

**Crystallographic Software Fayre (3)**

**R-1102 (9:00-17:00)**

Organizer: L. Cranswick

**Luncheon Seminar**

**12:45-13:30**

C-1001.2 : Sponsored by Sysmex Corp. (200 seats)

C-1003 : Sponsored by SPring-8 (200 seats)

**Commission on Small-Angle Scattering**

**R-1101 (12:30-14:45)**

**Programm Committee of European Crystallographic Association**

**R-1008 (12:30-14:45)**

**Commission on Aperiodic Crystals**

**R-0805 (13:00-14:30)**

**Music Session (3)**

**B-05SH (18:30-21:00)**

**IUCr General Assembly**

**F-12CH (19:00-21:00)**

**Poster Numbers:**

Poster number indicates Topic, Sub-topic and serial number, for example :

**P01.01.01**→Topic 01. *Instrumentation and Experimental Techniques* / Sub-Topic 01. *Conventional Sources of X-rays* / Serial Number within the main topic.

**Poster Presentation**

**28-29 August**

**Topics and Sub-topics**

**01 Instrumentation and Experimental Techniques**

1. Conventional Sources of X-rays
2. Synchrotron Radiation I: Instrumentation and Techniques
3. Synchrotron Radiation II: Applications
4. New X-ray Sources
5. Electron Diffraction (LEED, RHEED, PED, AED)
6. Cryo-Electron Microscopy
7. X-ray Imaging
8. Neutron Scattering I: Techniques and Instrumentation
9. Neutron Scattering II: Applications
10. Area Detectors (Multi-wire, Image Plate, CCD)
11. Data Accuracy and Detectors
12. Cryo-Crystallography: Techniques and Instrumentation
13. Fast (pico-second) Crystallography
14. Free Electron Lasers for X-rays

**04 Crystallography of Biological Macromolecules**

1. Peptide and Protein Crystallization
2. Enzymes and Enzyme Catalysis
4. Muscle and Motor Proteins
20. NMR Applications to Macromolecules

**08 Structure/Property Relationships**

1. Molecular Recognition
10. Polymorphism and Isomorphism: Identification and Characterization
11. Polymorphism: Applications
14. Structure-Property Relationships

**11 Crystallography in Material Science**

2. Catalysis: *In situ* Studies
5. Noncrystalline Materials
8. Polymers
9. Liquid Crystals
13. Battery and Fuel Cell Materials
14. Residual Stress Measurements
15. Pore Framework Materials

**15 Diffraction Physics and Optics**

1. Interferometry
2. Inelastic Scattering
3. Neutron Optics
4. X-ray Optics: Lenses, Guides and Focusing
5. Resonant Magnetic X-ray Diffraction
6. Anisotropic Resonant Scattering

7. Polarization: Generation and Exploitation
8. Dynamical Diffraction
9. Extinction and Absorption
10. N-beam Diffraction
11. Grazing Angle Incidence

### 21 Symmetry and its Generalizations

1. General Symmetry: Theory
2. Designer Symmetry: Theory and Practice
3. Pseudo-Symmetry: Recognition and Applications

### 22 Aperiodic and Incommensurate Structures

1. Data Collection and Structure Solution
2. Identification and Refinement
3. Results and Applications

### 23 Crystallographic Topology

1. Group Theory and Topology
2. Tiling
3. Quasicrystals
4. Networks
5. Critical Points

### 24 Databases

1. Creation and Exploitation
2. Coping with Rapid Expansions of Data: The Next Generation of Databases
3. Research Applications of the CSD
4. Research Applications of the PBD/ NADB

5. Research Applications of the ICSD
6. Research Applications of the PDF
7. Data Mining and Knowledge Generation
8. Bioinformatics: The Future

### 25 Industrial Crystallography

1. Instrumentation and Techniques
2. Stress-Strain Analysis
3. On Line Diffraction Analysis
4. Line Broadening
5. Amorphous and SAS
6. Microporous Materials
7. Nanomaterials
8. High Temperature Crystallography
9. Thick Coatings
10. Pharmaceutical Crystallography

### 29 Other Topics

### 01. INSTRUMENTATION AND EXPERIMENTAL TECHNIQUES

**P01.01.01(C171)** | H. Okuda: Two-dimensionally curved Ge for focusing crystals prepared by a hot plastic deformation

**P01.01.02(C171)** | J. D. Ferrara: New optics for molecular macromolecular crystallography

**P01.01.03(C171)** | C. Michaelsen: X-ray diffractometry with a microfocus source

**P01.04.04(C171)** | J. Graf: Small X-ray beams for small crystals: Pushing the limits of home-lab X-ray sources

**P01.04.05(C172)** | D. C. Frankel: Optimizing signal-to-noise on a home X-ray source for the analysis of microcrystals

**P01.04.06(C172)** | H. Kawata: Present status of energy recovery linac project in Japan

**P01.04.07(C172)** | Z. Amirkhanyan: Transition radiation of relativistic electron from the superlattice of dielectric permittivity

**P01.02.08(C173)** | A. Douangamath: A monochromatic station for macromolecular crystallography at diamond light source

**P01.02.09(C173)** | R. Flaig: Experience from operation and commissioning of the phase 1 MX beamlines at diamond light source

**P01.02.10(C173)** | J. Jeyaraman: Installation of high throughput protein crystallography data collection at SPring-8 BL12B2

**P01.02.11(C174)** | K. Larsson: Crystallography at MAX-lab

**P01.02.12(C174)** | D. Hall: Macromolecular crystallography at Diamond Light Source: Automation and pathogenic sample environment

**P01.02.13(C174)** | M. Hiraki: Approach for automated data collection at the photon factory protein crystallography beamlines

**P01.02.14(C175)** | L. E. Berman: A proposed suite of macromolecular crystallography facilities for NSLS-II

**P01.02.15(C175)** | N. Matsugaki: A new macromolecular crystallography beamline for softer X-ray at the Photon Factory

**P01.02.16(C175)** | Y. Yamada: AR-NE3A, a new pharmaceutical beamline for macromolecular crystallography at the Photon Factory

**P01.02.17(C176)** | N. Igarashi: Beamline developments for structural biology at the Photon Factory

**P01.03.18(C176)** | C. B. Trame: Experiences with automated crystal screening at the JCSG

**P01.03.19(C176)** | M. Wang: Automation of the protein crystallography beamline X06DA at the swiss light source

**P01.03.20(C177)** | G. Ueno: Beamline automation and mail-in data collection at SPring-8 structural biology beamlines

**P01.02.21(C177)** | C. Chao: Beamline automation and remote access at NSRRC BL-13

**P01.03.22(C177)** | M. Aslantas: New approaches to room-temperature synchrotron data collection in macromolecular crystallography

**P01.03.23(C177)** | D. K. Schneider: The PXRR integrates six beamlines for macromolecular crystallography at the NSLS into one resource

**P01.02.24(C178)** | S. Classen: SAXS and macromolecular crystallography at the SIBYLS beamline (12.3.1) of the Advanced Light Source

**P01.02.25(C178)** | G. L. Card: The new micro-focus beamline at SSRL: Current capabilities and future possibilities

**P01.02.26(C178)** | K. Igor: NorthEastern Collaborative Access Team (NE-CAT) beam lines at the advanced photon source

**P01.02.27(C179)** | R. Fourme: A beamline for anomalous diffraction at SOLEIL : Proxima 1

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**P01.03.28(C179)** | J. P. Rose: Pushing the envelop of sulfur SAS structure determination at UGA/SER-CAT

**P01.03.29(C179)** | R. F. Fischetti: Probing radiation damage with a 1-micron beam

**P01.03.30(C180)** | S. W. Wilkins: Towards protein structure determination using two-dimensional crystals and powders

**P01.02.31(C180)** | D. Ahn: 8C2 high resolution powder diffraction beamline at Pohang Light Source and its recent results

**P01.02.32(C180)** | N. A. Rae: Accurate powder diffraction standards: Determination of the lattice parameter of LaB<sub>6</sub> SRM(660)

**P01.02.33(C180)** | J. M. Sasaki: A halogen lamp furnace to synthesize nanoparticles: *In situ* X-ray absorption spectroscopy

**P01.03.34(C181)** | M. Tanaka: Vacuum-ultraviolet circular dichroism of amino acid films by polarizing-undulator based system

**P01.03.35(C181)** | W. Clegg: Bringing the power of synchrotron crystallography to the chemical community

**P01.02.36(C181)** | Y. Ohishi: X-ray focusing by using compound refractive lens optimized for high-pressure XRD at SPring-8

**P01.02.37(C182)** | J. Wiesmann: Total reflection and multilayer optics for synchrotrons and free-electron lasers

**P01.02.38(C182)** | J. P. Wright: Center of mass grain maps in 3D

**P01.07.39(C182)** | H. P. Bezirganyan: Grazing-angle incidence hard X-ray nanoscope

**P01.07.40(C183)** | M. M. Murshed: Application of synchrotron X-ray micro tomographic microscopy at low temperature

**P01.07.41(C183)** | J. Hodeau: Imaging and structural analysis of heterogeneous diluted materials by diffraction tomography

**P01.07.42(C183)** | K. Sakurai: Realtime imaging in X-ray fluorescence and X-ray diffraction

**P01.07.43(C184)** | P. Maj: Low noise multichannel ASIC for readout of SSD used in diffraction for powder and multilayer samples

**P01.08.44(C184)** | I. Tanaka: A new biological neutron diffractometer (iBIX) in J-PARC

**P01.08.45(C184)** | K. Kusaka: Optimization of design parameters of IBARAKI Biological Crystal Diffractometer (iBIX) in J-PARC

**P01.08.46(C185)** | K. Kurihara: Optics and shielding of IBARAKI Biological Crystal Diffractometer (iBIX) in J-PARC

**P01.10.47(C185)** | T. Hosoya: Development of a new detector and DAQ systems for iBIX

**P01.08.48(C185)** | T. Ohhara: Development of data processing software for a TOF single crystal neutron diffractometer at J-PARC

**P01.08.49(C186)** | T. Ishigaki: The current status of iMATERIA - Versatile neutron diffractometer at J-PARC

**P01.09.50(C186)** | P. F. Henry: Impact of modern neutron powder diffraction instrumentation on the study of hydrogenous materials

**P01.08.51(C186)** | C. Hoffmann: TOPAZ: A new time-of-flight laue diffractometer for new science

**P01.08.52(C187)** | R. O. Piltz: First results from the KOALA neutron Laue instrument

**P01.08.53(C187)** | M. Christensen: Mismatch cobaltite lattices investigated by white beam neutron diffraction

**P01.09.54(C187)** | M. Meven: Unconventional single crystal diffraction studies with hot neutrons on HEiDi at FRM II

**P01.08.55(C188)** | B. Deme: New design for D16 at the ILL

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**P01.08.56(C188)** | K. C. Littrell: CG2 general-purpose high-flux SANS instrument at HFIR at Oak Ridge National Laboratory

**P01.08.57(C188)** | S. Zhang: Neutron transmission strain tomography

**P01.08.58(C188)** | M. Strobl: BioRef - a time-of-flight reflectometer at Hahn-Meitner Institute Berlin

**P01.08.59(C189)** | V. M. Hutanu: The new polarised hot neutron single crystal diffractometer POLI-HEiDi at FRM II

**P01.09.60(C189)** | C. Pappas: Polarimetric neutron spin echo spectroscopy

**P01.08.61(C189)** | K. Shibata: The study of thermal diffuse scattering measured by pulsed neutron diffraction

**P01.09.62(C190)** | M. M. Jones: Simultaneous thermogravimetric and neutron diffraction characterization of hydrogen stores

**P01.08.63(C190)** | P. Mikula: Boost of multiple reflection effects - a new challenge for high-resolution neutron experiments

**P01.08.64(C190)** | M. B. Tamaki: Transmission neutron monochromator and coherent neutron scattering images

**P01.08.65(C191)** | A. M. Filhol: Anniversary - 10 years of McStas for instrument design and science

**P01.10.66(C191)** | M. Moon: Development of curved position-sensitive neutron detectors for FCD at HANARO

**P01.10.67(C191)** | Y. Ishikawa: Single crystal structure analysis by neutron 2D-PSD

**P01.10.68(C191)** | M. W. Tate: Pixel array detectors for high count rate X-ray imaging

**P01.11.69(C192)** | K. Hasegawa: Shutter-less continuous rotation data collection from protein crystals with the X-ray CMOS detector

**P01.10.70(C192)** | T. Taguchi: Novel pixel detector for in-house XRD applications

**P01.10.71(C192)** | J. Dohnalek: Protein diffraction experiments with Atlas CCD detector

**P01.11.72(C192)** | N. Boudet: The XPAD3 hybrid pixel detector applications

**P01.11.73(C193)** | A. J. Schierbeek: More signal, less noise : Making good use of bright sources & fast detectors

**P01.11.74(C193)** | M. R. Probert: DATAVIEW: A new post processing analysis tool

**P01.12.75(C193)** | A. Yamano: A hyperquenching tool

**P01.12.76(C193)** | S. K. Nayak: *In situ* crystallizations of Cl and Br substituted anilines and its intermolecular interactions

**P01.15.77(C194)** | K. Shiba: Relation of DLS distribution of protein samples with thermal stability

**P01.15.78(C194)** | J. N. Poulsen: Microseed matrix screening: A modified version

**P01.12.79(C194)** | B. Rupp: An open and flexible robotic system designed towards autonomous protein crystal harvesting

**P01.15.80(C195)** | J. M. Jenkins: Facilitating low volume protein crystallography set-ups using the mosquito® liquid handler

**P01.02.81(C195)** | H. J. Bernstein: A simplified unified approach for animations and movies using SBEVSL

**P01.02.82(C195)** | J. C. Nix: Remote data collection and rapid scheduling at the Molecular Biology Consortium beamline ALS 4.2.2

**P01.13.83(C196)** | S. L. Johnson: Femtosecond X-ray science at the Swiss Light Source

**P01.02.84(C196)** | D. J. Rodi: WAXS as a novel tool in drug discovery

**P01.13.85(C196)** | M. R. Warren: Time-resolved photo-crystallographic investigation of metastable species

**P01.13.86(C197)** | J. Hallmann: Picosecond crystallography of homogeneous [2+2] photodimerisation reactions

**P01.14.87(C197)** | G. Faigel: Modeling of single molecule imaging by X-ray free electron laser

**P01.11.88(C197)** | B. B. He: Geometry and resolution of area detectors for X-ray powder diffraction

**P01.15.89(C197)** | T. K. Mondal: Effect of pressure and temperature on the crystallization behavior of As Te glasses with selenium

**P01.11.90(C198)** | V. Y. Lunin: The modelling of experimental errors improves statistical description of merohedrally twinned data

**P01.11.91(C198)** | T. Ida: Statistical properties of measured X-ray intensities affected by counting loss of detection system

**P01.15.92(C198)** | E. Brostromer: The XtalFinder imaging system

**P01.15.93(C199)** | H. te Nijenhuis: Possibilities and limitations of X-ray diffraction using high energy X-rays on a laboratory system

**P01.08.94(C199)** | S. Torii: Super high resolution powder diffractometer at J-PARC

**P01.08.95(C199)** | R. Kajimoto: 4SEASONS: A high-intensity chopper spectrometer for inelastic neutron scattering at J-PARC/MLF

**P01.15.96(C200)** | P. Nollert: Preparation and imaging of lipidic cubic phase based protein crystallization experiments

**P01.15.97(C200)** | F. P. M. Gorrec: Protein crystallization at the laboratory of molecular biology: Robotics, procedures and developments

#### 04. CRYSTALLOGRAPHY OF BIOLOGICAL MACROMOLECULES

**P04.01.01(C230)** | K. Furuta: Photochemical neutral radical induced nucleation of proteins

**P04.01.02(C230)** | N. V. Pletneva: The three dimensional structure of red, yellow and green fluorescent proteins from *Zoanthus*

**P04.01.03(C231)** | P. Sledz: The role of protein methylation rescue method for protein crystallization

**P04.01.04(C231)** | A. Shahar: Progress in structure determination of the 18kDa TSPO and the outer matrix Matrilin 3 protein

**P04.01.05(C231)** | C. L. Rush: The role of chilectins in rheumatoid arthritis

**P04.01.06(C232)** | S. E. Broughton: A structural investigation in to the basis of Celiac disease

**P04.01.07(C232)** | H. Adachi: Purification, crystallization and preliminary X-ray analysis of photosystem II dimer from a red alga

**P04.01.08(C232)** | A. Park: Structural analysis of ATP:Cob(I) alamin adenosyltransferase

**P04.01.09(C233)** | G. Petrareanu: Expression, purification and crystallization of phosphoketolase from *Lactococcus lactis*

**P04.01.10(C233)** | Y. Li: Try to solve abscisic acid (ABA) receptor's structure and learn how ABA signal is transduced

**P04.01.11(C233)** | J. Hasek: Polymer and co-polymer surface modifying effects in the protein crystallization

**P04.01.12(C233)** | T. Mori: Structural basis for CD44 recognition by ERM proteins

**P04.01.13(C234)** | M. Isogai: Expression, purification and crystallization of Aurora kinase C

**P04.01.14(C234)** | S. Hu: Structural insights into the SM protein-syntaxin interactions

**P04.01.15(C234)** | M. Sugahara: Nucleant-mediated protein crystallization with microporous zeolite showing heteroepitaxial growth

**P04.01.16(C235)** | K. Tomoo: Crystallization and preliminary X-ray analysis of Ca<sup>2+</sup>-free primary Ca<sup>2+</sup>-sensor of Na<sup>+</sup>/Ca<sup>2+</sup>exchanger

**P04.01.17(C235)** | H. Wang: The crystal structure of villin domain 6

**P04.01.18(C235)** | H. Shimizu: Crystallization and X-ray structure analysis of Complex II from adult *Ascaris suum* mitochondria

**P04.01.19(C235)** | F. L. Imai: The crystal structure at 1.8 Å resolution of the calcium-bound human S100A13 at pH 7.5

**P04.01.20(C236)** | T. Ibuki: X-ray analysis of FliJ, a cytoplasmic component of the flagellar type III protein export apparatus

**P04.01.21(C236)** | K. Hara: Crystallographic study of zinc finger domain of EcoI involved in sister chromatid cohesion

**P04.01.22(C236)** | J. Duszkova: Crystallization of carbohydrate oxidase from *Microdochium nivale*

**P04.01.23(C237)** | M. Tsunoda: Crystal structure of actinohivin; A novel anti-human immunodeficiency virus protein

**P04.01.24(C237)** | S. R. Shouldice: Structural and functional analysis of an important *Pseudomonas aeruginosa* redox protein

**P04.01.25(C237)** | T. Yamada: Crystallization of serine proteases for neutron single crystal structure determination

**P04.01.26(C238)** | M. Horiuchi: Structural basis for the antiproliferative activity of the Tob-hCaf1 complex

**P04.01.27(C238)** | O. B. Clarke: Towards the structure of the  $\beta$  4 subunit of the human BK channel

**P04.01.28(C238)** | T. Yoshizawa: Crystallographic study of extracellular dermal glycoprotein of carrot

**P04.01.29(C239)** | A. Mikami: Crystallization of *Clostridium botulinum* serotype D neurotoxin complex

**P04.01.30(C239)** | S. Kamachi: Expression and crystallization of *Drosophila* Ecr/USP

**P04.01.31(C239)** | I. G. Munoz: Molecular basis of histone H3K4ME3 recognition by ING4

**P04.01.32(C240)** | A. Suzuki: A new type of precipitant, metal cyanide complex

**P04.01.33(C240)** | C. Sauter: Crystallization and crystallographic analysis in a microfluidic chip

**P04.01.34(C240)** | Y. Kim: Improving protein crystallization: A large-scale evaluation of protein reductive methylation

**P04.01.35(C241)** | A. D. Clark: Many are called but few are chosen: 20 years of crystallizing HIV-1 reverse transcriptase

**P04.01.36(C241)** | S. T. Partanen: Studies on enzymes belonging to the crotonase superfamily

**P04.01.37(C241)** | J. Yoo: Structure analysis of ligand-independent activation of Fushi tarazu factor-1 ligand binding domain

**P04.01.38(C242)** | K. Kawamura: X-ray diffuse scattering from protein crystals caused by the lattice defects

**P04.01.39(C242)** | M. Goto: Structure of membrane-bound quiohemoprotein alcohol dehydrogenase

**P04.01.40(C242)** | C. Chen: Rational crystallization of  $\beta$ -lactoglobulin and vitamin D<sub>3</sub> complex reveal a secondary binding site

**P04.01.41(C243)** | Y. Ohnishi: Large single crystal growth and preliminary neutron diffraction analysis of *Achromobacter* protease I

**P04.01.42(C243)** | C. Ishida: Purification and crystallization of a C-terminal domain of a human single-pass transmembrane protein

**P04.01.43(C243)** | S. Sugiyama: Crystallization and preliminary X-ray analysis of RNA aptamer in complex with human immunoglobulin G

**P04.01.44(C244)** | M. Yamakami: Growth of high-quality and large crystals of HIV protease for neutron crystallography

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**P04.01.45(C244)** | J. Tsai: X-ray crystallographic study of the C-terminal domain of Tic110 protein from *Cyanidioschyzon merolae*

**P04.01.46(C244)** | D. Choquesillo-Lazarte: Protein crystallization through screening of pH and precipitants using counterdiffusion technique

**P04.01.47(C244)** | Y. Hagiwara: Snapshots in the reaction pathway of bilin reductase PcyA

**P04.01.48(C245)** | A. Brandt: The crystal structure of lipase A from *Candida Antarctica*

**P04.01.49(C245)** | L. Li: Novel approaches in protein crystallization

**P04.01.50(C245)** | B. Jeong: A preliminary crystallographic study of CDCP2 from *Arabidopsis thaliana*

**P04.01.51(C246)** | J. Otani: Crystal structure of DNMT3A ADD domain

**P04.01.52(C246)** | H. Kawahara: The observation of individual protein molecules on a protein crystal under forced solution-flow

**P04.01.53(C246)** | R. Murai: Study on femtosecond laser-induced nucleation dynamics of proteins

**P04.01.54(C247)** | G. Sazaki: Single-molecule visualization on a protein crystal surface

**P04.01.55(C247)** | H. Hasenaka: Wavelength dependence of the crystallization by the laser irradiation

**P04.01.56(C247)** | N. Shimizu: Growth of large protein crystals for neutron crystallography by hanging a seed crystal

**P04.01.57(C248)** | B. R. Jeong: Crystallization and biochemical analysis of eIFA protein

**P04.01.58(C248)** | S. Cameron: The scottish structural proteomics facility

**P04.01.59(C248)** | N. Furubayashi: A dynamic light scattering system combined with a conventional chromatography for sample preparation

**P04.01.60(C249)** | H. Lee: SAXS and crystal structural analysis of *Helicobacter pylori* GroES

**P04.01.61(C249)** | Y. Zhai: Crystallographic study of the bacterial prolipoprotein posttranslational lipid modification system

**P04.01.62(C249)** | X. Pang: Preliminary crystallographic studies on ACAP1 BAR-PH and GAP-ANK domains

**P04.02.63(C249)** | C. Chakrabarti: A comparative study on substrate specificity, activity and thermal stability of some plant proteases

**P04.02.64(C250)** | H. Koskiniemi: Aromatic hydroxylases in polyketide antibiotic biosynthesis

**P04.02.65(C250)** | N. Watanabe: Mechanism of stereospecific substrate recognition by LL-diaminopimelate aminotransferase

**P04.02.66(C250)** | A. Bowyer: L-Threonine dehydrogenase (TDH) from *T. kodakaraensis*, an enzyme involved in amino acid metabolism

**P04.02.67(C251)** | A. S. Thakur: Structural studies of acyl-CoA thioesterase 7 and its role in inflammation

**P04.02.68(C251)** | W. Wong: Structural proteomics of secreted proteases from the ovine footrot pathogen, *Dichelobacter nodosus*

**P04.02.69(C251)** | J. Zheng: Structure determination of *E. coli* isocitrate dehydrogenase kinase/phosphatase

**P04.02.70(C252)** | J. Andrell: Structure of decameric PLP-dependent acid induced arginine decarboxylase from *Escherichia coli*

**P04.02.71(C252)** | M. Hoque: The substrate recognition and the catalytic reaction mechanisms of D-3-hydroxybutyrate dehydrogenase

**P04.02.72(C252)** | J. Peek: Using natural variations among shikimate dehydrogenases to study modes of substrate selectivity

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**P04.02.73(C253)** | M. Pascaru: Structure-function analysis of Eyes absent protein, aspartate dependent protein tyrosine phosphatase

**P04.02.74(C253)** | K. Banaszak: First crystallographic structure of mammalian phosphofructokinase from rabbit skeletal muscle

**P04.02.75(C253)** | C. Angkawidjaja: Crystal structure of a family I.3 lipase from *Pseudomonas* sp. MIS38 in a closed conformation

**P04.02.76(C254)** | T. Nakamura: Hypervalent intermediate of archaeal peroxiredoxin

**P04.02.77(C254)** | K. Matoba: Crystal structures of alkaline protease from *Pseudomonas aeruginosa* complexed with peptides

**P04.02.78(C254)** | S. Suh: Crystal structure of YlqF, a circularly permuted GTPase

**P04.02.79(C255)** | K. Kubota: Crystal structure of L-sorbose reductase from *Gluconobacter frateurii* at 2.4 Å resolution

**P04.02.80(C255)** | M. R. N. Murthy: Structural studies by X-ray on enzymes involved in propionate metabolism from membrane integrated protein leukotriene C<sub>4</sub> synthase

**P04.02.81(C255)** | T. Fujii: Crystal structure of tetrameric malate dehydrogenase from *Antarctic psychrophile*

**P04.02.82(C256)** | S. Kawano: Crystallographic analysis of complexes of bovine trypsin and Schiff base metal chelate

**P04.02.83(C256)** | Y. Higuchi: Evolution of nylon-oligomer-degrading enzyme based on high resolution crystal structure analysis

**P04.02.84(C256)** | X. Wang: Structural biology study in biosynthesis of plant natural products

**P04.02.85(C257)** | B. Ha: Structural basis for Ufm1 processing by UfSP1

**P04.02.86(C257)** | Y. Kikuchi: Crystal structure of the muramidase domain of FlgJ, a putative flagellar rod cap protein

**P04.02.87(C257)** | R. Bott: The three dimensional structure of an intact glucoamylase

**P04.02.88(C257)** | G. D. Brayer: Allostery and functional refolding in the Gram-negative hexameric Type II citrate synthases

**P04.02.89(C258)** | H. Ago: Crystal structure analysis of human membrane integrated protein leukotriene C<sub>4</sub> synthase

**P04.02.90(C258)** | K. Yamamoto: Structural insights into substrate specificity of isomaltase from *Saccharomyces cerevisiae*

**P04.02.91(C258)** | M. Konno: Mechanism for formation of Arg-AMP in help of tRNA on the basis of structure of ArgRS, tRNA and ATP

**P04.02.92(C259)** | S. Okazaki: Crystal structures of  $\alpha$ -amino- $\epsilon$ -caprolactam racemase from *Achromobacter obae*

**P04.02.93(C259)** | A. Ruf: FBPase allosteric transition: Crystal structures of liver and muscle isoforms from rodents and human

**P04.02.94(C259)** | M. Fujihashi: Catalytic promiscuity and mechanistic determinants of ODCase - A high-resolution investigation

**P04.02.95(C260)** | R. Obata: Crystal structures of arylmalonate decarboxylase - Implications for enantioselective reaction

**P04.02.96(C260)** | S. Tanaka: Study on the Ca<sup>2+</sup>-dependent maturation mechanism of subtilisin from a hyperthermophilic archaeon

**P04.02.97(C260)** | H. Ishikawa: Structural and functional analysis of TTHA0252, a novel RNase of the  $\beta$ -CASP family

**P04.02.98(C261)** | T. Wakamatsu: Structural basis for different substrate specificities of two ADP-ribose pyrophosphatase

**P04.02.99(C261)** | S. Chern: Dimerization is important for the GTPase activity of chloroplast translocon components

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**P11.08.73(C529)** | A. R. Esterman: Coordination polymers towards applications: Chirality by design

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