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- P002 **Transient fluctuation of phototropin LOV2 domain**
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- P004 **Time-resolved study of the interdomain signal transfer of blue light sensor protein YtvA**
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- P006 **Thermodynamic properties and volume fluctuations of cytochrome c in dioxane aqueous solutions**
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- P007 **Heat capacity of monoacylglycerol-cholesterol-water systems**
*Yasuhisa Yamamura; Takuya Adachi; Mafumi Hishida; Shigenori Nagatomo; Kazuya Saito
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Hiroyuki Oikawa¹; Yuta Suzuki¹; Masataka Saito¹; Kiyoto Kamagata¹; Munehito Arai^{2,3}; *Satoshi Takahashi¹
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*Kunihiko Ishii; Tahei Tahara
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- P012 **Redox-dependent conformational dynamics of protein disulfide isomerase coupled with exposure of its substrate binding region**
*Kouya Inagaki^{1,2}; Yoshinori Uekusa^{1,2}; Yukiko Kamiya^{1,2}; Tadashi Satoh¹; Koichi Kato^{1,2}
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- P013 **Giant Acceleration of diffusion in single molecule experiments**

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P015 Solution structure of the alternatively folded state of ubiquitin

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P018 Fluctuating and Remaining Structure in the Intrinsically Disordered Protein Monitored by

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P019 Water Model Tuning to Better Reproduce Rotational Diffusion and NMR Spectral Density of Protein

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P021 Distinguishing crystal-like amyloid fibrils and glass-like amorphous aggregates from their kinetics of formation

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*Hiroshi Sekiguchi¹; Yohei Yamamoto²; Mayuno Arita²; Yasuhito Suzuki³; Yuri Nishino⁴; Suzuko Kobayashi⁵; Kohei Ichianagi³; Tai Kubo⁵; Atsuo Miyazawa^{4,6}; Masafumi Yohda²; Naoto Yagi¹; Yuji C. Sasaki³

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P023 Terahertz spectroscopy of proteins by synchrotron radiation at UVSOR

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- P024 **Equilibrium expanded non-native alpha-helix intermediate of hNck2 SH3 domain at acidic pH**
*Yoshitaka Matsumura¹; Masaji Shinjo¹; Tsutomu Matsui²; Kaoru Ichimura¹; Jingxiang Liu³; Jianxing Song³; Hiroshi Kihara^{4,5}
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*Tsuyoshi Terakawa¹; Shoji Takada¹
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Matthew J. McGrath¹, I-F. Will Kuo², Shigehiko Hayashi¹, and *Shoji Takada¹
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*Koji Ono; Naoto Hori; Shoji Takada
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*Le Chang¹; Takeshi Ishikawa^{2,3}; Kazuo Kuwata³; Shoji Takada¹
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Kentaro Kido; *Kento Kasahara; Hirofumi Sato; Shigeyoshi Sakaki
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- P030 **α -helical mebrane protein folding simulations by replica-exchange Monte Carlo method**
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- P031 **Optimized force-field parameters of main-chain torsion-energy terms for each amino acid**
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- P032 **Statistical analysis of incipient relaxation process of photolyzed carbonmonoxy myoglobin by perturbation ensemble MD method**
*Masayoshi Takayanagi^{1,2,3}; Masataka Nagaoka^{2,3}
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- P034 **Ion effects on liquid structure of water monitored by terahertz time-domain spectroscopy**
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*Shigenori Nagatomo¹; Yukiko Ozeki¹; Yasuhisa Yamamura¹; Kazuya Saito¹
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Yamaguchi¹; Mikio Kataoka¹

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*Mayu Shimada; Yoichi Yamazaki; Hironari Kamikubo; Mariko Yamaguchi; Mikio Kataoka
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*Shin-ichi Tate

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*Katsuaki Oyama; Syun Isayama; Kazuki Terauchi

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*Takahiro Hoshaka, Atsushi Yamaguchi, Kaori Shiraga, Takayoshi Watanabe

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*Motoki Hino; Hideaki Ichihara; Yoko Matsumoto; Ryuichi Ueoka

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*Hideaki Ichihara; Motoki Hino; Yoko Matsumoto; Ryuichi Ueoka
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*Yuji Komizu; Mamiko Yukihara; Yoko Matsumoto; Ryuichi Ueoka
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*Ryuichi Ueoka; Yoko Matsumoto; Yuji Komizu; Hideaki Ichihara
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- P061 **Hybrid Liposomes Inhibit Tumor Growth and Lung Metastasis of Murine Osteosarcoma Cells**
*Hideki Kitajima; Yuji Komizu; Hideaki Ichihara; Koichi Goto; Ryuichi Ueoka
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- P062 **HAMLET and BAMLET induces cell death of Primary Effusion Lymphoma**
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- P064 **Effect of Cations on G-quadruplex Structure and Fluctuation of Telomeric DNA**
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P066 Selective reconstitution of bacteriorhodopsin in a binary liposome composed of DMPC and its partially fluorinated analog

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P069 Compartmentalization by confinement in multi-lamellar vesicles

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P070 Functional Analysis of Polyamine-Lipid/DNA Complex (Lipoplex) for Gene Delivery: Relationship between Metamorphosis of Lipoplex and its Function

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- P071 **Structure formation in binary surfactant mixture**
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- P073 **Membrane lipid-sensitive gating of the KcsA potassium channel**
Masayuki Iwamoto; *Shigetoshi Oiki
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- P074 **Structural investigation of voltage-sensing mechanism of voltage-dependent K⁺ channels**
Hitomi Harada¹; *Masanori Osawa¹; Shin-ichiro Ozawa¹; Tomomi Kimura¹; Tomohiro Nozaki¹; Ichio Shimada^{1,2}
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- P075 **Binding Modes of Cations in The KCSA Potassium Channel Proved 3D-RISM Theory**
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- P076 **6N-D water and small molecule distributions from 3D-RISM**
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- P077 **Effects of Macromolecular Crowding on the Sequential Glycan Processing Pathway**
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*Shun Hirota¹; Yoko Hattori¹; Satoshi Nagao¹; Hisao Osuka^{1,2}; Takuya Yamada¹; Takeshi Uni¹; Hirofumi Komori^{2,3}; Yasuhito Shomura^{2,3}; Hironari Kamikubo¹; Mikio Kataoka¹; Shigeru Negi⁴; Yukio Sugiura⁴; Kiyohiro Imai⁵; Yoshiki Higuchi^{2,3}

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P079 **Protein fluctuation in monomer determines prion strain conformations**

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P081 **Rotation of F₁-ATPase under high pressure**

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P082 **Chaperonin induces protein unfolding to change folding pathway**

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P083 **Development of anti-tumor complexes made from a protein in the molten globule state**

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- P084 **HYDROGEN-DEUTERIUM (H/D) EXCHANGE STUDIES ON FREE GROES AND THE GROES-SRI-ADP CHAPERONIN COMPLEX**
*Mahesh S. Chandak¹, Takashi Nakamura¹, Koki Makabe², Toshio Takenaka¹, Jin Chen¹, Koichi Kato¹ and Kunihiro Kuwajima¹
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- P085 **THERMODYNAMIC PARAMETERS ASSOCIATED WITH THE GroEL-GroES BINDING**
*Toshio Takenaka; Takashi Nakamura; Jin Chen; Kunihiro Kuwajima
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- P086 **Fluctuation-mediated regulation of the protein degradation by the proteasome**
*Tomonao Inobe¹; Kazunobu Takahashi¹; Andreas Matouschek²
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- P087 **Dynamic Functional Regulation of MAP kinase p38 α**
Yuji Tokunaga^{1,2}; *Koh Takeuchi³; Hideo Takahashi^{1,4}; Ichio Shimada^{1,2}
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- P088 **DNA-Binding Property of the Novel DNA-Binding Domain STPR in FMBP-1 of the Silkworm Bombyx mori**
*Tomoyasu Aizawa; Motosuke Tsutsumi; Dai Kurosawa; Arisa Nishino; Kosuke Yuhara; Masakatsu Kamiya; Takashi Kikukawa; Makoto Demura; Keiichi Kawno
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- P089 **Identification of α -Catenin Binding Site in Premolten Globule Type Intrinsically Disordered Protein, EspB from Enterohaemorrhagic E. coli**
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P090 **Conformational fluctuations affect the amyloidgenic propensity of immunoglobulin light chain variable domain: from thermodynamic stabilities of chimeric mutants**

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P091 **Conformational fluctuations affect the amyloidgenic propensity of immunoglobulin light chain variable domain: from kinetic folding/unfolding studies of chimeric mutants**

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P092 **Crucial role of conformational flexibility of proteins in enzymatic catalyses**

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P093 **Development of multipole electrostatic potential operator for QM/MM methods**

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P094 **Conformational Transition Pathway of Calmodulin N-terminal Domain Revealed by Biased Molecular Dynamics Simulations**

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P095 **Structural change and fluctuation in early intermediates of bovine rhodopsin**

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P096 **A theoretical study on the fluorescent state of enhanced green fluorescent protein**

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P097 **Protein structures and dynamics in the condensed phase: Hornet silk**

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P098 **The KcsA channel cytoplasmic domain effects on the inactivation gating**

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