

(P01) Structure of the *Streptococcus pyogenes* β -NAD⁺ glycohydrolase-inhibitor complex; J. Y. Yoon,¹ H.-J. Yoon,¹ and S. W. Suh^{1,2}; ¹Department of Chemistry, ²Department of Biophysics and Chemical Biology, College of Natural Sciences, Seoul National University, Seoul, 151-747, Korea.

(P02) X-ray free electron laser exposure of 2-D membrane protein crystals; B. Pedrini¹, C.-J. Tsai^{1,2}, G. Capitan², C. Padeste³, M. Frank⁴, R. Abela¹, G. F.X. Schertler², X.-D. Li²; ¹SwissFEL, Paul Scherrer Institute, 5232 Villigen, Switzerland, ²Laboratory of Biomolecular Research, Paul Scherrer Institute, 5232 Villigen, Switzerland, ³Lab for Micro- and Nanotechnology, Paul Scherrer Institute, 5232 Villigen, Switzerland, ⁴Physical and Life Sciences Directorate, Lawrence Livermore National Lab, Livermore, CA, USA

(P03) Experiences with archived raw diffraction images data: capturing cisplatin after chemical conversion of carboplatin in high salt conditions for a protein crystal; J. R. Helliwell¹, K. Diederichs², L. M. J. Kroon-Batenburg³, A. M. M. Schreurs³ and S. W. M. Tanley¹; ¹School of Chemistry, University of Manchester, Manchester M13 9PL, UK, ²Fachbereich Biologie, Universität Konstanz, Box M647, D-78457 Konstanz, Germany, ³Dept. of Crystal and Structural Chemistry, Bijvoet Center for Biomolecular Research, Utrecht University, Padualaan 8, 3584 CH Utrecht, The Netherlands

(P04) Structural polymorphism of Z-DNA induced by metal salts; T. Chatake¹ and T. Sunami²; ¹Research Reactor Institute, Kyoto University, Kumatori, Osaka, 590-0494, Japan, ²Molecular Modeling and Simulation Group, Quantum Beam Science Directorate, Japan Atomic Energy Agency, Kizugawa, Kyoto 619-0215, Japan.

(P05) A docking study of the Enhanced intracellular survival (Eis) protein from *Mycobacterium tuberculosis* in complex with dual-specificity protein phosphatase 16 (DUSP16) / mitogen-activated protein kinase phosphatase-7 (MKP-7) suggests dissociation of hexamers; H.-J. Yoon,¹ K. H. Kim,¹ H. Kim,² S. Jang,² and S. W. Suh^{1,3}; ¹Department of Chemistry, Seoul National University, ²Department of Chemistry, Sejong University, ³Department of Biophysics and Chemical Biology, Seoul National University, Korea.

(P06) The atomic structure of Sulfolobus Turreted Icosahedral Virus: a 75 megadalton particle that lives in boiling acid; J. E. Johnson¹, D. Veessler¹, T-S. Ng^{2,3}, A. K. Sendamarai^{4,5}, B. J. Eilers^{4,5}, C. M. Lawrence^{4,5}, S.-M. Lok^{2,3}, M. J. Young^{5,6}, and C.-y. Fu¹; ¹Department of Integrative Structural and Computational Biology, The Scripps Research Institute, La Jolla, California, USA. ²Program in Emerging Infectious Diseases, Duke-NUS Graduate Medical School, KTP Building, 8 college Road, Singapore. ³Center for Bioimaging Sciences, National University of Singapore, Singapore. ⁴Department of Chemistry

and Biochemistry, Montana State University, Bozeman, Montana, USA. ⁵Thermal Biology Institute, Montana State University, Bozeman, Montana, USA. ⁶Department of Plant Sciences and Plant Pathology, Montana State University, Bozeman, Montana, USA.

(P07) X-ray structure determination and deuteration of Nattokinase; Y. Yanagisawa¹, T. Chatake², Y. Morimoto², A. Katagiri¹, R. Kazama¹, T. Adachi¹, H. Sumi³; ¹Department of Pharmacy, Chiba Institute of Science, 3 Shiomi-cho, Choshi, Chiba, 288-0025, Japan, ²Research Reactor Institute, Kyoto University, Kumatori, Osaka, 590-0494, Japan, ³Department of Life Science, Kurashiki University of Science and the Arts, 2640 Nishinoura, Tsurajima-cho, Kurashiki, Okayama, 712-8505, Japan.

(P08) Development of specific inhibitors of African trypanosomes glycerol kinase for anti-trypanosomal drug design; E. O. Balogun¹, D. K. Inaoka², T. Shiba¹, Y. Kido², T. Nara³, T. Aoki³, T. Honma⁴, A. Tanaka⁴, M. Inoue⁵, S. Matsuoka⁵, P. A.M. Michels⁶, K. Kita², S. Harada¹; ¹Grad. Sch. of Sci. and Tech., Kyoto Inst. of Tech; ²Grad. Sch. of Med., The Univ. of Tokyo; ³Juntendo Univ. Sch. of Med. ⁴System and Struct. Biol. Center, RIKEN; ⁵Grad. Sch. of Pharm. Sci., The Univ. of Tokyo; ⁶Univ. catholique de Louvain, Belgium.

(P09) Structure of a membrane-bound stomatin-specific protease in complex with a substrate peptide; H. Yokoyama¹, N. Takizawa¹, D. Kobayashi¹, I. Matsui², and S. Fujii¹; ¹School of Pharmaceutical Sciences, University of Shizuoka, 52-1 Yada, Suruga-ku, Shizuoka 422-8526, Japan, ²Biomedical Research Institute, National Institute of Advanced Industrial Science and Technology (AIST), 1-1 Higashi, Tsukuba, Ibaraki 305-8566, Japan.

(P10) Application of iota-toxin and actin complex crystal as the ADP-ribosylation reaction chamber; T. Tsurumura and H. Tsuge; Faculty of Life Sciences, Kyoto Sangyo University, Kamigamo-Motoyama, Kyoto 603-8555, Japan

(P11) High-pressure-induced water penetration into dihydrofolate reductase from *Escherichia coli*; H. Yamada¹, T. Nagae¹, and N. Watanabe^{2, 3}; ¹Graduation School of Engineering, ²Venture Business Laboratory, ³Synchrotron radiation Research center, Nagoya University, Furo-cho, Chikusa-ku, Nagoya 464-8603 Japan.

(P12) Cryo-scanning electron microscopy for cross-sectioned biological specimens; Y. Nishino^{1, 3}, Y. Ito^{2, 3}, and A. Miyazawa^{1, 3}; ¹Graduate School of Life Science, University of Hyogo, 3-2-1, Koto, Kamigori-cho, Ako-gun, Hyogo 678-1297, Japan, ²Leica Microsystems, Shirokane Takanawa Station Building 6F, 1-27-6 Shirokane, Minato-ku, Tokyo 108-0072, Japan, ³RIKEN SPring-8 center, 1-1-1 Kouto, Sayo, Hyogo 679-5148, Japan

(P13) Crystal structure of a MAPKAP-K2 inhibitor TEI-I01800 bound to human Cyclin-dependent Kinase-2 (CDK2); A. Fujino, K. Fukushima, T. Kubota, T. Kosugi and M. T. Kamimura; *Teijin Institute for Bio-medical Research, 4-3-2 Asahigaoka, Hino-shi, Tokyo 191-8512, Japan*

(P14) Protein crystallization and observation of crystal growth in a magnetic field; A. Nakamura, J. Ohtsuka, and M. Tanokura; *Department of Applied Biological Chemistry, Graduate School of Agricultural and Life Sciences, The University of Tokyo, 1-1-1 Yayoi, Bunkyo-ku, Tokyo 113-8657, Japan*

(P15) Synchrotron radiation beamline for macromolecular assemblies operated by IPR (SPring-8 BL44XU); E. Yamashita¹, A. Higashiura¹, M. Yoshimura², M. Suzuki¹, K. Hasegawa³, Y. Furukawa³, T. Ohata³, T. Kumasaka³, G. Ueno⁴, M. Yamamoto⁴, S. Yoshikawa⁵, T. Tsukihara^{1,5}, and A. Nakagawa¹; ¹*Institute for Protein Research, Osaka University, 3-2 Yamadaoka, Suita, Osaka 565-0871, Japan*, ²*Taiwan NSRRC, Taiwan Beamline Office at SPring-8, 1-1-1 Kouto, Sayo-cho, Sayo-gun, Hyogo 679-5148, Japan*, ³*JASRI/SPring-8, 1-1-1 Kouto, Sayo-cho, Sayo-gun, Hyogo 679-5198, Japan*, ⁴*RIKEN/SPring-8, 1-1-1 Kouto, Sayo-cho, Sayo-gun, Hyogo 679-5148, Japan*, ⁵*Graduate School of Life Science, University of Hyogo, 3-2-1 Kouto, Kamigori-cho, Ako-gun, Hyogo 678-1297, Japan*

(P16) The crystal structure of GH3 β -glucosidase from *Aspergillus aculeatus*; S. Fushinobu¹, K. Suzuki¹, J. Sumitan², and T. Kawaguchi²; ¹*Department of Biotechnology, The University of Tokyo, 1-1-1 Yayoi, Bunkyo-ku, Tokyo 113-8657, Japan*, ²*Graduate School of Life and Environmental Sciences, Osaka Prefecture University, 1-1 Gakuen-cho, Naka-ku, Sakai, Osaka 599-8531, Japan*

(P17) Predicting the three-dimensional structure of actinin-4 mutants; N. Miura¹, M. Banno², K. Honda¹, A. Miyanaga¹, T. Yamada¹; ¹*National Cancer Center Research Institute, 5-1-1 Tsukiji, Chuo-ku, Tokyo 104-0045, Japan*, ²*Mitsui Knowledge Industry, 2-7-14 Higashinakano, Nakano-ku, Tokyo 164-8555, Japan*.

(P18) Open and closed structures of GalE-like L-Threonine dehydrogenase from *Cupriavidus necator* appeared from X-ray crystal structures and molecular dynamics simulation; S. Nakano^{1,2}, S. Okazaki^{1,2}, H. Tokiwa³ and Y. Asano^{1,2}; ¹*Biotechnology Research Center and Department of Biotechnology, Toyama Prefectural University, 5180 Kurokawa, Imizu, Toyama 939-0398, Japan*, ²*JST, ERATO, Asano Active Enzyme Molecule Project, 5180 Kurokawa, Imizu, Toyama 939-0398, Japan*, ³*Department of Chemistry, Rikkyo University, Nishi-ikebukuro, Toshimaku, Tokyo 171-8501, Japan*.

(P19) Structural studies of hemoglobin from pisces species Shortfin mako shark (*Isurus oxyrinchus*) at 1.9Å resolution; P. Ramesh^{1,2}, S.S. Sundaresan², and M. N. Ponnuswamy²; ¹*Laboratory of Structural Biology, Department of Molecular Cell Biology, Samsung Biomedical Research Institute,*

Sungkyunkwan University of School of Medicine, Suwon 440-746, Korea. ²Centre of Advanced Study in Crystallography and Biophysics, University of Madras, Maraimalai Campus (Guindy), Chennai - 600 025.

(P20) Protein unfolding at an air-water interface investigated by a simultaneous multiple angle-wavelength dispersive x-ray reflectometer; Y. F. Yano¹, E. Arakawa², W. Voegell³, and T. Matsushita³; ¹Department of Physics, Kinki University, 3-4-1 Kowakae, Higashiosaka City, Osaka 577-8502, Japan, ²Department of Physics, Tokyo Gakugei University, Koganei, Tokyo, Japan, ³Photon Factory, Institute of Materials Structure Science, KEK, Tsukuba, Ibaraki, Japan

(P21) Three dimensional structure base analysis of the wide range inhibitory activity of 1/2SLPI; K. Fukushima¹, H. Matsuda², M. Takimoto-Kamimura¹; ¹Teijin Institute for Bio-medical Research, 4-3-2, Asahigaoka, Hino-shi, Tokyo 191-8512, Japan, ²Material Analysis Research Laboratories, Teijin Limited, 4-3-2, Asahigaoka, Hino-shi, Tokyo 191-8512, Japan

(P22) Crystal structure of TM0056, a putative peptide binding protein from *Thermotoga maritima*; H.-J. Yoon,¹ S. W. Suh,^{1,2} H. J. Kim,³ and H. H. Lee³; ¹Department of Chemistry, Seoul National University, ²Department of Biophysics and Chemical Biology, Seoul National University, ³Department of Bio & Nano Chemistry, Kookmin University, Korea.

(P23) Hpy188I-DNA structures - snapshots of the GIY-YIG nuclease mediated catalysis; M. Sokolowska¹, H. Czapinska¹, and M. Bochtler^{1,2,3}; ¹International Institute of Molecular and Cell Biology, Trojdena 4, 02-109 Warsaw, Poland, ²Institute of Biochemistry and Biophysics PAS, Pawlinskiego 5a, 02-106 Warsaw, Poland, ³Schools of Chemistry and Biosciences, Main Building, Cardiff University, Cardiff CF10 3AT, UK.

(P24) High-resolution X-ray crystal structure of bovine H-protein using a high-pressure cryocooling method; A. Higashiura¹, K. Ohta², M. Masaki², M. Sato², K. Inaka³, H. Tanaka⁴ and A. Nakagawa¹; ¹Institute for Protein Research Osaka University, 3-2 Yamadaoka, Suita, Osaka 565-0871, Japan, ²Japan Aerospace Exploration Agency, 2-1-1 Sengen, Tsukuba, Ibaraki 305-8505, ³Maruwa Foods and Biosciences Inc., Nara 639-1123, Japan, ⁴Confocal Science Inc., Tokyo 101-0032, Japan

(P25) Visualization of the nucleotidyl-transfer reaction process by human DNA polymerase η ; T. Nakamura¹, Y. Zhao^{2,3}, Y. Yamagata¹, Y. J. Hua³, and W. Yang²; ¹Graduate School of Pharmaceutical Sciences, Kumamoto University, 5-1 Oe-honmachi, Chuo-ku, Kumamoto, 862-0973, Japan, ²Laboratory of Molecular Biology, National Institute of Diabetes and Digestive and Kidney Diseases, National Institutes of Health, Bethesda, Maryland, 20892, USA, ³Institute of Nuclear-Agricultural Sciences, Zhejiang

University, Hangzhou, 310029, China.

(P26) Structural insights into RISC assembly facilitated by dsRNA-binding domains of human RNA helicase A (DHX9); Q. Fu and Y. A. Yua^{*}; Department of Biological Sciences and Centre for Bioimaging Sciences, National University of Singapore, 14 Science Drive 4, Singapore, 117543, Singapore

(P27) Structural basis for the cytidyltransferase reaction catalyzed by yeast ECT; J. Ohtsuka,^a R. Fukuda,^b S. Wang,^a Y. Ono,^b W. C. Lee,^a K. Ito,^a K. Nagata,^a A. Ohta,^b and M. Tanokura^a; Departments of ^aApplied Biological Chemistry and ^bBiotechnology, Graduate School of Agricultural and Life Sciences, The University of Tokyo, Bunkyo-ku, Tokyo 113-8657, Japan.

(P28) Crystal structure of human CK2 α at 1.04 Å resolution; Takayoshi Kinoshita¹, Tetsuko Nakaniwa^{1,2}, Yusuke Sekiguchi¹, Yuri Sogabe¹, Atsushi Sakurai³, Shinya Nakamura³ and Isao Nakanishi³; ¹Graduate school of science, Osaka Prefecture University, 1-1 Gakuen-cho, Naka-ku, Sakai, Osaka 599-8570, Japan, ²Graduate school of science, Osaka University, 1-1 Machikaneyama, Toyonaka, Osaka 560-0043, Japan, ³Department of Pharmaceutical Sciences, Kinki University, 3-4-1 Kowakae, Higashi-osaka, Osaka 577-8502, Japan.

(P29) Crystal structures of branched-chain aminotransferase from *Deinococcus radiodurans* complexes with α -ketoisocaproate and L-glutamate suggest the radiation-resistance of this enzyme for catalysis; C.-D. Chen^{1,2}, P. Chuankhayan, Y.-C. Huang, Y.-C. Hsieh, H.-H. Guan, C.-J. Chen^{1,2,3,4}; ¹Life Science Group, Scientific Research Division, National Synchrotron Radiation Research Center, Hsinchu, Taiwan, ²Department of Physics, National Tsing Hua University, Hsinchu 30043, Taiwan, ³Institute of Biotechnology; ⁴University Center for Bioscience and Biotechnology, National Cheng Kung University, Tainan City 70101, Taiwan.

(P30) Insight into inflammation repression by enteropathogenic *Escherichia coli* from the structure of novel Zincin protease, NleC, as determined by X-ray crystallography and SAXS; M.M. Turco and M.C. Sousa; University of Colorado at Boulder, 296 UCB, Boulder, CO 80309, USA

(P31) Crystal structure of a complex of human Chymase with its benzimidazole derived inhibitor; Y. Matsumoto, S. Kakuda, M. Koizumi, T. Mizuno, Y. Muroga, T. Kawamura, and M. Takimoto-Kamimura; Teijin Institute for Bio-medical Research, 4-3-2, Asahigaoka, Hino-shi, Tokyo 191-8512, Japan

(P32) Improvement of Automated Protein Crystal Exchange System PAM for High-throughput Data Collection; M. Hiraki, Y. Yamada, L.M.G. Chavas, and N. Matsugaki; Structural Biology Research Center,

Photon Factory, Institute of Materials Structure Science, KEK, 1-1 Oho, Tsukuba, Ibaraki 305-0801, Japan

(P33) Development of on-line UV-Visible microspectrophotometer for the macromolecular crystallography beamline; N. Shimizu^{1,2}, T. Shimizu³, S. Baba¹, K. Hasegawa¹, M. Yamamoto³, and T. Kumasaka¹; ¹SPRING-8/JASRI, 1-1-1 Koto, Sayo-cho, Sayo-gun, Hyogo 679-5198, Japan. ²KEK-PF, 1-1 Oho, Tsukuba, Ibaraki 305-0801, Japan, ³RIKEN SPRING-8 Center, 1-1-1 Koto, Sayo-cho, Sayo-gun, Hyogo 679-5148, Japan.

(P34) Structure of the human muscle fatty acid-binding protein complexed with Hydrophobic ligands; M. Hirose^{1,2}, S. Sugiyama^{1,2}, H. Ishida^{1,3}, D. Matsuoka^{1,2}, T. Hara^{1,2}, E. Mizohata³, T. Inoue³, S. Matsuoka^{1,2}, M. Murata^{1,2}; ¹JST, ERATO, Lipid Active Structure Project, 1-1 Machikaneyama-cho, Toyonaka, Osaka 560-0043, Japan, ²Graduate School of Science, Osaka University, 1-1 Machikaneyama-cho, Toyonaka, Osaka 560-0043, Japan, ³Division of Applied Chemistry, Graduate School of Engineering, Osaka University, 2-1 Yamadaoka, Suita, Osaka 565-0871, Japan

(P35) New versatile crystal mounts using hydrophilic polymer glue with humidity control and fine capillary developed at SPRING-8; T. Kumasaka, N. Mizuno, and S. Baba; SPRING-8/JASRI, 1-1-1 Koto, Sayo, Hyogo 679-5198, Japan.

(P36) Atomic resolution structure of copper-containing nitrite reductase provides insights into the nature common to type 2 copper-containing enzymes; ^{1,2}Y. Fukuda, ³T. Tamada, ⁴H. Takami, ²T. Inoue and ¹M. Nojiri; ¹Graduate school of Science, Osaka University, 1-1 Machikaneyama, Toyonaka, Osaka, 560-0043, Japan, ²Graduate School of Engineering, 2-1 Yamadaoka, Suita, 565-0871, Japan, ³Molecular Biology Research Center, Quantum Beam Science Directorate, JAEA, 2-4 Shirane Shirakata, Tokai-mura, Naka-gun, Ibaraki, 319-1195, Japan, ⁴Environmental Metagenome Research Team, JAMSTEC, 3173-25 Showa-machi, Kanazawa-ku, Yokohama, Kanagawa, 236-0001, Japan.

(P37) The crystal structure of APOBEC3C including HIV-1 Vif-binding interface; S. Kitamura^{1,2}, H. Ode¹, M. Nakashima^{1,2}, M. Imahashi^{1,3}, Y. Naganawa¹, T. Kurosawa^{1,2}, Y. Yokomaku¹, T. Yamane², N. Watanabe^{2,4}, A. Suzuki², W. Sugiura^{1,3}, and Y. Iwatani^{1,3}; ¹Clinical Research Center, National Hospital Organization Nagoya Medical Center, 4-1-1 San-no-Maru, Naka-ku, Nagoya, Aichi 460-0001, Japan, ²Graduate School of Engineering, ³Graduate School of Medicine, and ⁴Synchrotron Radiation Research Center, Nagoya University, Furo-cho, Chikusa-ku, Nagoya, Aichi 464-8603, JAPAN.

(P38) Structure of AFUEI, an elastase inhibitor from *Aspergillus fumigatus*; M. Sakuma¹, K. Imada², Y. Okumura³, K. Uchiya³, A. Hijikata⁴, T. Shirai⁴, M. Homma¹ and T. Nikai³; ¹Division of Biological Science,

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(P39) Probing the equilibrium of Serpin conformations; M. Yamasaki^{1,2} and J. A. Huntington³; ¹The Hakubi Center for Advanced Research, University of Kyoto, Yoshida-Ushinomiya-cho Sakyo, Kyoto 606-8302, Japan ²Institute for Frontier Medical Sciences, University of Kyoto, 53 Kawahara-cho, Shogoin, Sakyo, Kyoto 606-8507, Japan ³Cambridge Institute for Medical Research, University of Cambridge, CB0 2XY, UK

(P40) Reaction mechanism of Serine Hydroxymethyltransferase based on crystal structures at ultra-high resolution; N.Yukawa¹, H.Ikushiro², H.Hayashi³, M.Goto⁴, N.Kamiya^{5,1}, I.Miyahara^{1,5}; ¹Graduate School of Science, Osaka City University, Sugimoto-cho, Sumiyoshi-ku, Osaka, 558-8585, Japan, ²Department of Biochemistry, Osaka Medical College, Daigaku-cho, Takatsuki, 569-8686, Japan, ³Department of Chemistry, Osaka Medical College, Daigaku-cho, Takatsuki, 569-8686, Japan, ⁴Graduate School of Science, Toho University, Miyama, Hunahashi, Chiba, 274-8510 Japan, ⁵The OCU Advanced Research Institute for Natural Science and Technology (OCARINA), Osaka City University, Sugimoto-cho, Sumiyoshi-ku, Osaka, 558-8585, Japan

(P41) Solution Structural Studies of Soluble Extracellular Domain of Amyloid Precursor Protein; S. Kanemura^{1,3}, M. Okumura^{2,3}, D. Imai^{1,3}, T. Hikima³, M. Niinobe⁴, Y. Hidaka⁵ and H. Yamaguchi^{1,3}; ¹School of Science and Technology, Kwansai Gakuin University, 2-1 Gakuen, Sanda, Hyogo 669-1337, Japan, ²Division of Protein Chemistry, Medical Institute of Bioregulation, Kyushu University, 3-1-1 Maidashi, Higashi-ku, Fukuoka 812-8582, Japan, ³RIKEN SPring-8 Center, RIKEN Harima Institute, 1-1-1 Koto, Sayo-cho, Sayo-gun, Hyogo 679-5148, Japan, ⁴Institute for Protein Research, Osaka University, 1-1 Yamadaoka, Suita, Osaka 565-0871, Japan, ⁵School of Science and Engineering, Kinki University, 3-4-1 Kowakae, Higashi-osaka, Osaka 577-8502, Japan

(P42) Reduction of repulsive intermolecular interaction of myoglobin by removal of the heme; H. Imamura¹, T. Morita¹, T. Sumi², Y. Isogai³, M. Kato⁴, K. Nishikawa¹; ¹Graduate School of Advanced Integration Science, Chiba University, 1-33 Yayoi, Inage, Chiba, 263-8522, Japan, ²Department of Computer Science and Engineering, Toyohashi University of Technology, 1-1 Hibi-rigaoka, Tempaku, Toyohashi, Aichi, 441-8580, Japan, ³Department of Biotechnology, Toyama Prefectural University, 5180 Kurokawa Imizu Toyama, 939-0398, Japan, ⁴Department of Pharmacy, Ritsumeikan University, 1-1-1

Nojihigashi, Kusatsu, Shiga, 525-8577, Japan.

(P43) Site-specific relaxation of peptide bond planarity - attributable to excessively-localized deuterium nuclei observed by neutron crystallography; K. Chiba-Kamoshida^{1,2}, T. Matsui¹, T. Chatake¹, T. Ohhara¹, I. Tanaka¹, K. Yutani³ and N. Niimura¹; ¹Advanced Science Research Centre, JAERI, Tokai, 319-1195, JAPAN; ²Age-Dimension Research Centre, AIST, Tsukuba, 305-8566, JAPAN; ³RIKEN SPring-8 Center, RIKRN Harima Institute, Sayo, Hyogo, 679-5148, JAPAN.

(P44) Atomic dynamics of ADPRase in the reaction pathway and pH titration; Y. Furuike¹, Y. Tomita¹, Y. Akita¹, I. Miyahara^{1,2}, and N. Kamiya^{2,1}; ¹Graduate School of Science, Osaka City University, ²The OCU Advanced Research Institute for Natural Science and Technology (OCARINA), Osaka City University, 3-3-138 Sugimoto, Sumiyoshi, Osaka 558-8585, Japan

(P45) Discovery of New Phase of the Structure of Lipids and DNA Complex by TEM; G. Tamura^{1,2}, N. Hosogi³, W. Shinoda⁴, P. Matsudaira^{1,2}, and K. Nagayama⁵; ¹Centre for Bio-Imaging Sciences (CBIS), National University of Singapore (NUS), 14 Science Drive 4, 117543, Singapore, ²Mechanobiology Institute (MBI), National University of Singapore (NUS), 5A Engineering Drive 1, 117411, Singapore, ³EM Application Department, EM Business Unit, JEOL Ltd., 3-1-2, Musashino, Akishima, Tokyo, 196-8558, Japan, ⁴Health Research Institute (HRI), National Institute of Advanced Industrial Science and Technology (AIST), 1-8-31 Midorigaoka, Ikeda, Osaka, 563-8577, Japan, ⁵National Institute of Physiological Sciences (NIPS), 5-1, Myodajji Higashiyama, Okazaki, Aichi, 444-8787, Japan

(P46) Toward realization of a high-speed classification system for one million single biomolecule diffraction patterns on K computer; A. Tokuhisa¹, J. Ara², Y. Joti³, Y. Ohno⁴, T. Kameyama⁴, K. Yamamoto⁴, A. Shimada⁴, M. Hatanaka⁴, G. Baias⁴, M. Yokokawa⁴, H. Shoji⁴, M. Kurokawa⁴, A. Hori⁴ and T. Hatsui¹; ¹RIKEN SPring-8 Center, 1-1-1, Kouto, Sayo-cho, Sayo-gun, Hyogo, 679-5148, JAPAN, ²The University of Tokyo, 7-3-1, Hongo, Bunkyo-ku, Tokyo, 113-0033, JAPAN, ³JASRI, 1-1-1 Kouto, Sayo-cho, Sayo-gun, Hyogo, 679-5198, JAPAN, ⁴RIKEN AICS, 7-1-26, Minami-machi, Minato-jima, Chuo-ku, Kobe, Hyogo, 650-0047, JAPAN

(P47) Crystal structure analysis of DING protein; Y. Tanaka, Z. Gai, A. Nakamura, N. Hirano, I. Tanaka, and M. Yao; Faculty of Advanced Life Science, Hokkaido University, Sapporo, 060-0810, Japan

(P48) Inhibition of electron transfer in photosystem II studied by crystal structure analysis and quantum chemical calculation; A. Tanaka¹, S. Suzuri¹, T. Asada², K. Kawakami³, Y. Umena^{3,5}, J.-R. Shen⁴, I. Miyahara^{1,3}, N. Kamiya^{3,1}; ¹Grad. of Sci., Osaka City Univ. 3-3-138 Sugimoto Sumiyoshi,

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(P49) Surface polarity and energy analyses of protein-protein interactions in crystals; S. Yamamura¹, M. Ootaki², S. Endo¹, T. Takahashi³ and Y. Sugawara¹; ¹School of Science, Kitasato University, Minami-ku, Sagami-hara, Kanagawa 252-0373, Japan, ²Institute of Radioisotope Research, St. Marianna University Graduate School of Medicine, Miyamae-ku, Kawasaki, Kanagawa 216-8511, Japan, ³College of Life Science, Ritsumeikan University, Kusatsu, Shiga 525-8577, Japan

(P50) Protein, hydrogen bonds and hydration waters towards neutron protein crystallography; A. Yamaguchi¹, N. Niimura³, T. Yamada³, T. Yokoyama⁴, S. Nakamura⁵, S. Kidokoro⁵, and I. Tanaka²; ¹Faculty of Engineering, Ibaraki University, 4-12-1, Naka-Narusawa, Hitachi, Ibaraki 316-8511, Japan, ²Graduate School of Science and Engineering, Ibaraki University, 4-12-1, Naka-Narusawa, Hitachi, Ibaraki 316-8511, Japan, ³Frontier Research Center for Applied Atomic Sciences, Ibaraki University, 162-1 Shirakata, Tokai, Ibaraki 319-1106, Japan, ⁴Faculty of Pharmaceutical Sciences, University of Toyama, 2630 Sugitani, Toyama 930-0914, Japan, ⁵Department of Bioengineering, Nagaoka University of Technology, 1603-1, Kamitomioka, Nagaoka, Niigata 940-2188, Japan

(P51) Current status of IBARAKI biological crystal diffractometer iBIX at J-PARC; K. Kusaka¹, T. Hosoya¹, T. Yamada¹, K. Tomoyori¹, T. Ohhara², M. Katagiri¹, K. Kurihara^{3,4}, I. Tanaka¹ and N. Niimura¹; ¹Frontier Research Center for Applied Atomic Sciences, Ibaraki University, Tokai, Ibaraki 319-1106, Japan, ²Center for Neutron Science & Technology, CROSS, Tokai, Ibaraki 319-1106, Japan, ³J-PARC Center, JAEA, Tokai Ibaraki 319-1195, Japan, ⁴Quantum Beam Science Directorate, JAEA, Tokai, Ibaraki 319-1195, Japan

(P52) Error estimation guided rebuilding of *de novo* models increases the success rate for *ab initio* phasing; R. Shrestha, D. Simoncini and K. Y. J. Zhang; Zhang Initiative Research Unit, Advanced Science Institute, RIKEN, 2-1 Hirosawa, Wako, Saitama 351-0198, Japan

(P53) SPring-8 BL41XU, a high flux macromolecular crystallography beamline; K. Hasegawa¹, N. Shimizu^{1,2}, H. Okumura¹, N. Mizuno¹, S. Baba¹, K. Hirata³, T. Takeuchi¹, H. Yamazaki¹, Y. Senba¹, H. Ohashi¹, M. Yamamoto³, and T. Kumasaka¹; ¹SPring-8/JASRI, 1-1-1 Kouto, Sayo-cho, Sayo-gun, Hyogo 679-5198, Japan. ²KEK-PF, 1-1 Oho, Tsukuba, Ibaraki 305-0801, Japan, ³RIKEN SPring-8 Center, 1-1-1 Kouto, Sayo-cho, Sayo-gun, Hyogo 679-5148, Japan.

(P54) Structure analysis of archaeal AMP phosphorylase reveals a unique mode of multimerization;

Y. Nishitani¹, R. Aono², A. Nakamura¹, T. Sato^{2,3}, H. Atoml^{2,3}, T. Imanaka⁴, and K. Miki¹; ¹Graduate School of Science, Kyoto University, Sakyo-ku, Kyoto 606-8502, Japan, ²Graduate School of Engineering, Kyoto University, Katsura, Nishikyo-ku, Kyoto 615-8510, Japan, ³JST, CREST, Sanbancho, Chiyoda-ku, Tokyo, Japan, ⁴College of Life Sciences, Ritsumeikan University, Noji-higashi, Kusatsu, Shiga 525-8577, Japan.

(P55) Crystal structure analysis of *Pyrococcus horikoshii* Deoxyhypusine Synthase; ZQ. Gai, C. Okada, J. Yu, H. Wakabayashi, K. Komoda, Y. Tanaka, I. Tanaka, and M. Yao; Faculty of Advanced Life Science, Hokkaido University, Sapporo, 060-0810, Japan

(P56) Where are my proteins? Suppressing extraneous effects in x-ray free-electron laser imaging; N. Duane Loh; PULSE Institute, SLAC National Accelerator Laboratory, Menlo Park, CA 94025, USA.

(P57) Crystal Structure of Mutated C-terminal Domain of *Clostridium perfringens* Enterotoxin with Higher Affinity for Claudin-4; H. Aoyama, A. Inoue, H. Tsujino, K. Matsuhisa, M. Kondoh, K. Yagi, and T. Uno; Graduate School of Pharmaceutical Sciences, Osaka University, Suita, Osaka 565-0871, Japan

(P58) Structural analysis of a hydrazide catalyzing enzyme from *Microbacterium* sp.; T. Akiyama¹, M. Ishii¹, A. Takuwa², Y. Sasaki¹, K. Oinuma², N. Takaya², and S. Yajima¹; ¹Tokyo University of Agriculture, 1-1-1 Sakuragaoka, Setegaya-ku, Tokyo 156-0054, Japan, ²Tsukuba University, 1-1-1 Tennodai, Tsukuba Ibaraki 305-0006, Japan.

(P59) Creation and structure determination of an artificial protein with three complete sequence repeats; M. Adachi¹, R. Shimizu¹, R. Kuroki¹, and M. Blabe²; ¹Quantum Beam Science Directorate, Japan Atomic Energy Agency, Shirakata-Shirane 2-4, Tokaimura, Ibaraki 319-1195, Japan, ²Department of Biomedical Sciences, Florida State University, Tallahassee FL 32306-4300, USA

(P60) Improvements toward highly precious diffraction experiments at the macromolecular micro-crystallography beamline BL-17A; Y. Yamada¹, L.M.G. Chavas¹, N. Igarashi¹, M. Hiraki¹, S. Wakatsuki^{1,2,3} and N. Matsugaki¹; ¹KEK-PF, 1-1 Oho, Tsukuba, Ibaraki 305-0801, Japan, ²Photon Science, SLAC, 2575 Sand Hill Rd, MS 69, Menlo Park, CA 94025-7015, USA, ³Structural Biology, School of Medicine, Stanford University, Beckman Center B105, 279 Campus Drive, Stanford, CA 94305-5126, USA

(P61) Crystal structures of human Toll-like receptor 8; U. Ohto¹, H. Tanji¹, T. Shibata², K. Miyake², and T. Shimizu¹; ¹Graduate School of Pharmaceutical Sciences, University of Tokyo, 7-3-1 Hongo, Bunkyo, Tokyo 113-0033, Japan, ²Division of Innate Immunity, Department of Microbiology and Immunology, Laboratory of Innate Immunity, Center for Experimental Medicine and Systems Biology, The Institute of

Medical Science, The University of Tokyo, 4-6-1 Shirokanedai, Minato-ku, Tokyo 108-8639, Japan.

(P62) DNA-mediated allosteric regulation in a complex of multiple transcription factors with DNA; M Shiina, K Hamada, T Inoue-Bungo, M Shimamura, A Uchiyama, S Baba, K Sato, and K Ogata; Department of Biochemistry, Yokohama City University Graduate School of Medicine, 3-9 Fukuura, Kanazawa-ku, Yokohama, Kanagawa 236-0004, Japan.

(P63) Crystal structure of endo-1,4- β -glucosylase from *Eisenia foetida*; T. Arimori¹, A. Itoh², M. Nakazawa², M. Ueda², and T. Tamada¹; ¹Quantum Beam Science Directorate, Japan Atomic Energy Agency, 2-4, Shirakata-Shirane, Tokai, Ibaraki 319-1195, Japan, ²Graduate School of Life and Environmental Sciences, Osaka Prefecture University, 1-1 Gakuen-cho, Sakai, Osaka 599-8531, Japan.

(P64) Crystal structure of UDP-glucose: anthocyanidin 3-O- glucosyl- transferase from *Clitoria ternatea*; T. Hiromoto, E. Honjo, T. Tamada, and R. Kuroki; Quantum Beam Science Directorate, Japan Atomic Energy Agency, 2-4 Shirakata-Shirane, Tokai, Ibaraki 319-1195, Japan

(P65) Fundamental studies for proton polarization technique in neutron protein crystallography; I. Tanaka^{1,2}, K. Kusaka², T. Chatake³, and N. Niimura²; ¹College of Engineering, Ibaraki Univ., 4-12-1, Naka-Narusawa, Hitachi, Ibaraki 316-8511, Japan, ²Frontier Research Center for Atomic Sciences, Ibaraki Univ., 162-1, Shirakata, Tokai, Ibaraki 319-1106, Japan, ³Research Reactor Institute, Kyoto Univ., 2, Asashironishi, Kumatori, Osaka 590-0494, Japan.

(P66) Development of simultaneous SAXS/WAXS data collection system based on PILATUS detectors at BL-6A of the Photon Factory; N. Igarashi¹, N. Shimizu¹, T. Mori¹, H. Ohta², Y. Nagatani¹, T. Kosuge¹ and K. Ito¹; ¹KEK-PF, 1-1 Oho, Tsukuba, Ibaraki 305-0801, Japan, ²Mitsubishi Electric SSC, 20F Carrot Tower, 4-1-1 Taishido, Setagaya-ku, Tokyo 154-8520, Japan.

(P67) Crystal structures of MqnD, a menaquinone biosynthetic enzyme, complexed with the product, 1,4-dihydroxy-6-naphthoate, and its analogs; R. Arai¹, K. Matsuo¹ and T. Dairi²; ¹Fac. of Tex. Sci. & Tech., Shinshu Univ., Ueda, Nagano 386-8567, Japan, ²Grad. Sch. of Eng., Hokkaido Univ., Sapporo, Hokkaido, 060-8628, Japan

(P68) Crystal structural analysis of *drosophila* nucleosome assembly protein; K. Hamada¹, M. Shiina¹, R. Nakashima¹, M. Saito¹, T. Ito², K. Ogata¹; ¹Department of Biochemistry, Yokohama City University Graduate School of Medicine, 3-9 Fukuura, Kanazawa, Yokohama 236-0004, Japan, ²Department of Biochemistry, Nagasaki University School of Medicine, 1-12-4 Sakamoto, Nagasaki 852-8523, Japan.

(P69) Crystal structure of channelrhodopsin, a light-gated cation channel; H. E. Kato¹, F. Zhang², O. Yizha², C. Ramakrishnan², T. Nishizawa¹, K. Hirata³, J. Ito⁴, Y. Aita⁴, T. Tsukazaki¹, S. Hayashi⁵, P. Hegemann⁶, A. D. Maturana⁴, R. Ishitani¹, K. Deisseroth², O. Nureki¹; ¹Department of Biophysics and Biochemistry, Graduate School of Science, The University of Tokyo, 2-11-16 Yayoi, Bunkyo-ku, Tokyo 113-0032, Japan, ²Department of Bioengineering and Howard Hughes Medical Institute, Stanford University, Stanford, California 94305, USA, ³RIKEN, SPring-8 Center, Hyogo 679-5148, Japan, ⁴Department of Bioengineering Sciences, Graduate School of Bioagricultural Sciences, Nagoya University, Furo-cho, Chikusa-ku, Nagoya, 464-8601, Japan, ⁵Department of Chemistry, Graduate School of Science, Kyoto University, Kyoto 606-8502, Japan, ⁶Institute of Biology, Experimental Biophysics, Humboldt-University, Invalidenstrae 42,D-10115 Berlin, Germany

(P70) Crystal Structure of Dimerized N-terminal Domain of MinC by Domain Swapping; J. Y. An^{1,2}, T. G. Kim^{1,2}, K. R. Park^{1,2}, J.-G. Lee^{1,2}, H.-S. Youn^{1,2}, J.-Y. Kang^{1,2}, Y.-J. Lee^{1,2}, G. B. Kang¹, and S. H. Eom^{1,2}; ¹School of Life Sciences, Gwangju Institute of Science and Technology, Gwangju 500-712, South Korea, ²Steitz Center for Structural Biology, Gwangju Institute of Science and Technology, Gwangju 500-712, South Korea.

(P71) The preliminary TOF neutron diffraction experiment of human α -thrombin-bivalirudin complex using iBIX at J-PARC; T. Yamada¹, K. Kusaka¹, T. Hosoya¹, T. Ohhara², K. Tomoyori¹, K. Kurihara³, I. Tanaka¹, M. Katagiri¹, and N. Niimura¹; ¹Frontier Research Center for Applied Atomic Sciences, Ibaraki University, IQBRC Bldg, 162-1 Shirakata, Tokai, Naka, Ibaraki, 319-1106, Japan, ²CROSS-Tokai, Research Center for Neutron Science and Technology, IQBRC Bldg, 162-1 Shirakata, Tokai, Naka, Ibaraki JAPAN 319-1106, Japan, ³Quantum Beam Science Directorate, JAEA, Tokai, Ibaraki 319-1195, Japan

(P72) Dynamic Fluid-Structure Interaction Simulation of High-brightness X-ray Generator; S.Ishiyama; Quantum Beam Science Directorate, Japan Atomic Energy Agency, Tokai-mura, Naka-gun, Ibaraki, 319-1195 Japan

(P73) Structure and thermal stability of liposome entrapping proteins; R. Kimura¹, M. Hirai¹, N. Ohta², A. Igarashi³, and S. Shimuzu³; ¹Graduate School of Engineering, Gunma University, 4-2 Aramaki, Maebashi, Gunma 371-8510, Japan, ²JASRI, Sayo-gun, Hyogo 679-5198, Japan, ³KEK-PF, Tsukuba, Ibaraki 305-0801, Japan.

(P74) Effect of crowded co-solutes on protein structure; K. Takeuchi¹, M. Hirai¹, N. Ohta², S. Shimuzu³, and A. Igarashi³; ¹Graduate School of Engineering, Gunma University, 4-2 Aramaki, Maebashi, Gunma 371-8510, Japan, ²JASRI, 1-1-1, Kuoto, Sayo-cho, Sayo-gun, Hyogo 679-5198, Japan, ³KEK-PF, 1-1 Oho,

Tsukuba, Ibaraki 305-0801, Japan.

(P75) Growing high-quality protein crystal in Kibo in the International Space Station; K. Ohta¹, S. Takahashi², N. Furubayashi³, B. Yan², Y. Wada¹, M. Yamada¹, K. Inaka³, H. Tanaka², H. Miyoshi¹, T. Kobayashi¹ and S. Kamigaichi¹; ¹JAXA, 2-1-1 Sengen, Tsukuba, Ibaraki 305-8505, Japan, ²Confocal Science Inc., 2-12-2 Iwamoto-cho, Chiyoda-ku, Tokyo 101-0032, Japan, ³Maruwa Foods and Biosciences Inc., 170-1 Tsutsui-cho, Yamatokoriyama, Nara 639-1123, Japan.

(P76) Numerical Model of Protein Crystal Growth in a Transient Homogeneous Field (Ground) and Transient Diffusive Field (Space); H. Tanaka¹, S. Sasaki², S. Takahashi¹, K. Inaka³, Y. Wada⁴, M. Yamada⁴, K. Ohta⁴, H. Miyoshi⁴, T. Kobayashi⁴ and S. Kamigaichi⁴; ¹Confocal Science Inc., 2-12-2 Iwamoto-cho, Chiyoda-ku, Tokyo 101-0032, Japan, ²Neo Force, 5-9-14 Tsurumaki, Setagaya-ku, Tokyo 154-0016, Japan, ³Maruwa Foods and Biosciences Inc., 170-1 Tsutsui-cho, Yamatokoriyama, Nara 639-1123, Japan, ⁴JAXA, 2-1-1 Sengen, Tsukuba, Ibaraki 305-8505, Japan.

(P77) Prediction of the positions and thermodynamic properties of hydrating water molecules on protein surfaces; its implications to drug design; O. Ichihara; Schrödinger K.K., 17F Marunouchi Trust Tower North, 1-8-1 Marunouchi, Chiyoda-ku, Tokyo 100-0005, Japan.

(P78) Molecular dynamics of *Manihot esculenta* hydroxynitrile lyase; S. Okazaki^{1,2}, S. Nakano^{1,2}, and Y. Asano^{1,2}; ¹Biotechnology Research Center and Department of Biotechnology, Toyama Prefectural University, 5180 Kurokawa, Imizu, Toyama 939-0398, Japan, ²JST, ERATO, Asano Active Enzyme Molecule Project, 5180 Kurokawa, Imizu, Toyama 939-0398, Japan.

(P79) Crystallization of inverting cellulase based on the crystallization phase diagram for neutron protein crystallography; A. Nakamura¹, T. Ishida¹, S. Fushinobu¹, K. Kusaka², I. Tanaka², K. Inaka³, M. Masaki⁴, K. Ohta⁴, S. Kaneko⁵, N. Niimura², M. Samajima¹ and K. Igarashi¹; ¹Graduate School of Agricultural and Life Sciences, The University of Tokyo, 1-1-1 Yayoi, Bunkyo-ku, Tokyo, 113-8657, Japan, ²Frontier Research Center for Applied Atomic Sciences, Ibaraki University, 164-1 Shirakita, Tokai-mura, Naka-gun, Ibaraki, 319-1106, Japan, ³MARUWA Foods and Biosciences, Inc., 170-1 Tutui, Yamatokoriyama, Nara, 639-1123, Japan, ⁴Japan Aerospace Exploration Agency, Tsukuba Space Center, 2-1-1 Sengen, Tsukuba, Ibaraki, 305-8505, Japan, ⁵National Food Research Institute, 1-2-12 Kannondai, Tsukuba, Ibaraki 304-8642, Japan.