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P001

Folding study of outer surface protein A

Koki Makabe, Takashi Nakamura and Kunihiro Kuwajima
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P002

Solvent effect on structural stability of human telomere

*Yutaka Maruyama¹; Taku Matsushita²; Masahiro Ohgidani²; Masayuki Takeda²; Osamu Tanoue²; Ryuichi Ueoka²; Fumio Hirata¹
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P003

Database analysis of protein structural changes upon ligand binding

Takayuki Amemiya^{1,2} ; *Akinori Kidera^{1,3}
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P004

Leu628 of the KIX Domain of CBP is a Key Residue for the Interaction with the MLL Transactivation Domain

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P005

Graded enhancement of p53 binding to CREB-binding protein (CBP) by multisite phosphorylation

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P006

Protein Interactions Monitored by NMR: Intrinsically Disordered p53 Transactivation Subdomains Interact with the TAZ2 Domain of CBP at Two Sites

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P007

Modulation of the Altered Functional Characteristics of Circularly Permuted GroEL through the Introduction of Disulfide Bonds

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P008

Probing the roles of conserved arginine-44 of Escherichia coli dihydrofolate reductase in its function and stability by systematic sequence perturbation analysis

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P009

Specificity and nonlinearity in large-amplitude motion of allosteric proteins

Wenfei Li ; *Shoji Takada

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P010

Free energy landscape analysis of biomolecules by massive parallel multi-scale simulation

*Ryuhei Harada^{1,2}; Akio Kitao^{1,2}

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P011

Challenge to reproduction of hyper-mobile water around monovalent ions: Classical molecular dynamics study

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P012

Alteration of lipid constituent in cancer cell membrane induced by hybrid liposome

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P013

Protein salting-out observed at an air-water interface

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P014

Ensemble modeling of p53 intrinsically disordered N-terminal domain by combining multi-scale simulations with NMR experiments

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P015

Elucidation of protein fluctuation by relaxation dispersion NMR spectroscopy and water-amide proton exchange

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P016

Fluctuation Controls Enzymatic Activity of Staphylococcal Nuclease

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P017

Functionally rotating mechanism of a multidrug transporter studied by coarse-grained simulation

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P018

Emission Spectral Analysis of Europium(III) Probes Attached to Proteins

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P019

Large fluctuations of DNA bases induced by binding to homologous pairing proteins

Tohru Terada
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P020

Lateral Diffusion of Phospholipid Molecules Separated from the Rotational and the Translational Diffusion of a Fluid Bilayer Vesicle

Noriyuki Yoshii; *Emiko Okamura
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P021

Temperature effect on the fluctuation of titin I27 domain: the DHS analysis of the mechanical unfolding free energy landscape

*Yukinori Taniguchi¹; Zu Thur Yew²; Emanuele Paci²; Masaru Kawakami¹

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P022

Monomer-dimer fluctuation of transmembrane helices as detected by single-molecule fluorescence microscopy

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P023

Design of novel metal-binding proteins based on influenza M2 protein

*Yoshihiro Iida¹; Atsuo tamura¹

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P024

Localization of amyloid-destabilizing mutations in the N-terminal domain of Rnq1 in *Saccharomyces cerevisiae*

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P025

Application of fluorescence lifetime correlation measurements to biological molecules

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P026

Stabilization of BPTI-[5,55] through decrease of local backbone fluctuations and development of hetero-microseeding for crystallizing low-stability proteins

Yutaka Kuroda, Mohamed M Islam, Kei Kobayashi
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P027

Clustering of Lipid Rafts in Plasma Membranes by Hybrid Liposomes for Leukemia Cells Leading to Apoptosis

*Yuji Komizu; Sayuri Nakata; Koichi Goto; Yoko Matsumoto;
Ryuichi Ueoka
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P028

Detecting coupled motions in protein with Molecular Dynamics simulation

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P029

Anomalous Diffusion in Supported Planar Lipid Bilayers on Nano-Structured Oxide Substrates

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P030

Fluctuation and function of polyglutamine tract binding protein-1

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Keiichi Kawano³
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P031

MD simulations and QM calculations of water around small solute

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P032

Calorimetric Study of Conformational Fluctuation of Alkyl Chain in Lamellar Phase of Monoacylglycerol/water systems

Yasuhisa Yamamura, Shin Nakada, Maika Iwami, Airi Katagiri, Syuma Yasuzuka, Kazuya Saito

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P033

Contribution of an arginine residue of Zif268 zinc finger on the structure and DNA binding

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P034

The role of the cytoplasmic domain in pH-dependent gating by the KcsA channel

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P035

Novel method for saturation mutagenesis of proteins using cell-free translation system

*Takayoshi Watanabe; Toshiya Mineura; Takahiro Hoshika

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P036

Effect of cations on G-quadruplex structure and fluctuation of telomeric DNA

Taku Matsushita¹; Masahiro Ohgidani¹; Masayuki Takeda¹; Osamu Tanoue¹; Yutaka Maruyama²; Fumio Hirata²; Ryuichi Ueoka¹

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P037

Structural analysis on folding intermediate of srcSH3

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DYNAMIC EQUILIBRIUM OF LYS48-LINKED DI-UBIQUITIN IN SOLUTION ASSESSED BY NMR

*Takashi Hirano¹; Olivier Serve²; Maho Yagi^{1,2}; Tsunehiro Mizushima¹; Koichi Kato^{1,2}

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P039

Conformational Fluctuations Associated with Variable Domains of Pathogenic and Nonpathogenic Immunoglobulin Light Chains

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P040

Fluctuation of Ion and Water Flux through the KcsA Potassium Channel

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P041

Effect of pressure on beta-hairpin peptides

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P042

Property of Glycan-processing Enzyme under Extracellular Matrix Conditions

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EVALUATION OF AGING-RELATED DISEASES BY N-LINKED GLYCANS UNDER MOLECULAR CROWDING CONDITIONS

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P044

Direct manipulation of a single potassium channel gate with an atomic force microscope probe

*Toru Ide¹; Minako Hirano¹; Mitsunori Kitta²

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P045

Remarkable Therapeutic Effects of Hybrid Liposomes on the Growth of Gastric Carcinoma along with Apoptosis

*Hideaki Ichihara, Yusuke Matsuoka, Yuji Komizu, Yoko Matsumoto, Ryuichi Ueoka

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P046

Time-resolved observation of protein-protein interaction between blue-light receptor PixD and response regulator PixE

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P047

Fluctuation in the mechanism of HIV protease inhibitors between HIV protease and proteasome

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P048

Folding of a helical miniprotein studied by multicanonical replica-exchange molecular dynamics simulations

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P049

Kinetic intermediates of beta2-microglobulin fibril elongation probed by pulse-labeling H/D exchange combined with NMR analysis

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Laser-induced Propagation and Destruction of Amyloid beta Fibrils

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**THE MOLTEN GLOBULE STATE AND ITS BIOLOGICAL
FUNCTION IN α -LACTALBUMIN**

*Takashi Nakamura^{1,2}; Koki Makabe^{1,2,3}; Tomoyasu Aizawa⁴;
Keiichi Kawano⁴; Makoto Demura⁴; Kunihiro Kuwajima^{1,2,3}
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Molecular Science; 3Department of Functional Molecular Science,
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Science, Graduate School of Life Science, Hokkaido University*

P052

**Microsecond-resolved time traces of protein folding by
single-molecule fluorescence detection**

*Hiroyuki Oikawa¹; Kiyoto Kamagata¹; Satoshi Takahashi¹
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Tohoku University*

P053

**Time-resolved study on the protein-protein interaction of
Anabaena sensory rhodopsin**

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Masahide Terazima¹
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University; 2Nagoya Institute of Technology; 3Texas University*

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**An application of RISM method incorporating intramolecular
fluctuation**

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Yokogawa³; Hirofumi Sato¹; Shigeyoshi Sakaki⁴
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**Comparison of DNA hydration patterns obtained using two
distinct computational methods, MD simulation and 3D-RISM
theory**

Yoshiteru Yonetani¹; Yutaka Maruyama²; Fumio Hirata²;
Hidetoshi Kono¹
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P056

Sequence dependent kinetics of hydration water molecules in the minor groove of DNA

Yoshiteru Yonetani; Hidetoshi Kono
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Conversion from BLUF Protein to LOV Protein ?

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Pressure-induced fluctuations of local protein structures: Generalized-ensemble simulation study

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Protein Fluctuation Revealed by Pressure Dependence of Intramolecular FRET

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FRET analysis of protein structures by double-incorporation of nonnatural amino acids

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The investigation of the relationship between non-local interaction and the effect of single alanine insertion in staphylococcal nuclease

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P062

Classification of the functional element of dihydrofolate reductase by the systematic alanine insertion

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Bacterial flagellar filament: A metastable structure in polymorphic transformation

*Fumio Hayashi; Kenji Oosawa
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Effect of partial fluorination of hydrophobic chains in phosphatidylcholine on structure and function of bacteriorhodopsin reconstituted into artificial lipid vesicles

*Masashi Sonoyama¹; Masaru Yoshino¹; Takashi Kikukawa²; Yasunori Yokoyama³; Toshiyuki Takagi⁴; Hiroshi Takahashi¹; Makoto Demura²; Teruhiko Baba⁴; Toshiyuki Kanamori⁴
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Chiroptical studies of amyloid-forming proteins in condensed phase and the interactions with membranes

*Reiko Kuroda; Takunori Harada; Natsuyo Asano; Ishrat Jahan
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Probing the collective mode of proteins using low-frequency Raman spectroscopy

*Taku Muneda; Ryuichi Wada; Kato Minoru

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light induced large structural fluctuation of BLUF protein TePixD revealed by high-pressure TG method

*Kunisato Kuroi¹; Keisuke Tanaka¹; Yoshifumi Kimura¹; Koji Okajima^{2,3}; Masahiko Ikeuchi²; Satoru Tokutomi³; Masahide Terazima¹

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P068

Paramagnetic NMR approach to the analysis of conformations and dynamics of N-glycans

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Spectroscopic characterization of inter-molecular interaction of amyloid β promoted on GM1 clusters

Maho Yagi^{1,2}; *Koichi Kato^{1,2}

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pH-INDUCED FOLDING AND UNFOLDING OF HORSE APOMYOGLOBIN IN THE SUBMILLISECOND TIME RANGE

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HIGH-ENERGY STATE MUTANT OF UBIQUITIN

Soichiro Kitazawa¹, Maho Yagi^{2,3}, Kenji Sugase⁴, Koichi Kato^{2,3},
Ryo Kitahara¹

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P072

FRET analysis of structural changes in Staphylococcal nuclease

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Iijima² ; Yoichi Yamazaki¹ ; Hironari Kamikubo¹ ; Takahiro
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P073

**Measurements of Loop Formation in the Denatured State of
Staphylococcal Nuclease**

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Mikio Kataoka¹;

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and Technology*

P074

**Photoreaction dynamics of photosensor protein: Phototropin2
LOV1 domain**

Yuki Kawaguchi¹; Kong Sam-Geun²; Masamitsu Wada²; Masahide
Terazima¹

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science, Kyusyu University*

P075

**Multi-scale simulation of a molecular motor actomyosin: toward
understanding the weak-to-strong binding transition**

*Kei-ichi Okazaki; Jun Ohnuki; Takato Sato; Mitsunori Takano
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University*

P076

Volume fluctuation of proteins as revealed by isothermal compressibility

*Tadashi Kamiyama

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P077

FUNCTIONAL ANALYSIS OF POLYAMINE-LIPID/DNA COMPLEX (LIPOPLEX) AS GENE CARRIER: RELATIONSHIP BETWEEN METAMORPHOSIS OF LIPOPLEX AND ITS FUNCTION

*Takehisa Dewa¹; Kiyoshi Kato¹; Yusuke Kouzuma¹; Yosuke Okita¹; Tomohiro Asai²; Naoto Oku²; Hideo Fujimoto¹; Mamoru Nango¹

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Molecular Recognition Controlled by a Detailed Balance: A Host-Guest Mechanism for 25,26,27,28-Tetramethoxycalix[4]arene in Sodium and Potassium Perchlorate Salt Solutions

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P079

Solvent penetration in the photoactive yellow protein studied by 3D-RISM theory

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P080

Dissecting a bimolecular process of ATP binding to the chaperonin GroEL

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P081

Low-frequency dynamic of ATP and its related compounds studied by terahertz time-domain spectroscopy

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P082

New approach to investigate the molecular recognition of protein toward structure-based drug design based on 3D-RISM theory

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P083

The statistical mechanics study of potassium channels.

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P084

Cytochrome c polymerization by successive domain swapping at the C-terminal helix

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Local Solvation Thermodynamics Analysis of Amyloid-Beta Protein Misfolding

Song-Ho Chong; Chewook Lee; and Sihyun Ham
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P086

Effect of secondary structural formation on low-frequency dynamics of poly-L-glutamic acid studied by terahertz time-domain spectroscopy

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P087

Temperature dependence of vibrational dynamics in aqueous solutions

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P088

Vibrational Dynamics of [RuCl₅(NO)]²⁻ in Aqueous Solution Studied by Nonlinear Infrared Spectroscopy

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Low-frequency Dynamics of Myoglobin by Terahertz Time-Domain Spectroscopy

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P090

Solvation dynamics in aqueous solution by fluorescence up-conversion method: deuterium effect, temperature dependence, probe molecule dependence

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P091

Low-frequency dynamics of biological molecules studied by terahertz time-domain spectroscopy

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