], Yukari Kujime[1], Megumi Sakayari[1], Masato Okubo[1], Chitose Kurihaara[1], Koji Nakade[1], Takehide Urata[1], and Yuichi Obata[1] ([1] Gene Engineering Division, RIKEN BioResource Center)

2. **Arabidopsis transcriptome and epigenome analysis in abiotic stress responses**

   Akihiro Matsui[1], Jong-Myong Kim[1], Taiko Kim To[1], Kentaro Nakaminami[1], Junko Ishida[1], Taeko Morosawa[1], Maho Tanaka[1], Shuhei Kobayashi[1,2], Chau Thi Cam Nguyen[1,2], Kazuo Shinozaki[3], Tetsuro Toyoda[4], and ○Motoaki Seki[1,2] ([1]RIKEN Plant Science Center, Plant Genomic Network Research Team, [2]Kihara Institute for Biological Research, Yokohama City University, [3]RIKEN Plant Science Center, Gene Discovery Research Group, [4]RIKEN BASE)

3. **Towards complete understanding of cellular systems**

   Hirotada Mori (Graduate School of Biological Sciences, Nara Institute of Science and Technology)

4-13. **Progress in the whole-cell project of an extreme thermophile, *Thermus thermophilus* HB8**

   Synchrotron-Radiation System Biology Research Group (RIKEN SPring-8 Center)

14. **Whole-cell proteome analysis of *T. thermophilus* HB8 by accurate mass and time tag technique**

   ○Kwang Kim[1], Hiroki Okanishi[1], Yoshio Takahata[2], Ryoji Masui[1,3], and Seiki Kuramitsu[1,2,3] ([1]Dept. Biol. Sci., Grad. Sch. Sci., Osaka Univ., [2]Grad. Sch. Frontier Biosciences, Osaka Univ., [3]RIKEN SPring-8 Center, Harima Institute.)

15. **Identification of phosphoprotein and structural analysis of the phosphorylation site in *Thermus thermophilus* HB8**

   ○Yoshio Takahata[1], Masao Inoue[2], Yota Iio[2], Kwang Kim[2], Yasushi Ishihama[3], Ryoji Masui[2,4], and Seiki Kuramitsu[1,2,4] ([1]Grad. Sch. Frontier Biosci., Osaka Univ., [2]Grad. Sch. Sci., Osaka Univ., [3]Grad. Sch. Pharmaceut. Sci., Kyoto Univ., [4]RIKEN SPring-8 Center, Harima Inst.)

16. **Global transcriptome analysis of protein phosphorylation mutants from *Thermus thermophilus* HB8**

   ○Yota Iio[1], Yoshio Takahata[2], Masao Inoue[1], Kim Kwang[1], Kenji Fukui[3], Yoshihiro Agari[3], Akeo Shinkai[3], Ryoji Masui[1,3], and Seiki Kuramitsu[1,2,3] ([1] Dept. Biol. Sci., Grad. Sch. Sci., Osaka Univ., [2] Grad. Sch. Frontier Biosciences, Osaka Univ., [3]RIKEN SPring-8 Center, Harima Inst.)

17. **Identification of acetylated proteins in *Thermus thermophilus* HB8**

   ○Hiroki Okanishi[1],Kwang Kim[1], Ryoji Masui[1,2], and Seiki Kuramitsu[1,2] ([1]Dept. Biol. Sci., Grad. Sch. Sci., Osaka Univ., [2]RIKEN Spring-8 Center)

18. **Characteristic distribution pattern of chaperonin substrates on the metabolic network**

   Kazuhiro Takemoto (PRESTO, JST; U. Tokyo)

19. **TthA0610/1422; A protein-folding system in periplasmic space in *Thermus thermophilus* HB8**

   ○Takashi Tamura, Takamasa Yoshida, Yuma Mori, Akio Ebihara, Seiki Kuramitsu, and Kenji Inagaki (Dept of Bioscience, Grad. Sch. Nat. Sci. & Tech., Okayama Univ.)

20. Isolation and genomic analysis of a *myoviridae* bacteriophage fMN1 of the extreme thermophile *Thermus thermophilus*

○Masatada Tamakoshi[1,2], Takayuki Izumi[1], Motoki Sugisawa[1], Kenshiro Oshima[3], Toh Hidehiro[4], Kaoru Mitsuoka[5], Masahira Hattori[3], and Akihiko Yamagishi[1] ([1]Dept.Mol.Biol., Tokyo Univ. of Pharm. Life Sci., [2]RIKEN SPring-8 Center, Harima Institute, [3]Grad.Sch. of Frontier Sci., Univ. of Tokyo, [4]Med .Inst. of Bioregulation., Kyushu Univ., [5]Biomed. Information Res. Center (BIRC), Nat. Inst .of Advanced Industrial Sci. and Tech. (AIST))

21. Visualization of the Type IV pili proteins, PilD and PilT, tagged with superfolder green fluorescent protein in *Thermus thermophilus*

○Sayaka Miyashita[1], Noriko Hara[1], Masatada Tamakoshi[2], and Ayumi Koike-Takeshita[1] ([1]Kanagawa inst. of Tech., [2]Tokyo Univ. Pharm. And Life Sci.)

22. Structural analysis of membrane proteins involved in iron uptake

○Hiroshi Sugimoto, Youichi Naoe, and Yoshitsugu Shiro (Biometal Science Laboratory, RIKEN Spring-8 Center)

23. Crystal structure of the catalytic domain of multidomain PHB depolymerase

Tamao Hisano (RIKEN SPring-8 Center)

24. Protein micro-crystallography at the micro focus beamline BL32XU at SPring-8

○Kunio Hirata[1], Yoshiaki Kawano[1], Koichi Hashimoto[1], Go Ueno[1], Takaaki Hikima[1], Hironori Murakami[1], Nobutaka Shimizu[1,2], Kazuya Hasegawa[2], Takashi Kumasaka[2], and Masaki Yamamoto[1] ([1]SR Life Science Instrumentation Unit, RIKEN SPring-8 Center, [2]Structural Biology Group, SPring8/JASRI.)

25. Remote access to SPring-8 structural biology beamlines

○Go Ueno[1], Kazuya Hasegawa[2], Takaaki Hikima[1], Hironori Murakami[1], Yukito Furukawa[2], Takashi Kumasaka[1,2], and Masaki Yamamoto[1] ([1]RIKEN SPring-8 Center, [2]SPring-8/JASRI)

26. Research and development of RNA/RNP bio-molecular imaging technology at SPring-8/SACLA

○Yoshitaka Bessho[1], Yasumasa Joti[2], Takashi Kimura[3], Aya Kitamura[1], Shoji Takeuchi[4], Yoshinori Nishino[3] ([1]RIKEN Spring-8 Center., [2]XFEL division, JASRI, [3]RIES, Hokkaido Univ., [4]Tokyo Univ.)

27. Simulation study to examine the possibility of high-resolution biomolecular imaging with SACLA

Yasumasa Joti (XFEL Division, JASRI)

28. Structure analysis of biological macromolecules

Koji Yonekura (RIKEN SPring-8 Center)

29. RIKEN SPring-8 Center Protein Crystallography Database

○Naoki Kunishima, Michihiro Sugahara, Tomoyuki Tanaka, Hisashi Naitow, Akeo Shinkai, Seiki Kuramitsu, and Yukuhiko Asada (RIKEN Harima SPring-8 Center)

30. DNA repair system of *Thermus thermophilus* HB8

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

31. The partial reconstitution of DNA mismatch repair

○Atsuhiro Shimada[1], Kenji Fukui[2], Noriko Nakagawa[1,2], Ryoji Masui[1,2], and Seiki Kuramitsu[1,2] ([1]Dept. Biol. Sci., Grad. Sch. Sci., Osaka Univ., [2]RIKEN

SPring-8 Center, Harima Inst.)

32. The molecular regulatory mechanism of the DNA mismatch repair endonuclease

○Hitoshi Iino[1], Kwang Kim[2], Tatsuya Yamamoto[3], Atsuhiro Shimada[2], Ryoji Masui[1,2], Seiki Kuramitsu[1,2], and Kenji Fukui[1] ([1]RIKEN SPring-8 Center, [2]Grad. Sch. of Sci. Osaka Univ., [3]Keio Univ. Sch. of Med.)

33. The study of the interaction between MutL and other MMR proteins

○Yoshito Hata[1], Atsuhiro Shimada[1], Ryoji Masui[1,2], Kenji Fukui[2], and Seiki Kuramitsu[1,2] ([1]Dept. Biol. Sci., Grad. Sch. Sci., Osaka Univ., [2]RIKEN SPring-8 Center, Harima Inst.)

34. Structural and functional analysis of bacterial DNA polymerase X

○Shuhei Nakane[1], Noriko Nakagawa[1,2], Ryoji Masui[1,2], and Seiki Kuramitsu[1,2] ([1]Dept. Biol., Grad. Sch. Sci., Osaka Univ., [2]RIKEN SPring-8 Center, Harima Inst.)

35. Molecular and cellular functional analysis of exonuclease TTHA0118 from *Thermus thermophilus* HB8

○Yuri Uemura[1], Taisuke Wakamatsu[1], Atsuhiro Shimada[2], Ryoji Masui[2,3], and Seiki Kuramitsu[1,2,3] ([1]Grad. Sch. Frontier Biosci., Osaka Univ., [2]Grad. Sch. Sci., Osaka Univ., [3]RIKEN SPring-8 Center, Harima Inst.)

36. Functional analysis of nucleoid associated protein HU from *Thermus thermophilus* HB8

○Yuya Nishida[1], Noriko Nakagawa[2, 3], Ryoji Masui[2, 3], and Seiki Kuramitsu[1, 2, 3] ([1]Grad. Sch. Frontier Biosci., Osaka Univ., [2]RIKEN SPring-8 Center, Harima Inst., [3]Grad. Sch. Sci., Osaka Univ.)

37. Reconstitution of homologous recombination *in vitro* by *T. thermophilus* proteins

○Jin Inoue[1, 2], Takehiko Shibata[1, 2], and Tsutomu Mikawa[1, 2] ([1]RIKEN Adv. Sci. Inst., [2]Grad. School of Nanobioscience, Yokohama City Univ.)

38. The inhibition mechanism of RecX for the recombination activity of RecA

○Saya Okui[1], Jin Inoue[1,2], Takasi ito[3], Takehiko Shibata[1,2], Tsutomu Mikawa[2] ([1]Grad. Sch. Nanobiosci., Yokohama City Univ., [2]RIKEN Adv. Sci. Inst., [3]Dept.of chem.,Tokyo Metropolitan Univ.)

39. Regulation of D-loop reaction by recombination mediators

○Takeshi Shinohara[1], Jin Inoue[1,2], Tatsuhiko Inoue[3], Ryouji Masui[3], Seiki Kuramitsu[3], Takehiko Shibata[1,2], and Tsutomu Mikawa[2] ([1]Grad. Sch. Nanobiosci., Yokohama City Univ., [2]RIKEN Adv. Sci. Inst.)

40. Functional analysis of RadA/Sms, a RecA-like ATPase involved in homologous recombination

○Masao Inoue[1], Kenji Fukui[2], Noriko Nakagawa[1,2], Ryoji Masui[1,2], and Seiki Kuramitsu[1,2] ([1]Dept. Biol. Sci., Grad. Sch. Sci., Osaka Univ., [2]RIKEN SPring-8 Center, Harima Inst.)

41. Cellular and molecular functional analysis of bacterial Rad52_Rad22 family protein from *Thermus thermophilus* HB8

○Tatsuhiko Inoue[1], Noriko Nakagawa[2,3], Ryoji Masui[2,3], and Seiki Kuramitsu[1,2,3] ([1]Grad. Sch. Frontier Biosci., Osaka Univ., [2]Grad. Sch. Sci., Osaka Univ., [3]RIKEN SPring-8 Center, Harima Inst.)

42. Study of transcriptional regulatory system of *T. thermophilus* HB8: Structure and function of two TetR family proteins

○Akeo Shinkai, Yoshihiro Agari, and Keiko Sakamoto (RIKEN SPring-8 Center, Harima Inst.)

43. **X-ray crystal structure of hypothetical protein TTHB210, controlled by σ^E/anti-σ^E regulatory system in *Thermus thermophilus* HB8**

    ○Yoshihiro Agari[1], Seiki Kuramitsu[1,2], and Akeo Shinkai[1] ([1]RIKEN Spring-8 Center, Harima Inst., [2]Grad. Sch. Sci., Osaka Univ.)

44. **Functional and structural characterization of the TetR family transcriptional repressor PaaR from *Thermus thermophilus* HB8**

    ○Keiko Sakamoto[1], Yoshihiro Agari[1], Seiki Kuramitsu[1, 2], and Akeo Shinkai[1] ([1]RIKEN SPring-8 Center, Harima Inst. [2]Grad. Sch. of Sci., Osaka Univ.)

45. **Global analysis of RNases from *Thermus thermophilus* HB8**

    ○Hiromasa Ohyama[1], Yoshihiro Agari[2], Kenji Fukui[2], Noriko Nakagawa[1,2], Akeo Shinkai[2], Seiki Kuramitsu[1,2], and Ryoji Masui[1, 2] ([1]Dept. Biol. Sci., Grad. Sch. Sci., Osaka Univ., [2]RIKEN SPring-8 Center, Harima Inst.)

46. **LdrP, a cAMP-independent CRP/FNR family transcriptional regulator, is the master switch for the light-inducible gene expression in *Thermus thermophilus***

    ○Hideaki Takano[1], Yoshihiro Agari[2], Ryuta Yamazaki[1], Teruhiko Beppu[1], Akeo Shinkai[2], and Kenji Ueda[1] ([1]Life Science Research Center, College of Bioresource Sciences, Nihon University, [2] RIKEN SPring-8 Center, Harima Institute)

47. **Crystal structure of the bifunctional tRNA modification enzyme MnmC from *Escherichia coli***

    ○Aya Kitamura[1], Toru Sengoku[2], Madoka Nishimoto[2], Shigeyuki Yokoyama[2,3,4], and Yoshitaka Bessho[1,2] ([1]RIKEN Spring-8 Center, Harima Institute, [2]RIKEN Systems and Structural Biology Center, [3]Laboratory of Structural Biology, [4]Department of Biophysics and Biochemistry, Graduate School of Science, The University of Tokyo)

48. **The crystal structure analysis and establishment of activity measurement system of *Thermus thermophilus* tRNA (Um34,Cm34) methyltransferase [YibK]**

    ○Takashi Matsugi[1], Akira Hirata[1], and Hiroyuki Hori[1,2] ([1]Dept.of Materials Sci. and Biotechnol., Grad. Sch. of Sci. and Eng., Ehime Univ., [2]VBL, Ehime Univ.)

49. **Elucidation of substrate tRNA recognition mechanism by tRNA(m1A58) methyltransferase[TrmI] from *Thermus thermophilus***

    ○Hiroyuki Takuma[1], Masayuki Minoji[1], Natumi Ushio[1], Chie Tomikawa[1], Akira Hirata[1] ,Chikako Iwashita[1], Ochi Anna[1], and Hiroyuki Hori[1,2] ([1]Dept. of Materials Sci. and Biotechnol., Grad. Sch. of Sci. and Eng., Ehime Univ., [2]VBL, Ehime Univ.)

50. **Dissecting enzyme mechanisms in the purine nucleotides biosynthetic pathway**

    ○Gota Kawai[1,2], Mayumi Kusano[1], Seiki Baba[2,3], Mayumi Kanagawa[2], and Gen-ichi Sampei[2,4] ([1]Chiba Inst. Tech., [2]RIKEN SPring-8 Center, [3]SPring8/JASRI, [4]Univ. Electro-Commun.)

51. **Crystal structure of PurF from *Sulfolobus tokodaii***

    ○Ryota Miyazawa[1], Ryosuke Umebayashi[1], Yuki Yanagida[1], Kiyoshi Okada[1], Mayumi Kanagawa[2], Seiki Baba[2,3], Gota Kawai[2,4], and Gen-ichi Sampei[1,2] ([1] Univ. Electro-Commun., [2]RIKEN SPring-8 Center, [3]Spring-8/JASRI, [4]Chiba Inst. Tech.)

52. Gene expression analysis of the purine nucleotide biosynthetic operons in *Thermus thermophilus* HB8

○Hideya Yamamoto[1], Taiga Watanabe[1], Syusaku Matsuura[1], Kenta Nakajima[1], Gota Kawai[2,3], and Gen-ichi Sampei[1,3] ([1] Univ. Electro-Commun., [2] Chiba Inst. Tech., [3] RIKEN SPring-8 Center)

53. Crystal structure of the GMP synthetase from *Sulfolobus tokodaii*

○Hironobu Washio[1], Yusuke saito[1], Takuya Watanabe[1], Noriaki Kagotani[1], Satoko Tamura[1], Sakiko Suzuki[1], Mayumi Kanagawa[2], Baba Seiki[2], Gen-ichi Sanpei[2, 4], and Gota Kawai[1, 2] ([1]Chiba Inst. Tech., [2]RIKEN SPring-8 Center, [3]SPring8/JASRI, [4]Univ. of Electro-Commun.)

54. Analysis of nucleoside metabolism in *Thermus thermophilus* HB8 suggests the diversity of this metabolism

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

55. Metabolic pathway for sym-homospermidine production in *Thermus thermophilus*

Tairo Oshima (Institute of Environmental Microbiology, Kyowa-kako)

56. Mechanism of leucine-induced allosteric activation of glutamate dehydrogenase

○Takeo Tomita[1], and Makoto Nishiyama[1,2] ([1]Biotechnology Research Center, The University of Tokyo, [2]RIKEN SPring-8 Center)

57. Leucine-mediated signal transduction in *Thermus thermophilus*

○Hajime Matsushita[1], Takeo Tomita[1], Tomohisa Kuzuyama[1], and Makoto Nishiyama[1, 2] ([1]Biotechnology Research Center, The University of Tokyo, [2]RIKEN SPring-8 center)

58. A regulator PutR regulates the expression of the genes in amino acid metabolisms

○Masatoshi Shimizu[1], Takeo Tomita[1], Tomohisa Kuzuyama[1], and Makoto Nishiyama[1, 2] ([1]Biotechnology Research Center, The University of Tokyo, [2]RIKEN SPring-8 Center)

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

○Yuko Kanemaru[1], Fumihito Hasebe[1], Takeo Tomita[1], and Tomohisa Kuzuyama[1], Makoto Nishiyama[1, 2] ([1]Biotechnology Research Center, The University of Tokyo, [2]RIKEN SPring-8 Center)

60. *In vivo, in vitro*, and X-ray crystallographic analyses suggested the involvement of an uncharacterized TIM barrel protein in a protection against oxidative stress

Shuhei Nakane[1], Taisuke Wakamatsu[2], Ryoji Masui[1,3], Seiki Kuramitsu[1,3], and ○Kenji Fukui[3] ([1]Grad. Sch. Sci., Osaka Univ., [2]Grad. Sch. Frontier Biosci., Osaka Univ., [3]RIKEN SPring-8 Center.)

61. Prediction of protein function utilizing its structural information

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62. Studies of signaling mechanism of general stress response mechanism in *Bacillus subtilis*

○Nao Miyano, Takeshi Hoshino, Masatomo Makino, Nobutaka Shimizu, and Takashi Kumasaka (JASRI/SPring-8)

63. Crystal structure of the tandem-type universal stress protein TTHA0350 from *Thermus thermophilus* HB8

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64. Possible role of phospholylation in CMP kinase function based on its crystal strutures

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