Kenji Sugase

List of Publications by Year
in descending order

71	2,459	393982 19	205818 48
papers	citations	h-index	g-index

72	72	72	3352
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Structural Insights into Methylated DNA Recognition by the Methyl-CpG Binding Domain of MBD6 from Arabidopsis thaliana. ACS Omega, 2022, 7, 3212-3221.	1.6	7
2	Counter-flow phenomena studied by nuclear magnetic resonance (NMR) velocimetry and flow simulations. Physics of Fluids, 2022, 34, .	1.6	5
3	Structural dynamics of double-stranded DNA with epigenome modification. Nucleic Acids Research, 2021, 49, 1152-1162.	6.5	8
4	Structural Dynamic Heterogeneity of Polyubiquitin Subunits Affects Phosphorylation Susceptibility. Biochemistry, 2021, 60, 573-583.	1.2	4
5	Transient Diffusive Interactions with a Protein Crowder Affect Aggregation Processes of Superoxide Dismutase 1 Î²-Barrel. Journal of Physical Chemistry B, 2021, 125, 2521-2532.	1.2	7
6	Glycyrrhizin Derivatives Suppress Cancer Chemoresistance by Inhibiting Progesterone Receptor Membrane Component 1. Cancers, 2021, 13, 3265.	1.7	16
7	Backbone resonance assignments of the A2 domain of mouse von Willebrand factor. Biomolecular NMR Assignments, 2021, 15, 427-431.	0.4	0
8	Molecular recognition and deubiquitination of cyclic K48-linked ubiquitin chains by OTUB1. Biochemical and Biophysical Research Communications, 2021, 562, 94-99.	1.0	1
9	Multiple-State Monitoring of SOD1 Amyloid Formation at Single-Residue Resolution by Rheo-NMR Spectroscopy. Journal of the American Chemical Society, 2021, 143, 10604-10613.	6.6	10
10	Effects of Weak Nonspecific Interactions with ATP on Proteins. Journal of the American Chemical Society, 2021, 143, 11982-11993.	6.6	40
11	Expression, solubility monitoring, and purification of the co-folded LUBAC LTM domain by structure-guided tandem folding in autoinducing cultures. Protein Expression and Purification, 2021, 187, 105953.	0.6	3
12	Rigorous analysis of the interaction between proteins and low water-solubility drugs by qNMR-aided NMR titration experiments. Physical Chemistry Chemical Physics, 2021, 23, 21484-21488.	1.3	2
13	Visualizing protein motion in Couette flow by all-atom molecular dynamics. Biochimica Et Biophysica Acta - General Subjects, 2020, 1864, 129383.	1.1	6
14	Pinpoint analysis of a protein in slow exchange using F1F2-selective ZZ-exchange spectroscopy: assignment and kinetic analysis. Journal of Biomolecular NMR, 2020, 74, 205-211.	1.6	3
15	Quantitative monitoring of ubiquitination/deubiquitination reaction cycles by 18O-incorporation. Biochemical and Biophysical Research Communications, 2020, 529, 418-424.	1.0	1
16	Conformational exchange in the potassium channel blocker ShK. Scientific Reports, 2019, 9, 19307.	1.6	4
17	Structural and thermodynamic basis for the recognition of the substrate-binding cleft on hen egg lysozyme by a single-domain antibody. Scientific Reports, 2019, 9, 15481.	1.6	36
18	NMR resonance assignments of the NZF domain of mouse HOIL-1L free and bound to linear di-ubiquitin. Biomolecular NMR Assignments, 2019, 13, 149-153.	0.4	1

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19	Backbone and side-chain resonance assignments of the methyl-CpG-binding domain of MBD6 from Arabidopsis thaliana. Biomolecular NMR Assignments, 2019, 13, 59-62.	0.4	1
20	Overview of Relaxation Dispersion NMR Spectroscopy to Study Protein Dynamics and Proteinâ€Ligand Interactions. Current Protocols in Protein Science, 2018, 92, e57.	2.8	10
21	Isolation and characterization of a minimal building block of polyubiquitin fibrils. Scientific Reports, 2018, 8, 2711.	1.6	0
22	Elucidating Functional Dynamics by R 1Ï•and R 2 Relaxation Dispersion NMR Spectroscopy. , 2018, , 197-225.		0
23	Resolving biomolecular motion and interactions by R2 and R1Ï•relaxation dispersion NMR. Methods, 2018, 148, 28-38.	1.9	11
24	Hydrogen-Deuterium Exchange Profiles of Polyubiquitin Fibrils. Polymers, 2018, 10, 240.	2.0	2
25	Practical considerations for investigation of protein conformational dynamics by 15N R 1Ï•relaxation dispersion. Journal of Biomolecular NMR, 2017, 67, 201-209.	1.6	4
26	F 1 F 2-selective NMR spectroscopy. Journal of Biomolecular NMR, 2017, 68, 41-52.	1.6	11
27	Backbone resonance assignments of monomeric SOD1 in dilute and crowded environments. Biomolecular NMR Assignments, 2017, 11, 81-84.	0.4	5
28	Elucidation of potential sites for antibody engineering by fluctuation editing. Scientific Reports, 2017, 7, 9597.	1.6	15
29	High-Sensitivity Rheo-NMR Spectroscopy for Protein Studies. Analytical Chemistry, 2017, 89, 7286-7290.	3.2	19
30	Real-Time Observation of the Interaction between Thioflavin T and an Amyloid Protein by Using High-Sensitivity Rheo-NMR. International Journal of Molecular Sciences, 2017, 18, 2271.	1.8	9
31	Biological and Physicochemical Functions of Ubiquitylation Revealed by Synthetic Chemistry Approaches. International Journal of Molecular Sciences, 2017, 18, 1145.	1.8	4
32	Exploration of the Conformational Dynamics of Major Histocompatibility Complex Molecules. Frontiers in Immunology, 2017, 8, 632.	2.2	11
33	Use of glass capillaries to suppress thermal convection in NMR tubes in diffusion measurements. Magnetic Resonance in Chemistry, 2016, 54, 729-733.	1.1	12
34	Ubiquitylation Directly Induces Fold Destabilization of Proteins. Scientific Reports, 2016, 6, 39453.	1.6	24
35	Quantitative analysis of proteinâ€“ligand interactions by NMR. Progress in Nuclear Magnetic Resonance Spectroscopy, 2016, 96, 47-57.	3.9	82
36	Efficient identification and analysis of chemical exchange in biomolecules by R1Ï•relaxation dispersion with Amaterasu. Bioinformatics, 2016, 32, 2539-2541.	1.8	5

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37	The helical propensity of the extracellular loop is responsible for the substrate specificity of Fe(III)â€phytosiderophore transporters. FEBS Letters, 2016, 590, 4617-4627.	1.3	9
38	Dynamics of the Extended String-Like Interaction ofÂTFIIE with the p62 Subunit of TFIIH. Biophysical Journal, 2016, 111, 950-962.	0.2	9
39	Haem-dependent dimerization of PGRMC1/Sigma-2 receptor facilitates cancer proliferation and chemoresistance. Nature Communications, 2016, 7, 11030.	5.8	153
40	Dual Function of Phosphoubiquitin in E3 Activation of Parkin. Journal of Biological Chemistry, 2016, 291, 16879-16891.	1.6	12
41	Revealing the peptide presenting process of human leukocyte antigen through the analysis of fluctuation. Biophysics (Nagoya-shi, Japan), 2015, 11, 103-106.	0.4	0
42	Distal Regulation of Heme Binding of Heme Oxygenase-1 Mediated by Conformational Fluctuations. Biochemistry, 2015, 54, 340-348.	1.2	14
43	Conformational propensities of intrinsically disordered proteins influence the mechanism of binding and folding. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 9614-9619.	3.3	222
44	Dynamic changes in CCAN organization through CENP-C during cell-cycle progression. Molecular Biology of the Cell, 2015, 26, 3768-3776.	0.9	62
45	Extracting protein dynamics information from overlapped NMR signals using relaxation dispersion difference NMR spectroscopy. Journal of Biomolecular NMR, 2015, 63, 367-373.	1.6	5
46	Backbone assignments of the apo and Zn(II) protoporphyrin IX-bound states of the soluble form of rat heme oxygenase-1. Biomolecular NMR Assignments, 2015, 9, 197-200.	0.4	4
47	Peptide-dependent Conformational Fluctuation Determines the Stability of the Human Leukocyte Antigen Class I Complex. Journal of Biological Chemistry, 2014, 289, 24680-24690.	1.6	37
48	Solid-State NMR Spectra of Lipid-Anchored Proteins under Magic Angle Spinning. Journal of Physical Chemistry B, 2014, 118, 2405-2413.	1.2	8
49	Solution Structure of the Ubiquitin-associated (UBA) Domain of Human Autophagy Receptor NBR1 and Its Interaction with Ubiquitin and Polyubiquitin. Journal of Biological Chemistry, 2014, 289, 13890-13902.	1.6	60
50	Quantitative Analysis of Locationâ€and Sequenceâ€Dependent Deamination by APOBEC3G Using Realâ€Time NMR Spectroscopy. Angewandte Chemie - International Edition, 2014, 53, 2349-2352.	7.2	14
51	Fast and accurate fitting of relaxation dispersion data using the flexible software package GLOVE. Journal of Biomolecular NMR, 2013, 56, 275-283.	1.6	71
52	Solution Structure of the Q41N Variant of Ubiquitin as a Model for the Alternatively Folded N₂ State of Ubiquitin. Biochemistry, 2013, 52, 1874-1885.	1.2	26
53	The Monomerâ€“Seed Interaction Mechanism in the Formation of the Î²2-Microglobulin Amyloid Fibril Clarified by Solution NMR Techniques. Journal of Molecular Biology, 2012, 422, 390-402.	2.0	35
54	Design Strategy for High Free-Energy States of Proteins Based on High-Pressure NMR Study: Alternatively Folded Conformation of Ubiquitin. Biophysical Journal, 2012, 102, 25a.	0.2	0

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55	Boosting Protein Dynamics Studies Using Quantitative Nonuniform Sampling NMR Spectroscopy. Journal of Physical Chemistry B, 2011, 115, 13740-13745.	1.2	30
56	Elucidating slow binding kinetics of a protein without observable bound resonances by longitudinal relaxation NMR spectroscopy. Journal of Biomolecular NMR, 2011, 50, 219-227.	1.6	4
57	Lipopolysaccharide induces raft domain expansion in membrane composed of a phospholipid-cholesterol-sphingomyelin ternary system. Innate Immunity, 2011, 17, 256-268.	1.1	13
58	Calcitonin in a protochordate, Cionaâ€ƒintestinalisâ€ƒâ€“â€ƒthe prototype of the vertebrate calcitonin/calcitonin geneâ€related peptide superfamily. FEBS Journal, 2009, 276, 4437-4447.	2.2	53
59	Overexpression of post-translationally modified peptides in Escherichia coli by co-expression with modifying enzymes. Protein Expression and Purification, 2008, 57, 108-115.	0.6	30
60	Specific transporter for iron(III): Phytosiderophore complex involved in iron uptake by barley roots. Pure and Applied Chemistry, 2008, 80, 2689-2697.	0.9	18
61	S03A3 Metastable structure detected by relaxation dispersion NMR spectroscopy(Visualising) Tj ETQq1 1 0.784314 rgBT /Overlock 10	0.6	0
62	Solution structure of agelenin, an insecticidal peptide isolated from the spider Agelena opulenta, and its structural similarities to insectâ€specific calcium channel inhibitors. FEBS Letters, 2007, 581, 3789-3794.	1.3	11
63	Structural element responsible for the Fe(III)â€“phytosiderophore specific transport by HvYS1 transporter in barley. FEBS Letters, 2007, 581, 4298-4302.	1.3	48
64	Tailoring Relaxation Dispersion Experiments for Fast-Associating Protein Complexes. Journal of the American Chemical Society, 2007, 129, 13406-13407.	6.6	52
65	Mechanism of coupled folding and binding of an intrinsically disordered protein. Nature, 2007, 447, 1021-1025.	13.7	984
66	Solution structure of IsTX. FEBS Journal, 2004, 271, 3855-3864.	0.2	17
67	Restriction of a Peptide Turn Conformation and Conformational Analysis of Guanidino Group Using Arginine-Proline Fused Amino Acids:â€‰Application to Mini Atrial Natriuretic Peptide on Binding to the Receptor. Journal of Medicinal Chemistry, 2004, 47, 489-492.	2.9	14
68	Designing Analogues of Mini Atrial Natriuretic Peptide Based on Structural Analysis by NMR and Restrained Molecular Dynamics. Journal of Medicinal Chemistry, 2002, 45, 881-887.	2.9	4
69	Structureâ€“activity relationships for mini atrial natriuretic peptide by proline-Scanning mutagenesis and shortening of peptide backbone. Bioorganic and Medicinal Chemistry Letters, 2002, 12, 1245-1247.	1.0	8
70	Synthesis of the cyclic heptapeptide Substance P antagonist, dihydro-WIN67689 and determination of the stereochemistry of the modified tyrosine moiety. Tetrahedron Letters, 1999, 40, 9097-9100.	0.7	5
71	13C-13C and 13C-15N Dipolar Correlation NMR of Uniformly Labeled Organic Solids for the Complete Assignment of Their 13C and 15N Signals: An Application to Adenosine. Journal of the American Chemical Society, 1995, 117, 11351-11352.	6.6	47