

Kentaro Ishii

List of Publications by Year in descending order

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42
papers

677
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643344

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#	ARTICLE	IF	CITATIONS
1	Characterization of Adeno-Associated Virus Capsid Proteins with Two Types of VP3-Related Components by Capillary Gel Electrophoresis and Mass Spectrometry. <i>Human Gene Therapy</i> , 2021, 32, 1403-1416.	1.4	12
2	Comprehensive Size Distribution and Composition Analysis of Adeno-Associated Virus Vector by Multiwavelength Sedimentation Velocity Analytical Ultracentrifugation. <i>Journal of Pharmaceutical Sciences</i> , 2021, 110, 3375-3384.	1.6	34
3	Supramolecular tholos-like architecture constituted by archaeal proteins without functional annotation. <i>Scientific Reports</i> , 2020, 10, 1540.	1.6	8
4	Allosteric regulation accompanied by oligomeric state changes of <i>Trypanosoma brucei</i> GMP reductase through cystathionine- β -synthase domain. <i>Nature Communications</i> , 2020, 11, 1837.	5.8	10
5	Structural characterization of HypX responsible for CO biosynthesis in the maturation of NiFe-hydrogenase. <i>Communications Biology</i> , 2019, 2, 385.	2.0	13
6	A head-to-toe dimerization has physiological relevance for ligand-induced inactivation of protein tyrosine receptor type Z. <i>Journal of Biological Chemistry</i> , 2019, 294, 14953-14965.	1.6	12
7	Mutational and Combinatorial Control of Self-Assembling and Disassembling of Human Proteasome $\hat{\alpha}$ Subunits. <i>International Journal of Molecular Sciences</i> , 2019, 20, 2308.	1.8	6
8	SDS-induced oligomerization of Lys49-phospholipase A2 from snake venom. <i>Scientific Reports</i> , 2019, 9, 2330.	1.6	15
9	Identification of IgG1 Aggregation Initiation Region by Hydrogen Deuterium Mass Spectrometry. <i>Journal of Pharmaceutical Sciences</i> , 2019, 108, 2323-2333.	1.6	14
10	Temperature-controlled repeatable scrambling and induced-sorting of building blocks between cubic assemblies. <i>Nature Communications</i> , 2019, 10, 1440.	5.8	11
11	Cooperative Binding of KaiB to the KaiC Hexamer Ensures Accurate Circadian Clock Oscillation in Cyanobacteria. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4550.	1.8	18
12	Polarizability and isotope effects on dispersion interactions in water. <i>Communications Chemistry</i> , 2019, 2, .	2.0	4
13	ATP hydrolysis by KaiC promotes its KaiA binding in the cyanobacterial circadian clock system. <i>Life Science Alliance</i> , 2019, 2, e201900368.	1.3	14
14	Hyperthermostable cube-shaped assembly in water. <i>Communications Chemistry</i> , 2018, 1, .	2.0	22
15	RecA requires two molecules of Mg ²⁺ ions for its optimal strand exchange activity in vitro. <i>Nucleic Acids Research</i> , 2018, 46, 2548-2559.	6.5	12
16	Native mass spectrometry for understanding dynamic protein complex. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2018, 1862, 275-286.	1.1	20
17	Expression, Functional Characterization, and Preliminary Crystallization of the Cochaperone Prefoldin from the Thermophilic Fungus <i>Chaetomium thermophilum</i> . <i>International Journal of Molecular Sciences</i> , 2018, 19, 2452.	1.8	4
18	Structural Dynamics of the PET-Degrading Cutinase-like Enzyme from <i>Saccharomonospora viridis</i> AHK190 in Substrate-Bound States Elucidates the Ca ²⁺ -Driven Catalytic Cycle. <i>Biochemistry</i> , 2018, 57, 5289-5300.	1.2	59

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19	Dynamic structural states of ClpB involved in its disaggregation function. <i>Nature Communications</i> , 2018, 9, 2147.	5.8	55
20	Bifacial Nucleobases for Hexaplex Formation in Aqueous Solution. <i>Journal of the American Chemical Society</i> , 2018, 140, 8456-8462.	6.6	21
21	Native MS Ionization Process and Non-Covalent Interactions of Protein Complex. <i>Journal of the Mass Spectrometry Society of Japan</i> , 2018, 66, 222-225.	0.0	0
22	Analytical ultracentrifugation with fluorescence detection system reveals differences in complex formation between recombinant human TNF and different biological TNF antagonists in various environments. <i>MAbs</i> , 2017, 9, 664-679.	2.6	27
23	A Comprehensive Study of the Interaction between Peptidoglycan Fragments and the Extracellular Domain of <i>Mycobacterium tuberculosis</i> Ser/Thr Kinase PknB. <i>ChemBioChem</i> , 2017, 18, 2094-2098.	1.3	12
24	Mass Spectrometric Characterization of HIV-1 Reverse Transcriptase Interactions with Non-nucleoside Reverse Transcriptase Inhibitors. <i>Biological and Pharmaceutical Bulletin</i> , 2016, 39, 450-454.	0.6	5
25	New insight into the dynamical system of β -crystallin oligomers. <i>Scientific Reports</i> , 2016, 6, 29208.	1.6	32
26	Structural characterization of the circadian clock protein complex composed of KaiB and KaiC by inverse contrast-matching small-angle neutron scattering. <i>Scientific Reports</i> , 2016, 6, 35567.	1.6	24
27	Small-molecule inhibition of PTPRZ reduces tumor growth in a rat model of glioblastoma. <i>Scientific Reports</i> , 2016, 6, 20473.	1.6	47
28	Mass spectrometric analysis of protein-ligand interactions. <i>Biophysics and Physicobiology</i> , 2016, 13, 87-95.	0.5	33
29	Application of Site-Specific Spin Labeling for NMR Detecting Inhibitor-Induced Conformational Change of HIV-1 Reverse Transcriptase. <i>ChemMedChem</i> , 2016, 11, 363-366.	1.6	15
30	Disassembly of the self-assembled, double-ring structure of proteasome β 7 homo-tetradecamer by β 6. <i>Scientific Reports</i> , 2015, 5, 18167.	1.6	23
31	pH-Dependent Assembly and Segregation of the Coiled-Coil Segments of Yeast Putative Cargo Receptors Emp46p and Emp47p. <i>PLoS ONE</i> , 2015, 10, e0140287.	1.1	7
32	Analysis of Higher Order Structures of Proteins by Mass Spectrometry. <i>Seibutsu Butsuri</i> , 2015, 55, 270-273.	0.0	1
33	Site-directed spin labeling-electron spin resonance mapping of the residues of cyanobacterial clock protein KaiA that are affected by KaiA-KaiC interaction. <i>Genes To Cells</i> , 2014, 19, 297-324.	0.5	7
34	The Roles of the Dimeric and Tetrameric Structures of the Clock Protein KaiB in the Generation of Circadian Oscillations in Cyanobacteria. <i>Journal of Biological Chemistry</i> , 2012, 287, 29506-29515.	1.6	35
35	Phase-dependent generation and transmission of time information by the KaiABC circadian clock oscillator through SasA-KaiC interaction in cyanobacteria. <i>Genes To Cells</i> , 2012, 17, 398-419.	0.5	25
36	3D1334 Structural Changes in Cyanobacterial Clock Protein KaiC Interacting with KaiA as Detected by Site-Directed Spin-Labeling ESR(3D Protein: Structure & Function 3, The 49th Annual Meeting of the Tj ETQq0 0 0 r g B / Overlock 10 Tf 5		

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37	2P316 Specific residues involved in interaction between cyanobacterial clock protein KaiA and KaiC revealed by SDSL-ESR analysis(The 48th Annual Meeting of the Biophysical Society of Japan). Seibutsu Butsuri, 2010, 50, S138.	0.0	0
38	1P312 1H1505 Direct interaction between cyanobacterial circadian clock proteins revealed by SDSL-ESR analysis(Nonequilibrium state & Biological rhythm,Oral Presentations,The 48th Annual Meeting of the) Tj ETQq0 0 0 rgBT /Overlock 10 T	0.0	0
39	2P315 Information flow from the central oscillator to the main output pathway in the cyanobacterial circadian clock(The 48th Annual Meeting of the Biophysical Society of Japan). Seibutsu Butsuri, 2010, 50, S138.	0.0	0
40	Direct interaction between KaiA and KaiB revealed by a site-directed spin labeling electron spin resonance analysis. Genes To Cells, 2010, 15, 269-280.	0.5	19
41	2TP3-05 Novel interaction sites on cyanobacterial circadian clock proteins revealed by ESR(The 47th) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T	0.0	0
42	2P-307 Synechocystis sp. strain PCC6803 has the kaiAB1C1 circadian clock gene and clock gene homologues, kaiC2B2 and kaiB3 and kaiC3 genes(The 46th Annual Meeting of the Biophysical Society of) Tj ETQq0000 rgBT /Overlock 10 T	0.0	0