

# Kenji Ogura

## List of Publications by Year in descending order

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44  
papers

1,791  
citations

236925

25  
h-index

265206

42  
g-index

45  
all docs

45  
docs citations

45  
times ranked

2050  
citing authors

#	ARTICLE	IF	CITATIONS
1	Ligand-driven conformational changes of MurD visualized by paramagnetic NMR. <i>Scientific Reports</i> , 2015, 5, 16685.	3.3	30
2	Practical applications of hydrostatic pressure to refold proteins from inclusion bodies for NMR structural studies. <i>Protein Engineering, Design and Selection</i> , 2013, 26, 409-416.	2.1	11
3	Conformational change of Sos-derived proline-rich peptide upon binding Grb2 N-terminal SH3 domain probed by NMR. <i>Scientific Reports</i> , 2013, 3, 2913.	3.3	7
4	NMR Analyses of the Interaction between the FYVE Domain of Early Endosome Antigen 1 (EEA1) and Phosphoinositide Embedded in a Lipid Bilayer. <i>Journal of Biological Chemistry</i> , 2012, 287, 34936-34945.	3.4	27
5	Conformational dynamics of yeast calmodulin in the Ca <sup>2+</sup> -bound state probed using NMR relaxation dispersion. <i>FEBS Letters</i> , 2012, 586, 2548-2554.	2.8	3
6	Convenient method for resolving degeneracies due to symmetry of the magnetic susceptibility tensor and its application to pseudo contact shift-based protein-protein complex structure determination. <i>Journal of Biomolecular NMR</i> , 2012, 53, 53-63.	2.8	37
7	Solution structures of yeast <i>Saccharomyces cerevisiae</i> calmodulin in calcium-bound and target peptide-bound states reveal similarities and differences to vertebrate calmodulin. <i>Genes To Cells</i> , 2012, 17, 159-172.	1.2	15
8	Structural Basis of Atg8 Activation by a Homodimeric E1, Atg7. <i>Molecular Cell</i> , 2011, 44, 462-475.	9.7	156
9	An NMR strategy for fragment-based ligand screening utilizing a paramagnetic lanthanide probe. <i>Journal of Biomolecular NMR</i> , 2011, 51, 395-408.	2.8	56
10	Phosphoinositide-incorporated lipid-protein nanodiscs: A tool for studying protein-lipid interactions. <i>Analytical Biochemistry</i> , 2011, 410, 77-83.	2.4	31
11	The NMR structure of the autophagy-related protein Atg8. <i>Journal of Biomolecular NMR</i> , 2010, 47, 237-241.	2.8	49
12	Structure determination of proteins in 2H <sub>2</sub> O solution aided by a deuterium-decoupled 3D HCA(N)CO experiment. <i>Journal of Biomolecular NMR</i> , 2010, 47, 243-248.	2.8	3
13	Solution Structure of a Novel Cdc42 Binding Module of Bem1 and Its Interaction with Ste20 and Cdc42. <i>Journal of Biological Chemistry</i> , 2010, 285, 19346-19353.	3.4	24
14	Attachment of an NMR-invisible solubility enhancement tag using a sortase-mediated protein ligation method. <i>Journal of Biomolecular NMR</i> , 2009, 43, 145-150.	2.8	103
15	Two-point anchoring of a lanthanide-binding peptide to a target protein enhances the paramagnetic anisotropic effect. <i>Journal of Biomolecular NMR</i> , 2009, 44, 157-166.	2.8	86
16	NMR Structure of the Heterodimer of Bem1 and Cdc24 PB1 Domains from <i>Saccharomyces Cerevisiae</i> . <i>Journal of Biochemistry</i> , 2009, 146, 317-325.	1.7	12
17	Solution structure of the Grb2 SH2 domain complexed with a high-affinity inhibitor. <i>Journal of Biomolecular NMR</i> , 2008, 42, 197-207.	2.8	20
18	The Cooperative Role of OsCnfU-1A Domain I and Domain II in the Iron Sulphur Cluster Transfer Process as Revealed by NMR. <i>Journal of Biochemistry</i> , 2007, 142, 113-121.	1.7	10

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19	Structural basis for the transforming activity of human cancer-related signaling adaptor protein CRK. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 503-510.	8.2	113
20	The NMR structure of the domain II of a chloroplastic NifU-like protein OsNifU1A. <i>Journal of Biomolecular NMR</i> , 2007, 38, 161-164.	2.8	9
21	Activation of the superoxide-producing phagocyte NADPH oxidase requires co-operation between the tandem SH3 domains of p47phox in recognition of a polyproline typeII helix and an adjacent I±-helix of p22phox. <i>Biochemical Journal</i> , 2006, 396, 183-192.	3.7	32
22	NMR Solution Structure of the Tandem Src Homology 3 Domains of p47 Complexed with a p22 -derived Proline-rich Peptide. <i>Journal of Biological Chemistry</i> , 2006, 281, 3660-3668.	3.4	72
23	NMR Study on the Major Mite Allergen Der f 2: Its Refined Tertiary Structure, Epitopes for Monoclonal Antibodies and Characteristics Shared by ML Protein Group Members. <i>Journal of Biochemistry</i> , 2005, 137, 255-263.	1.7	61
24	Refolding and purification of recombinant OsNifU1A domain II that was expressed by <i>Escherichia coli</i> . <i>Protein Expression and Purification</i> , 2005, 43, 149-156.	1.3	3
25	Solution Structure of the Tandem Src Homology 3 Domains of p47 in an Autoinhibited Form. <i>Journal of Biological Chemistry</i> , 2004, 279, 29752-29760.	3.4	51
26	Solution Structure of Atypical Protein Kinase C PB1 Domain and Its Mode of Interaction with ZIP/p62 and MEK5. <i>Journal of Biological Chemistry</i> , 2004, 279, 31883-31890.	3.4	74
27	A molecular mechanism for autoinhibition of the tandem SH3 domains of p47phox, the regulatory subunit of the phagocyte NADPH oxidase. <i>Genes To Cells</i> , 2004, 9, 443-456.	1.2	63
28	Letter to the Editor: Sequence-specific Resonance Assignments of the Tandem SH3 Domains in an Autoinhibitory form of p47phox. <i>Journal of Biomolecular NMR</i> , 2004, 29, 451-452.	2.8	0
29	Backbone assignments of Grb2 complexed with ligand peptides for SH3 and SH2 domains. <i>Journal of Biomolecular NMR</i> , 2003, 27, 185-186.	2.8	3
30	The PB1 domain and the PC motif-containing region are structurally similar protein binding modules. <i>EMBO Journal</i> , 2003, 22, 4888-4897.	7.8	38
31	Crystallization and preliminary crystallographic analysis of the autoinhibited form of the tandem SH3 domain of p47phox. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 1479-1480.	2.5	12
32	Solution structure of N-terminal SH3 domain of Vav and the recognition site for Grb2 C-terminal SH3 domain. <i>Journal of Biomolecular NMR</i> , 2002, 22, 37-46.	2.8	18
33	Solution structure of Grb2 reveals extensive flexibility necessary for target recognition. <i>Journal of Molecular Biology</i> , 2001, 306, 527-537.	4.2	59
34	Solution Structure of the SH2 Domain of Grb2/Ash Complexed with EGF Receptor-Derived Phosphotyrosine-Containing Peptide. <i>Journal of Biochemistry</i> , 1999, 125, 1151-1159.	1.7	6
35	Solution structure of human acidic fibroblast growth factor and interaction with heparin-derived hexasaccharide. <i>Journal of Biomolecular NMR</i> , 1999, 13, 11-24.	2.8	49
36	The structure of an aggregate form of bacteriochlorophyllc showing the Qy absorption at 705 nm as determined by the ring-current effects on <sup>1</sup> H and <sup>13</sup> C nuclei and by <sup>1</sup> H- <sup>1</sup> H intermolecular NOE correlations. , 1999, 5, 63-77.		18

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37	Solution structure of the SH2 domain of Grb2 complexed with the Shc-derived phosphotyrosine-containing peptide. <i>Journal of Molecular Biology</i> , 1999, 289, 439-445.	4.2	63
38	The Structure of the Aggregate Form of Bacteriochlorophyll <i>c</i> Showing the Q <sub>y</sub> Absorption above 740 nm as Determined by the Ring-current Effects on <sup>1</sup> H and <sup>13</sup> C Nuclei and by <sup>1</sup> H- <sup>13</sup> C Intermolecular NOE Correlations. <i>Photochemistry and Photobiology</i> , 1998, 67, 239-248.	2.5	3
39	The Structure of the Aggregate Form of Bacteriochlorophyll <i>c</i> Showing the Q <sub>y</sub> Absorption above 740 nm as Determined by the Ring-current Effects on <sup>1</sup> H and <sup>13</sup> C Nuclei and by <sup>1</sup> H- <sup>13</sup> C Intermolecular NOE Correlations. <i>Photochemistry and Photobiology</i> , 1998, 67, 239.	2.5	42
40	Conformation of an Shc-derived phosphotyrosine-containing peptide complexed with the Grb2 SH2 domain. <i>Journal of Biomolecular NMR</i> , 1997, 10, 273-278.	2.8	19
41	Fully <sup>13</sup> C-Refocused Multidimensional <sup>13</sup> C-Edited Pulse Schemes Using Broadband Shaped Inversion and Refocusing Pulses. <i>Journal of Magnetic Resonance Series B</i> , 1996, 112, 63-68.	1.6	30
42	An improved double-tuned and isotope-filtered pulse scheme based on a pulsed field gradient and a wide-band inversion shaped pulse. <i>Journal of Biomolecular NMR</i> , 1996, 8, 492-8.	2.8	96
43	Structure of the N-terminal SH3 domain of GRB2 complexed with a peptide from the guanine nucleotide releasing factor Sos. <i>Nature Structural and Molecular Biology</i> , 1994, 1, 891-897.	8.2	103
44	Solution structure and ligand-binding site of the carboxy-terminal SH3 domain of GRB2. <i>Structure</i> , 1994, 2, 1029-1040.	3.3	74