

Masanori Osawa

List of Publications by Year in descending order

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56
papers

2,132
citations

279701

23
h-index

233338

45
g-index

60
all docs

60
docs citations

60
times ranked

2672
citing authors

#	ARTICLE	IF	CITATIONS
1	A novel target recognition revealed by calmodulin in complex with Ca ²⁺ -calmodulin-dependent kinase kinase. <i>Nature Structural Biology</i> , 1999, 6, 819-824.	9.7	228
2	Solution structure of Calmodulin-W-7 complex: the basis of diversity in molecular recognition. <i>Journal of Molecular Biology</i> , 1998, 276, 165-176.	2.0	152
3	Mechanism of mRNA deadenylation: evidence for a molecular interplay between translation termination factor eRF3 and mRNA deadenylases. <i>Genes and Development</i> , 2007, 21, 3135-3148.	2.7	150
4	The role of calcium-binding proteins in the control of transcription: structure to function. <i>BioEssays</i> , 2002, 24, 625-636.	1.2	132
5	Calcium-regulated DNA Binding and Oligomerization of the Neuronal Calcium-sensing Protein, Calsenilin/DREAM/KChIP3. <i>Journal of Biological Chemistry</i> , 2001, 276, 41005-41013.	1.6	116
6	Structural basis underlying the dual gate properties of KcsA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 6216-6221.	3.3	113
7	Target-induced conformational adaptation of calmodulin revealed by the crystal structure of a complex with nematode Ca ²⁺ /calmodulin-dependent kinase kinase peptide 1 Edited by K. Morikawa. <i>Journal of Molecular Biology</i> , 2001, 312, 59-68.	2.0	102
8	Mg ²⁺ and Ca ²⁺ Differentially Regulate DNA Binding and Dimerization of DREAM. <i>Journal of Biological Chemistry</i> , 2005, 280, 18008-18014.	1.6	95
9	Structural basis of the collagen-binding mode of discoidin domain receptor 2. <i>EMBO Journal</i> , 2007, 26, 4168-4176.	3.5	95
10	NMR Analyses of the Interaction between CCR5 and Its Ligand Using Functional Reconstitution of CCR5 in Lipid Bilayers. <i>Journal of the American Chemical Society</i> , 2010, 132, 6768-6777.	6.6	68
11	Structural Insights into Activation of Phosphatidylinositol 4-Kinase (Pik1) by Yeast Frequenin (Frq1). <i>Journal of Biological Chemistry</i> , 2007, 282, 30949-30959.	1.6	63
12	Calmodulin and STIM proteins: Two major calcium sensors in the cytoplasm and endoplasmic reticulum. <i>Biochemical and Biophysical Research Communications</i> , 2015, 460, 5-21.	1.0	61
13	ATP-dependent modulation of MgtE in Mg ²⁺ homeostasis. <i>Nature Communications</i> , 2017, 8, 148.	5.8	54
14	Functional Equilibrium of the KcsA Structure Revealed by NMR*. <i>Journal of Biological Chemistry</i> , 2012, 287, 39634-39641.	1.6	50
15	NMR Analyses of the Cl ⁻ Binding and Conformational Rearrangements of the Cytoplasmic Pore of G Protein-activated Inwardly Rectifying Potassium Channel 1 (GIRK1). <i>Journal of Biological Chemistry</i> , 2011, 286, 2215-2223.	1.6	48
16	Evidence for calmodulin inter-domain compaction in solution induced by W-7 binding. <i>FEBS Letters</i> , 1999, 442, 173-177.	1.3	46
17	Molecular Interactions of Yeast Frequenin (Frq1) with the Phosphatidylinositol 4-Kinase Isoform, Pik1. <i>Journal of Biological Chemistry</i> , 2003, 278, 4862-4874.	1.6	45
18	Cross-saturation and transferred cross-saturation experiments. <i>Progress in Nuclear Magnetic Resonance Spectroscopy</i> , 2009, 54, 123-140.	3.9	44

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19	Structural mechanism underlying G protein family-specific regulation of G protein-gated inwardly rectifying potassium channel. <i>Nature Communications</i> , 2019, 10, 2008.	5.8	44
20	Dynamic regulation of GDP binding to G proteins revealed by magnetic field-dependent NMR relaxation analyses. <i>Nature Communications</i> , 2017, 8, 14523.	5.8	36
21	Functional dynamics of proteins revealed by solution NMR. <i>Current Opinion in Structural Biology</i> , 2012, 22, 660-669.	2.6	32
22	Structural Basis for Modulation of Gating Property of G Protein-gated Inwardly Rectifying Potassium Ion Channel (GIRK) by α -family G Protein $\beta\gamma$ Subunit ($G\beta\gamma$). <i>Journal of Biological Chemistry</i> , 2012, 287, 19537-19549.	1.6	30
23	NMR Method for Characterizing Microsecond-to-Millisecond Chemical Exchanges Utilizing Differential Multiple-Quantum Relaxation in High Molecular Weight Proteins. <i>Journal of the American Chemical Society</i> , 2016, 138, 2302-2311.	6.6	27
24	Quantitative Characterization of Tob Interactions Provides the Thermodynamic Basis for Translation Termination-coupled Deadenylation Regulation. <i>Journal of Biological Chemistry</i> , 2010, 285, 27624-27631.	1.6	22
25	Cross-saturation and transferred cross-saturation experiments. <i>Quarterly Reviews of Biophysics</i> , 2014, 47, 143-187.	2.4	22
26	Characterization of the multimeric structure of poly(A)-binding protein on a poly(A) tail. <i>Scientific Reports</i> , 2018, 8, 1455.	1.6	22
27	Evidence for the Direct Interaction of Spermine with the Inwardly Rectifying Potassium Channel. <i>Journal of Biological Chemistry</i> , 2009, 284, 26117-26126.	1.6	19
28	Biological role of the two overlapping poly(A)-binding protein interacting motifs 2 (PAM2) of eukaryotic releasing factor eRF3 in mRNA decay. <i>Rna</i> , 2012, 18, 1957-1967.	1.6	19
29	Nickel binding to NikA: an additional binding site reconciles spectroscopy, calorimetry and crystallography. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2007, 63, 221-229.	2.5	18
30	Structural basis for the inhibition of voltage-dependent K ⁺ channel by gating modifier toxin. <i>Scientific Reports</i> , 2015, 5, 14226.	1.6	18
31	NMR structure of human fibronectin EDA. <i>Journal of Biomolecular NMR</i> , 2001, 21, 281-284.	1.6	16
32	GZD824 Inhibits GCN2 and Sensitizes Cancer Cells to Amino Acid Starvation Stress. <i>Molecular Pharmacology</i> , 2020, 98, 669-676.	1.0	16
33	Amino Acid Selective Cross-Saturation Method for Identification of Proximal Residue Pairs in a Protein-Protein Complex. <i>Journal of the American Chemical Society</i> , 2008, 130, 12168-12176.	6.6	14
34	Nanodiscs for Structural Biology in a Membranous Environment. <i>Chemical and Pharmaceutical Bulletin</i> , 2019, 67, 321-326.	0.6	12
35	Functional dynamics of cell surface membrane proteins. <i>Journal of Magnetic Resonance</i> , 2014, 241, 86-96.	1.2	11
36	Structural basis for the ethanol action on G-protein-activated inwardly rectifying potassium channel 1 revealed by NMR spectroscopy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 3858-3863.	3.3	10

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37	Functional roles of Mg ²⁺ binding sites in ion-dependent gating of a Mg ²⁺ channel, MgtE, revealed by solution NMR. <i>ELife</i> , 2018, 7, .	2.8	10
38	Backbone resonance assignments for G protein β 3 subunit in the GTP-bound state. <i>Biomolecular NMR Assignments</i> , 2012, 6, 217-220.	0.4	9
39	Structural basis for the binding of the membrane-proximal C-terminal region of chemokine receptor CCR2 with the cytosolic regulator FROUNT . <i>FEBS Journal</i> , 2014, 281, 5552-5566.	2.2	9
40	Identification of novel inhibitors of Keap1/Nrf2 by a promising method combining protein-protein interaction-oriented library and machine learning. <i>Scientific Reports</i> , 2021, 11, 7420.	1.6	9
41	Structure determination of a protein assembly by amino acid selective cross-saturation. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 179-190.	1.5	8
42	Peptide Toxins Targeting KV Channels. <i>Handbook of Experimental Pharmacology</i> , 2021, 267, 481-505.	0.9	7
43	Backbone resonance assignments for the cytoplasmic regions of G protein-activated inwardly rectifying potassium channel 1 (GIRK1). <i>Biomolecular NMR Assignments</i> , 2009, 3, 125-128.	0.4	5
44	Spatial distribution of cytoplasmic domains of the Mg ²⁺ -transporter MgtE, in a solution lacking Mg ²⁺ , revealed by paramagnetic relaxation enhancement. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2012, 1824, 1129-1135.	1.1	5
45	Backbone resonance assignments for G protein β 3 subunit in the GDP-bound state. <i>Biomolecular NMR Assignments</i> , 2014, 8, 237-241.	0.4	5
46	Mechanism of hERG inhibition by gating-modifier toxin, APETx1, deduced by functional characterization. <i>BMC Molecular and Cell Biology</i> , 2021, 22, 3.	1.0	5
47	Paip2A inhibits translation by competitively binding to the RNA recognition motifs of PABPC1 and promoting its dissociation from the poly(A) tail. <i>Journal of Biological Chemistry</i> , 2022, 298, 101844.	1.6	4
48	Disulfide mapping the voltage-sensing mechanism of a voltage-dependent potassium channel. <i>Scientific Reports</i> , 2016, 6, 37303.	1.6	2
49	Backbone resonance assignments for the ligand binding subunit of the histidine permease complex (HisJ) from <i>Escherichia coli</i> , under histidine-bound and unbound states. <i>Biomolecular NMR Assignments</i> , 2010, 4, 17-20.	0.4	1
50	Backbone resonance assignments for the cytoplasmic region of the Mg ²⁺ transporter MgtE in the Mg ²⁺ -unbound state. <i>Biomolecular NMR Assignments</i> , 2013, 7, 93-96.	0.4	1
51	Conformational equilibrium shift underlies altered K ⁺ channel gating as revealed by NMR. <i>Nature Communications</i> , 2020, 11, 5168.	5.8	1
52	Comprehensive Approach of ¹⁹ F Nuclear Magnetic Resonance, Enzymatic, and In Silico Methods for Site-Specific Hit Selection and Validation of Fragment Molecules that Inhibit Methionine ¹³ C-Lyase Activity. <i>Journal of Medicinal Chemistry</i> , 2021, 64, 14299-14310.	2.9	1
53	2SBP-05 Structural Basis for Regulation of G Protein-activated Inwardly Rectifying Potassium Channel 1 (GIRK1) by G Proteins(New Development of Structural Cell Biology in Signal) TjETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 102 Td (Tr <i>Seibutsu Butsuri</i> . 2014. 54. S131.	0.0	0
54	Nuclear Magnetic Resonance Approaches for Characterizing Protein-Protein Interactions. <i>Methods in Molecular Biology</i> , 2018, 1684, 115-128.	0.4	0

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55	Solution NMR Study on Functional Mechanism of Membrane Proteins. Seibutsu Butsuri, 2013, 53, 236-241.	0.0	0
56	CHAPTER 26. Large Protein Complexes Revealed by Solution-State NMR: G Proteins and G Protein-Activated Inwardly Rectifying Potassium Ion Channel. New Developments in NMR, 2014, , 501-532.	0.1	0