

Masanori Osawa

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

55
papers

1,778
citations

22
h-index

42
g-index

60
ext. papers

2,004
ext. citations

6.5
avg, IF

4.13
L-index

#	Paper	IF	Citations
55	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 , 101844	5.4	0
54	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	4.9	1
53	Peptide Toxins Targeting KV Channels. <i>Handbook of Experimental Pharmacology</i> , 2021 , 267, 481-505	3.2	1
52	Comprehensive Approach of F Nuclear Magnetic Resonance, Enzymatic, and Methods for Site-Specific Hit Selection and Validation of Fragment Molecules that Inhibit Methionine Lyase Activity. <i>Journal of Medicinal Chemistry</i> , 2021 , 64, 14299-14310	8.3	
51	Mechanism of hERG inhibition by gating-modifier toxin, APETx1, deduced by functional characterization. <i>BMC Molecular and Cell Biology</i> , 2021 , 22, 3	2.7	1
50	GZD824 Inhibits GCN2 and Sensitizes Cancer Cells to Amino Acid Starvation Stress. <i>Molecular Pharmacology</i> , 2020 , 98, 669-676	4.3	3
49	Conformational equilibrium shift underlies altered K channel gating as revealed by NMR. <i>Nature Communications</i> , 2020 , 11, 5168	17.4	0
48	Structural mechanism underlying G protein family-specific regulation of G protein-gated inwardly rectifying potassium channel. <i>Nature Communications</i> , 2019 , 10, 2008	17.4	14
47	Nanodiscs for Structural Biology in a Membranous Environment. <i>Chemical and Pharmaceutical Bulletin</i> , 2019 , 67, 321-326	1.9	11
46	Characterization of the multimeric structure of poly(A)-binding protein on a poly(A) tail. <i>Scientific Reports</i> , 2018 , 8, 1455	4.9	9
45	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	11.5	8
44	Nuclear Magnetic Resonance Approaches for Characterizing Protein-Protein Interactions. <i>Methods in Molecular Biology</i> , 2018 , 1684, 115-128	1.4	
43	Functional roles of Mg binding sites in ion-dependent gating of a Mg channel, MgtE, revealed by solution NMR. <i>ELife</i> , 2018 , 7,	8.9	5
42	Dynamic regulation of GDP binding to G proteins revealed by magnetic field-dependent NMR relaxation analyses. <i>Nature Communications</i> , 2017 , 8, 14523	17.4	26
41	ATP-dependent modulation of MgtE in Mg homeostasis. <i>Nature Communications</i> , 2017 , 8, 148	17.4	31
40	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, 2302-11	16.4	24
39	Disulfide mapping the voltage-sensing mechanism of a voltage-dependent potassium channel. <i>Scientific Reports</i> , 2016 , 6, 37303	4.9	2

38	Structural basis for the inhibition of voltage-dependent K ⁺ channel by gating modifier toxin. <i>Scientific Reports</i> , 2015 , 5, 14226	4.9	12
37	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	3.4	43
36	Functional dynamics of cell surface membrane proteins. <i>Journal of Magnetic Resonance</i> , 2014 , 241, 86-96		7
35	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 Transduction,Symposium,The 52th Annual Meeting of the Biophysical Society of Japan(BSJ2014)). <i>Seibutsu Butsuri</i> , 2014 , 54, 513-1	0	
34	Cross-saturation and transferred cross-saturation experiments. <i>Quarterly Reviews of Biophysics</i> , 2014 , 47, 143-87	7	18
33	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, 5552-66	5.7	8
32	Backbone resonance assignments for G protein (β3) subunit in the GDP-bound state. <i>Biomolecular NMR Assignments</i> , 2014 , 8, 237-41	0.7	5
31	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, 93-6	0.7	
30	Solution NMR Study on Functional Mechanism of Membrane Proteins. <i>Seibutsu Butsuri</i> , 2013 , 53, 236-241		
29	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, 1129-35	4	5
28	Functional dynamics of proteins revealed by solution NMR. <i>Current Opinion in Structural Biology</i> , 2012 , 22, 660-9	8.1	29
27	Backbone resonance assignments for G protein (β3) subunit in the GTP-bound state. <i>Biomolecular NMR Assignments</i> , 2012 , 6, 217-20	0.7	5
26	Functional equilibrium of the KcsA structure revealed by NMR. <i>Journal of Biological Chemistry</i> , 2012 , 287, 39634-41	5.4	47
25	Structural basis for modulation of gating property of G protein-gated inwardly rectifying potassium ion channel (GIRK) by i/o-family G protein βsubunit (Gβo). <i>Journal of Biological Chemistry</i> , 2012 , 287, 19537-49	5.4	29
24	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, 1957-67	5.8	17
23	Structure determination of a protein assembly by amino acid selective cross-saturation. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011 , 79, 179-90	4.2	7
22	NMR analyses of the Gbetagamma 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, 2215-23	5.4	40
21	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, 6216-21	11.5	100

20	Quantitative characterization of Tob interactions provides the thermodynamic basis for translation termination-coupled deadenylase regulation. <i>Journal of Biological Chemistry</i> , 2010 , 285, 27624-31	5.4	20
19	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, 6768-77	16.4	65
18	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	0.7	1
17	Evidence for the direct interaction of spermine with the inwardly rectifying potassium channel. <i>Journal of Biological Chemistry</i> , 2009 , 284, 26117-26	5.4	17
16	Backbone resonance assignments for the cytoplasmic regions of G protein-activated inwardly rectifying potassium channel 1 (GIRK1). <i>Biomolecular NMR Assignments</i> , 2009 , 3, 125-8	0.7	5
15	Cross-saturation and transferred cross-saturation experiments. <i>Progress in Nuclear Magnetic Resonance Spectroscopy</i> , 2009 , 54, 123-140	10.4	39
14	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, 12168-76	16.4	12
13	Nickel binding to NikA: an additional binding site reconciles spectroscopy, calorimetry and crystallography. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2007 , 63, 221-9		15
12	Structural basis of the collagen-binding mode of discoidin domain receptor 2. <i>EMBO Journal</i> , 2007 , 26, 4168-76	13	88
11	Structural insights into activation of phosphatidylinositol 4-kinase (Pik1) by yeast frequenin (Frq1). <i>Journal of Biological Chemistry</i> , 2007 , 282, 30949-59	5.4	52
10	Mechanism of mRNA deadenylation: evidence for a molecular interplay between translation termination factor eRF3 and mRNA deadenylases. <i>Genes and Development</i> , 2007 , 21, 3135-48	12.6	136
9	Mg ²⁺ and Ca ²⁺ differentially regulate DNA binding and dimerization of DREAM. <i>Journal of Biological Chemistry</i> , 2005 , 280, 18008-14	5.4	84
8	Molecular interactions of yeast frequenin (Frq1) with the phosphatidylinositol 4-kinase isoform, Pik1. <i>Journal of Biological Chemistry</i> , 2003 , 278, 4862-74	5.4	39
7	The role of calcium-binding proteins in the control of transcription: structure to function. <i>BioEssays</i> , 2002 , 24, 625-36	4.1	117
6	NMR structure of human fibronectin EDA. <i>Journal of Biomolecular NMR</i> , 2001 , 21, 281-4	3	15
5	Calcium-regulated DNA binding and oligomerization of the neuronal calcium-sensing protein, calsenilin/DREAM/KChIP3. <i>Journal of Biological Chemistry</i> , 2001 , 276, 41005-13	5.4	104
4	Target-induced conformational adaptation of calmodulin revealed by the crystal structure of a complex with nematode Ca(2+)/calmodulin-dependent kinase kinase peptide. <i>Journal of Molecular Biology</i> , 2001 , 312, 59-68	6.5	91
3	A novel target recognition revealed by calmodulin in complex with Ca ²⁺ -calmodulin-dependent kinase kinase. <i>Nature Structural Biology</i> , 1999 , 6, 819-24		197

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| 2 | Evidence for calmodulin inter-domain compaction in solution induced by W-7 binding. <i>FEBS Letters</i> , 1999 , 442, 173-7 | 3.8 | 36 |
| 1 | Solution structure of calmodulin-W-7 complex: the basis of diversity in molecular recognition. <i>Journal of Molecular Biology</i> , 1998 , 276, 165-76 | 6.5 | 137 |