

# Hidehito Tochio

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9021131/publications.pdf>

Version: 2024-02-01

88  
papers

5,123  
citations

117625

34  
h-index

88630

70  
g-index

94  
all docs

94  
docs citations

94  
times ranked

6829  
citing authors

#	ARTICLE	IF	CITATIONS
1	Characterizing conformational ensembles of multi-domain proteins using anisotropic paramagnetic NMR restraints. <i>Biophysical Reviews</i> , 2022, 14, 55-66.	3.2	2
2	Conformational Space Sampled by Domain Reorientation of Linear Diubiquitin Reflected in Its Binding Mode for Target Proteins. <i>ChemPhysChem</i> , 2021, 22, 1505-1517.	2.1	8
3	Tracking the 3D Rotational Dynamics in Nanoscopic Biological Systems. <i>Journal of the American Chemical Society</i> , 2020, 142, 7542-7554.	13.7	34
4	Contribution of Coiled-Coil Assembly to Ca <sup>2+</sup> /Calmodulin-Dependent Inactivation of TRPC6 Channel and its Impacts on FSGS-Associated Phenotypes. <i>Journal of the American Society of Nephrology: JASN</i> , 2019, 30, 1587-1603.	6.1	23
5	An innate interaction between IL-18 and the propeptide that inactivates its precursor form. <i>Scientific Reports</i> , 2019, 9, 6160.	3.3	15
6	Cooperative Domain Formation by Homologous Motifs in HOIL-1L and SHARPIN Plays A Crucial Role in LUBAC Stabilization. <i>Cell Reports</i> , 2018, 23, 1192-1204.	6.4	84
7	Intramolecular interaction suggests an autosuppression mechanism for the innate immune adaptor protein MyD88. <i>Chemical Communications</i> , 2018, 54, 12318-12321.	4.1	3
8	Impairment of Calcium-dependent inactivation of TRPC6 Mediated by Calmodulin Underlies Renal Channelopathy. <i>Proceedings for Annual Meeting of the Japanese Pharmacological Society</i> , 2018, WCP2018, PO1-3-25.	0.0	0
9	Hexaphyrin as a Potential Theranostic Dye for Photothermal Therapy and <sup>19</sup> F Magnetic Resonance Imaging. <i>ChemBioChem</i> , 2017, 18, 951-959.	2.6	16
10	Selective Labeling of Proteins on Living Cell Membranes Using Fluorescent Nanodiamond Probes. <i>Nanomaterials</i> , 2016, 6, 56.	4.1	24
11	Structural analysis of the TKB domain of ubiquitin ligase Cbl-b complexed with its small inhibitory peptide, Cblin. <i>Archives of Biochemistry and Biophysics</i> , 2016, 594, 1-7.	3.0	7
12	UCP3 is associated with Hax-1 in mitochondria in the presence of calcium ion. <i>Biochemical and Biophysical Research Communications</i> , 2016, 472, 108-113.	2.1	8
13	Suppression of Nonspecific Proteinâ€™Nanodiamond Adsorption Enabling Specific Targeting of Nanodiamonds to Biomolecules of Interest. <i>Chemistry Letters</i> , 2015, 44, 354-356.	1.3	27
14	Selective autophagic receptor p62 regulates the abundance of transcriptional coregulator ARIP4 during nutrient starvation. <i>Scientific Reports</i> , 2015, 5, 14498.	3.3	8
15	Optically Detected Magnetic Resonance of Nanodiamonds &In Vivo&; Implementation of Selective Imaging and Fast Sampling. <i>Journal of Nanoscience and Nanotechnology</i> , 2015, 15, 1014-1021.	0.9	18
16	Magnetic Resonance Imaging of Tumor with a Self-Traceable Phosphorylcholine Polymer. <i>Journal of the American Chemical Society</i> , 2015, 137, 799-806.	13.7	16
17	The unexpected role of polyubiquitin chains in the formation of fibrillar aggregates. <i>Nature Communications</i> , 2015, 6, 6116.	12.8	75
18	The structural basis for receptor recognition of human interleukin-18. <i>Nature Communications</i> , 2014, 5, 5340.	12.8	107

#	ARTICLE	IF	CITATIONS
19	Purification, crystallization and preliminary X-ray crystallographic analysis of human IL-18 and its extracellular complexes. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 1351-1356.	0.8	10
20	Functional assessment of the mutational effects of human IRAK4 and MyD88 genes. <i>Molecular Immunology</i> , 2014, 58, 66-76.	2.2	24
21	Effective production of fluorescent nanodiamonds containing negatively-charged nitrogen-vacancy centers by ion irradiation. <i>Diamond and Related Materials</i> , 2014, 49, 33-38.	3.9	18
22	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.	3.4	60
23	A Structured Monodisperse PEG for the Effective Suppression of Protein Aggregation. <i>Angewandte Chemie - International Edition</i> , 2013, 52, 2430-2434.	13.8	66
24	Quantitative comparison of protein dynamics in live cells and in vitro by in-cell <sup>19</sup> F-NMR. <i>Chemical Communications</i> , 2013, 49, 2801.	4.1	47
25	Pruning the ALS-Associated Protein SOD1 for in-Cell NMR. <i>Journal of the American Chemical Society</i> , 2013, 135, 10266-10269.	13.7	44
26	1SCP-05 Optically detected magnetic resonance spectroscopy of nitrogen-vacancy centers for subnanoscopic measurement in vivo (1SCP Challenges to in vivo biophysics, Symposium, The 51th Annual) Tj ETQq0 0 0 rgBT /Overlock 10 T		
27	Recognition of modification status on a histone H3 tail by linked histone reader modules of the epigenetic regulator UHRF1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 12950-12955.	7.1	178
28	2SB-02 Protein NMR spectroscopy in the cellular environment (2SB Symposium organized by younger) Tj ETQq0 0 0 rgBT /Overlock 10 T	0.1	0
29	Watching protein structure at work in living cells using NMR spectroscopy. <i>Current Opinion in Chemical Biology</i> , 2012, 16, 609-613.	6.1	21
30	Substrate/Product-Targeted NMR Monitoring of Pyrimidine Catabolism and Its Inhibition by a Clinical Drug. <i>ACS Chemical Biology</i> , 2012, 7, 535-542.	3.4	11
31	Real-Time Background-Free Selective Imaging of Fluorescent Nanodiamonds in Vivo. <i>Nano Letters</i> , 2012, 12, 5726-5732.	9.1	177
32	NMR analysis of Lys63-linked polyubiquitin recognition by the tandem ubiquitin-interacting motifs of Rap80. <i>Journal of Biomolecular NMR</i> , 2012, 52, 339-350.	2.8	17
33	Molecular analysis of the binding mode of Toll/interleukin-1 receptor (TIR) domain proteins during TLR2 signaling. <i>Molecular Immunology</i> , 2012, 52, 108-116.	2.2	14
34	TRAM Is Involved in IL-18 Signaling and Functions as a Sorting Adaptor for MyD88. <i>PLoS ONE</i> , 2012, 7, e38423.	2.5	32
35	Crystal Structure of the Ubiquitin-associated (UBA) Domain of p62 and Its Interaction with Ubiquitin. <i>Journal of Biological Chemistry</i> , 2011, 286, 31864-31874.	3.4	117
36	In-Cell NMR Spectroscopy in Protein Chemistry and Drug Discovery. <i>Current Topics in Medicinal Chemistry</i> , 2011, 11, 68-73.	2.1	18

#	ARTICLE	IF	CITATIONS
37	Turn-on Detection of Targeted Biochemical Reactions by Triple Resonance NMR Analysis Using Isotope-labeled Probe. <i>Chemistry Letters</i> , 2010, 39, 926-928.	1.3	8
38	3P019 Structural and thermodynamic analyses of histone H3 recognition by UHRF1 (Protein: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 707 S148.	0.1	0
39	<sup>1</sup> H, <sup>13</sup> C, and <sup>15</sup> N resonance assignment of the TIR domain of human MyD88. <i>Biomolecular NMR Assignments</i> , 2010, 4, 123-125.	0.8	6
40	Purification, crystallization and preliminary crystallographic studies of Lys48-linked polyubiquitin chains. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 834-837.	0.7	4
41	Structural basis for regulation of poly- $\epsilon$ -SUMO chain by a SUMO-like domain of Nip45. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 1491-1502.	2.6	28
42	Solution structure of a zinc-finger domain that binds to poly-ADP-ribose. <i>Genes To Cells</i> , 2010, 15, 101-110.	1.2	17
43	Structure and Mutagenesis Studies of the C-terminal Region of Licensing Factor Cdt1 Enable the Identification of Key Residues for Binding to Replicative Helicase Mcm Proteins. <i>Journal of Biological Chemistry</i> , 2010, 285, 15931-15940.	3.4	25
44	A Common Substrate Recognition Mode Conserved between Katanin p60 and VPS4 Governs Microtubule Severing and Membrane Skeleton Reorganization. <i>Journal of Biological Chemistry</i> , 2010, 285, 16822-16829.	3.4	34
45	Distance Determination in Proteins inside <i>Xenopus laevis</i> Oocytes by Double Electron-Electron Resonance Experiments. <i>Journal of the American Chemical Society</i> , 2010, 132, 8228-8229.	13.7	120
46	Structural basis for the multiple interactions of the MyD88 TIR domain in TLR4 signaling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 10260-10265.	7.1	197
47	Molecular Basis for SUMOylation-dependent Regulation of DNA Binding Activity of Heat Shock Factor 2. <i>Journal of Biological Chemistry</i> , 2009, 284, 2435-2447.	3.4	36
48	High-resolution multi-dimensional NMR spectroscopy of proteins in human cells. <i>Nature</i> , 2009, 458, 106-109.	27.8	410
49	Self-assembling nanoprobe that displays off/on <sup>19</sup> F nuclear magnetic resonance signals for protein detection and imaging. <i>Nature Chemistry</i> , 2009, 1, 557-561.	13.6	204
50	3P-091 Molecular basis for SUMOylation-dependent regulation of DNA binding activity of Heat Shock Factor 2 (Nucleic acid binding proteins, The 47th Annual Meeting of the Biophysical Society of Japan). <i>Seibutsu Butsuri</i> , 2009, 49, S166.	0.1	0
51	The solution structure of the C-terminal domain of NfeD reveals a novel membrane-anchored OB-fold. <i>Protein Science</i> , 2008, 17, 1915-1924.	7.6	10
52	Recognition of hemi-methylated DNA by the SRA protein UHRF1 by a base-flipping mechanism. <i>Nature</i> , 2008, 455, 818-821.	27.8	432
53	Paramagnetic Relaxation-Based <sup>19</sup> F MRI Probe To Detect Protease Activity. <i>Journal of the American Chemical Society</i> , 2008, 130, 794-795.	13.7	234
54	Kinetic and Thermodynamic Evidence for Flipping of a Methyl-CpG Binding Domain on Methylated DNA. <i>Biochemistry</i> , 2008, 47, 3266-3271.	2.5	21

#	ARTICLE	IF	CITATIONS
55	Structure of the Small Ubiquitin-like Modifier (SUMO)-interacting Motif of MBD1-containing Chromatin-associated Factor 1 Bound to SUMO-3. <i>Journal of Biological Chemistry</i> , 2008, 283, 35966-35975.	3.4	68
56	Expression, Purification and Structural Analysis of Human IL-18 Binding Protein: A Potent Therapeutic Molecule for Allergy. <i>Allergology International</i> , 2008, 57, 367-376.	3.3	19
57	1P-044 Thermodynamic analysis of the hemi-methylated CpG DNA recognition by SRA domain of mouse NP95(The 46th Annual Meeting of the Biophysical Society of Japan). <i>Seibutsu Butsuri</i> , 2008, 48, S27.	0.1	0
58	1P-043 The Ubiquitin Associated Domain Of p62 In The Solution Exists In A Monomer-Dimer Equilibrium(The 46th Annual Meeting of the Biophysical Society of Japan). <i>Seibutsu Butsuri</i> , 2008, 48, S27.	0.1	0
59	Magnetic resonance-based visualization of gene expression in mammalian cells using a bacterial polyphosphate kinase reporter gene. <i>BioTechniques</i> , 2007, 42, 209-215.	1.8	7
60	Fluoroscopic assessment of protein leakage during <i>Xenopus</i> oocytes in-cell NMR experiment by co-injected EGFP. <i>Analytical Biochemistry</i> , 2007, 371, 247-249.	2.4	14
61	Crystal Structure of SUMO-3-modified Thymine-DNA Glycosylase. <i>Journal of Molecular Biology</i> , 2006, 359, 137-147.	4.2	51
62	2P127 SUMO-3 (Small Ubiquitin-like Modifier) Recognition by a SUMO Binding Motif(31. Protein folding) <i>Tj ETQq0 0 0 rgBT /Overlock 1</i> 2006, 46, S327.	0.1	0
63	S1f2-3 In vitro and in cell NMR studies of modifier proteins(S1-f2: "Functions and dynamics of protein) <i>Tj ETQq1 1 0.784314 rgBT /Overlock 1</i> <i>Butsuri</i> , 2006, 46, S119.	0.1	0
64	A novel magnetic resonance-based method to measure gene expression in living cells. <i>Nucleic Acids Research</i> , 2006, 34, e51-e51.	14.5	14
65	Heteronuclear multidimensional NMR and homology modelling studies of the C-terminal nucleotide-binding domain of the human mitochondrial ABC transporter ABCB6. <i>Journal of Biomolecular NMR</i> , 2006, 35, 53-71.	2.8	9
66	In-cell NMR spectroscopy of proteins inside <i>Xenopus laevis</i> oocytes. <i>Journal of Biomolecular NMR</i> , 2006, 36, 179-188.	2.8	120
67	Fine-tuning of protein domain boundary by minimizing potential coiled coil regions. <i>Journal of Biomolecular NMR</i> , 2006, 37, 53-63.	2.8	5
68	Crystal structure of thymine DNA glycosylase conjugated to SUMO-1. <i>Nature</i> , 2005, 435, 979-982.	27.8	193
69	Structure of the UBA Domain of Dsk2p in Complex with Ubiquitin. <i>Structure</i> , 2005, 13, 521-532.	3.3	126
70	Molecular Mechanism of a Temperature-Sensitive Phenotype in Peroxisomal Biogenesis Disorder. <i>Pediatric Research</i> , 2005, 58, 263-269.	2.3	15
71	Plc1p, Arg82p, and Kcs1p, Enzymes Involved in Inositol Pyrophosphate Synthesis, Are Essential for Phosphate Regulation and Polyphosphate Accumulation in <i>Saccharomyces cerevisiae</i> . <i>Journal of Biological Chemistry</i> , 2005, 280, 25127-25133.	3.4	101
72	Structural characterization of the MIT domain from human Vps4b. <i>Biochemical and Biophysical Research Communications</i> , 2005, 334, 460-465.	2.1	35

#	ARTICLE	IF	CITATIONS
73	High-throughput construction method for expression vector of peptides for NMR study suited for isotopic labeling. <i>Protein Engineering, Design and Selection</i> , 2004, 17, 305-314.	2.1	24
74	Structure of the Ubiquitin-interacting Motif of S5a Bound to the Ubiquitin-like Domain of HR23B. <i>Journal of Biological Chemistry</i> , 2004, 279, 4760-4767.	3.4	79
75	Intracellular Phosphate Serves as a Signal for the Regulation of the PHO Pathway in <i>Saccharomyces cerevisiae</i> . <i>Journal of Biological Chemistry</i> , 2004, 279, 17289-17294.	3.4	129
76	Structural basis for distinct roles of Lys63- and Lys48-linked polyubiquitin chains. <i>Genes To Cells</i> , 2004, 9, 865-875.	1.2	147
77	Supramodular structure and synergistic target binding of the N-terminal tandem PDZ domains of PSD-95. <i>Journal of Molecular Biology</i> , 2003, 327, 203-214.	4.2	128
78	Backbone dynamics of the 8 kDa dynein light chain dimer reveals molecular basis of the protein's functional diversity. <i>Journal of Biomolecular NMR</i> , 2002, 23, 103-114.	2.8	26
79	Structural basis of diverse sequence-dependent target recognition by the 8 kDa dynein light chain <sup>11</sup> Edited by P. E. Wright. <i>Journal of Molecular Biology</i> , 2001, 306, 97-108.	4.2	129
80	Formation of a native-like $\beta^2$ -hairpin finger structure of a peptide from the extended PDZ domain of neuronal nitric oxide synthase in aqueous solution. <i>FEBS Journal</i> , 2000, 267, 3116-3122.	0.2	25
81	Solution structure and backbone dynamics of the second PDZ domain of postsynaptic density-95. <i>Journal of Molecular Biology</i> , 2000, 295, 225-237.	4.2	105
82	Formation of nNOS/PSD-95 PDZ dimer requires a preformed $\beta^2$ -finger structure from the nNOS PDZ domain. <i>Journal of Molecular Biology</i> , 2000, 303, 359-370.	4.2	116
83	Solution structure of the extended neuronal nitric oxide synthase PDZ domain complexed with an associated peptide. <i>Nature Structural Biology</i> , 1999, 6, 417-421.	9.7	134
84	Solution structure of a protein inhibitor of neuronal nitric oxide synthase. <i>Nature Structural Biology</i> , 1998, 5, 965-969.	9.7	49
85	Protein Inhibitor of Neuronal Nitric-oxide Synthase, PIN, Binds to a 17-Amino Acid Residue Fragment of the Enzyme. <i>Journal of Biological Chemistry</i> , 1998, 273, 33472-33481.	3.4	75
86	Assignment of Backbone Resonances for Larger Proteins Using the $^{13}\text{C}\alpha\text{-}^1\text{H}$ Coherence of a $^1\text{H}\alpha\text{-}, ^2\text{H-}, ^{13}\text{C-},$ and $^{15}\text{N-}$ Labeled Sample. <i>Journal of the American Chemical Society</i> , 1997, 119, 872-880.	13.7	33
87	[21] Induced structural changes in protein-DNA complexes. <i>Methods in Enzymology</i> , 1995, 261, 524-541.	1.0	13
88	Cytokine-inducing glycolipids in the lipoteichoic acid fraction from <i>Enterococcus hirae</i> ATCC 9790. <i>FEMS Immunology and Medical Microbiology</i> , 1995, 12, 97-112.	2.7	2