

# Kenji Sugase

## List of Publications by Year in descending order

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Version: 2024-02-01

71  
papers

2,459  
citations

393982

19  
h-index

205818

48  
g-index

72  
all docs

72  
docs citations

72  
times ranked

3352  
citing authors

#	ARTICLE	IF	CITATIONS
1	Mechanism of coupled folding and binding of an intrinsically disordered protein. <i>Nature</i> , 2007, 447, 1021-1025.	13.7	984
2	Conformational propensities of intrinsically disordered proteins influence the mechanism of binding and folding. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 9614-9619.	3.3	222
3	Haem-dependent dimerization of PGRMC1/Sigma-2 receptor facilitates cancer proliferation and chemoresistance. <i>Nature Communications</i> , 2016, 7, 11030.	5.8	153
4	Quantitative analysis of protein-ligand interactions by NMR. <i>Progress in Nuclear Magnetic Resonance Spectroscopy</i> , 2016, 96, 47-57.	3.9	82
5	Fast and accurate fitting of relaxation dispersion data using the flexible software package GLOVE. <i>Journal of Biomolecular NMR</i> , 2013, 56, 275-283.	1.6	71
6	Dynamic changes in CCAN organization through CENP-C during cell-cycle progression. <i>Molecular Biology of the Cell</i> , 2015, 26, 3768-3776.	0.9	62
7	Solution Structure of the Ubiquitin-associated (UBA) Domain of Human Autophagy Receptor NBR1 and Its Interaction with Ubiquitin and Polyubiquitin. <i>Journal of Biological Chemistry</i> , 2014, 289, 13890-13902.	1.6	60
8	Calcitonin in a protochordate, <i>Ciona intestinalis</i> is the prototype of the vertebrate calcitonin/calcitonin gene-related peptide superfamily. <i>FEBS Journal</i> , 2009, 276, 4437-4447.	2.2	53
9	Tailoring Relaxation Dispersion Experiments for Fast-Associating Protein Complexes. <i>Journal of the American Chemical Society</i> , 2007, 129, 13406-13407.	6.6	52
10	Structural element responsible for the Fe(III)-phytosiderophore specific transport by HvYS1 transporter in barley. <i>FEBS Letters</i> , 2007, 581, 4298-4302.	1.3	48
11	<sup>13</sup> C- <sup>13</sup> C and <sup>13</sup> C- <sup>15</sup> N Dipolar Correlation NMR of Uniformly Labeled Organic Solids for the Complete Assignment of Their <sup>13</sup> C and <sup>15</sup> N Signals: An Application to Adenosine. <i>Journal of the American Chemical Society</i> , 1995, 117, 11351-11352.	6.6	47
12	Effects of Weak Nonspecific Interactions with ATP on Proteins. <i>Journal of the American Chemical Society</i> , 2021, 143, 11982-11993.	6.6	40
13	Peptide-dependent Conformational Fluctuation Determines the Stability of the Human Leukocyte Antigen Class I Complex. <i>Journal of Biological Chemistry</i> , 2014, 289, 24680-24690.	1.6	37
14	Structural and thermodynamic basis for the recognition of the substrate-binding cleft on hen egg lysozyme by a single-domain antibody. <i>Scientific Reports</i> , 2019, 9, 15481.	1.6	36
15	The Monomer-Seed Interaction Mechanism in the Formation of the <sup>125</sup> I-Microglobulin Amyloid Fibril Clarified by Solution NMR Techniques. <i>Journal of Molecular Biology</i> , 2012, 422, 390-402.	2.0	35
16	Overexpression of post-translationally modified peptides in <i>Escherichia coli</i> by co-expression with modifying enzymes. <i>Protein Expression and Purification</i> , 2008, 57, 108-115.	0.6	30
17	Boosting Protein Dynamics Studies Using Quantitative Nonuniform Sampling NMR Spectroscopy. <i>Journal of Physical Chemistry B</i> , 2011, 115, 13740-13745.	1.2	30
18	Solution Structure of the Q41N Variant of Ubiquitin as a Model for the Alternatively Folded N <sub>2</sub> State of Ubiquitin. <i>Biochemistry</i> , 2013, 52, 1874-1885.	1.2	26

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19	Ubiquitylation Directly Induces Fold Destabilization of Proteins. <i>Scientific Reports</i> , 2016, 6, 39453.	1.6	24
20	High-Sensitivity Rheo-NMR Spectroscopy for Protein Studies. <i>Analytical Chemistry</i> , 2017, 89, 7286-7290.	3.2	19
21	Specific transporter for iron(III): Phytosiderophore complex involved in iron uptake by barley roots. <i>Pure and Applied Chemistry</i> , 2008, 80, 2689-2697.	0.9	18
22	Solution structure of IsTX. <i>FEBS Journal</i> , 2004, 271, 3855-3864.	0.2	17
23	Glycyrrhizin Derivatives Suppress Cancer Chemoresistance by Inhibiting Progesterone Receptor Membrane Component 1. <i>Cancers</i> , 2021, 13, 3265.	1.7	16
24	Elucidation of potential sites for antibody engineering by fluctuation editing. <i>Scientific Reports</i> , 2017, 7, 9597.	1.6	15
25	Restriction of a Peptide Turn Conformation and Conformational Analysis of Guanidino Group Using Arginine-Proline Fused Amino Acids: Application to Mini Atrial Natriuretic Peptide on Binding to the Receptor. <i>Journal of Medicinal Chemistry</i> , 2004, 47, 489-492.	2.9	14
26	Quantitative Analysis of Location- and Sequence-Dependent Deamination by APOBEC3G Using Real-Time NMR Spectroscopy. <i>Angewandte Chemie - International Edition</i> , 2014, 53, 2349-2352.	7.2	14
27	Distal Regulation of Heme Binding of Heme Oxygenase-1 Mediated by Conformational Fluctuations. <i>Biochemistry</i> , 2015, 54, 340-348.	1.2	14
28	Lipopolysaccharide induces raft domain expansion in membrane composed of a phospholipid-cholesterol-sphingomyelin ternary system. <i>Innate Immunity</i> , 2011, 17, 256-268.	1.1	13
29	Use of glass capillaries to suppress thermal convection in NMR tubes in diffusion measurements. <i>Magnetic Resonance in Chemistry</i> , 2016, 54, 729-733.	1.1	12
30	Dual Function of Phosphoubiquitin in E3 Activation of Parkin. <i>Journal of Biological Chemistry</i> , 2016, 291, 16879-16891.	1.6	12
31	Solution structure of agelenin, an insecticidal peptide isolated from the spider <i>Agelena opulenta</i> , and its structural similarities to insect-specific calcium channel inhibitors. <i>FEBS Letters</i> , 2007, 581, 3789-3794.	1.3	11
32	F 1 F 2-selective NMR spectroscopy. <i>Journal of Biomolecular NMR</i> , 2017, 68, 41-52.	1.6	11
33	Exploration of the Conformational Dynamics of Major Histocompatibility Complex Molecules. <i>Frontiers in Immunology</i> , 2017, 8, 632.	2.2	11
34	Resolving biomolecular motion and interactions by R2 and R1ρ-relaxation dispersion NMR. <i>Methods</i> , 2018, 148, 28-38.	1.9	11
35	Overview of Relaxation Dispersion NMR Spectroscopy to Study Protein Dynamics and Protein-Ligand Interactions. <i>Current Protocols in Protein Science</i> , 2018, 92, e57.	2.8	10
36	Multiple-State Monitoring of SOD1 Amyloid Formation at Single-Residue Resolution by Rheo-NMR Spectroscopy. <i>Journal of the American Chemical Society</i> , 2021, 143, 10604-10613.	6.6	10

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37	The helical propensity of the extracellular loop is responsible for the substrate specificity of Fe(III)-phytosiderophore transporters. <i>FEBS Letters</i> , 2016, 590, 4617-4627.	1.3	9
38	Dynamics of the Extended String-Like Interaction of $\alpha$ TFIIIE with the p62 Subunit of TFIIF. <i>Biophysical Journal</i> , 2016, 111, 950-962.	0.2	9
39	Real-Time Observation of the Interaction between Thioflavin T and an Amyloid Protein by Using High-Sensitivity Rheo-NMR. <i>International Journal of Molecular Sciences</i> , 2017, 18, 2271.	1.8	9
40	Structure-activity relationships for mini atrial natriuretic peptide by proline-Scanning mutagenesis and shortening of peptide backbone. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2002, 12, 1245-1247.	1.0	8
41	Solid-State NMR Spectra of Lipid-Anchored Proteins under Magic Angle Spinning. <i>Journal of Physical Chemistry B</i> , 2014, 118, 2405-2413.	1.2	8
42	Structural dynamics of double-stranded DNA with epigenome modification. <i>Nucleic Acids Research</i> , 2021, 49, 1152-1162.	6.5	8
43	Transient Diffusive Interactions with a Protein Crowder Affect Aggregation Processes of Superoxide Dismutase 1 $\beta$ -Barrel. <i>Journal of Physical Chemistry B</i> , 2021, 125, 2521-2532.	1.2	7
44	Structural Insights into Methylated DNA Recognition by the Methyl-CpG Binding Domain of MBD6 from <i>Arabidopsis thaliana</i> . <i>ACS Omega</i> , 2022, 7, 3212-3221.	1.6	7
45	Visualizing protein motion in Couette flow by all-atom molecular dynamics. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2020, 1864, 129383.	1.1	6
46	Synthesis of the cyclic heptapeptide Substance P antagonist, dihydro-WIN67689 and determination of the stereochemistry of the modified tyrosine moiety. <i>Tetrahedron Letters</i> , 1999, 40, 9097-9100.	0.7	5
47	Extracting protein dynamics information from overlapped NMR signals using relaxation dispersion difference NMR spectroscopy. <i>Journal of Biomolecular NMR</i> , 2015, 63, 367-373.	1.6	5
48	Efficient identification and analysis of chemical exchange in biomolecules by $R_1\rho$ -relaxation dispersion with <i>Amaterasu</i> . <i>Bioinformatics</i> , 2016, 32, 2539-2541.	1.8	5
49	Backbone resonance assignments of monomeric SOD1 in dilute and crowded environments. <i>Biomolecular NMR Assignments</i> , 2017, 11, 81-84.	0.4	5
50	Counter-flow phenomena studied by nuclear magnetic resonance (NMR) velocimetry and flow simulations. <i>Physics of Fluids</i> , 2022, 34, .	1.6	5
51	Designing Analogues of Mini Atrial Natriuretic Peptide Based on Structural Analysis by NMR and Restrained Molecular Dynamics. <i>Journal of Medicinal Chemistry</i> , 2002, 45, 881-887.	2.9	4
52	Elucidating slow binding kinetics of a protein without observable bound resonances by longitudinal relaxation NMR spectroscopy. <i>Journal of Biomolecular NMR</i> , 2011, 50, 219-227.	1.6	4
53	Backbone assignments of the apo and Zn(II) protoporphyrin IX-bound states of the soluble form of rat heme oxygenase-1. <i>Biomolecular NMR Assignments</i> , 2015, 9, 197-200.	0.4	4
54	Practical considerations for investigation of protein conformational dynamics by $^{15}\text{N}$ $R_1\rho$ -relaxation dispersion. <i>Journal of Biomolecular NMR</i> , 2017, 67, 201-209.	1.6	4

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55	Biological and Physicochemical Functions of Ubiquitylation Revealed by Synthetic Chemistry Approaches. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1145.	1.8	4
56	Conformational exchange in the potassium channel blocker ShK. <i>Scientific Reports</i> , 2019, 9, 19307.	1.6	4
57	Structural Dynamic Heterogeneity of Polyubiquitin Subunits Affects Phosphorylation Susceptibility. <i>Biochemistry</i> , 2021, 60, 573-583.	1.2	4
58	Pinpoint analysis of a protein in slow exchange using F1F2-selective ZZ-exchange spectroscopy: assignment and kinetic analysis. <i>Journal of Biomolecular NMR</i> , 2020, 74, 205-211.	1.6	3
59	Expression, solubility monitoring, and purification of the co-folded LUBAC LTM domain by structure-guided tandem folding in autoinducing cultures. <i>Protein Expression and Purification</i> , 2021, 187, 105953.	0.6	3
60	Hydrogen-Deuterium Exchange Profiles of Polyubiquitin Fibrils. <i>Polymers</i> , 2018, 10, 240.	2.0	2
61	Rigorous analysis of the interaction between proteins and low water-solubility drugs by qNMR-aided NMR titration experiments. <i>Physical Chemistry Chemical Physics</i> , 2021, 23, 21484-21488.	1.3	2
62	NMR resonance assignments of the NZF domain of mouse HOIL-1L free and bound to linear di-ubiquitin. <i>Biomolecular NMR Assignments</i> , 2019, 13, 149-153.	0.4	1
63	Backbone and side-chain resonance assignments of the methyl-CpG-binding domain of MBD6 from <i>Arabidopsis thaliana</i> . <i>Biomolecular NMR Assignments</i> , 2019, 13, 59-62.	0.4	1
64	Quantitative monitoring of ubiquitination/deubiquitination reaction cycles by <sup>18</sup> O-incorporation. <i>Biochemical and Biophysical Research Communications</i> , 2020, 529, 418-424.	1.0	1
65	Molecular recognition and deubiquitination of cyclic K48-linked ubiquitin chains by OTUB1. <i>Biochemical and Biophysical Research Communications</i> , 2021, 562, 94-99.	1.0	1
66	S03A3 Metastable structure detected by relaxation dispersion NMR spectroscopy(Visualising) Tj ETQq0 0 0 rgBT /Overlock 1Q Tf 50 302	0.0	0
67	Design Strategy for High Free-Energy States of Proteins Based on High-Pressure NMR Study: Alternatively Folded Conformation of Ubiquitin. <i>Biophysical Journal</i> , 2012, 102, 25a.	0.2	0
68	Revealing the peptide presenting process of human leukocyte antigen through the analysis of fluctuation. <i>Biophysics (Nagoya-shi, Japan)</i> , 2015, 11, 103-106.	0.4	0
69	Isolation and characterization of a minimal building block of polyubiquitin fibrils. <i>Scientific Reports</i> , 2018, 8, 2711.	1.6	0
70	Elucidating Functional Dynamics by R 1ρ and R 2 Relaxation Dispersion NMR Spectroscopy. , 2018, , 197-225.		0
71	Backbone resonance assignments of the A2 domain of mouse von Willebrand factor. <i>Biomolecular NMR Assignments</i> , 2021, 15, 427-431.	0.4	0