

# Hidehito Tochio

## List of Publications by Year in descending order

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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  | 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       |
| 2  | High-resolution multi-dimensional NMR spectroscopy of proteins in human cells. <i>Nature</i> , 2009, 458, 106-109.   | 27.8 | 410       |
| 3  | 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       |
| 4  | Self-assembling nanoprobe that display 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       |
| 5  | 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       |
| 6  | Crystal structure of thymine DNA glycosylase conjugated to SUMO-1. <i>Nature</i> , 2005, 435, 979-982.   | 27.8 | 193       |
| 7  | 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       |
| 8  | Real-Time Background-Free Selective Imaging of Fluorescent Nanodiamonds in Vivo. <i>Nano Letters</i> , 2012, 12, 5726-5732.  | 9.1  | 177       |
| 9  | Structural basis for distinct roles of Lys63- and Lys48-linked polyubiquitin chains. <i>Genes To Cells</i> , 2004, 9, 865-875.   | 1.2  | 147       |
| 10 | 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       |
| 11 | Structural basis of diverse sequence-dependent target recognition by the 8 kDa dynein light chain 11. Edited by P. E. Wright. <i>Journal of Molecular Biology</i> , 2001, 306, 97-108.   | 4.2  | 129       |
| 12 | 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       |
| 13 | 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       |
| 14 | Structure of the UBA Domain of Dsk2p in Complex with Ubiquitin. <i>Structure</i> , 2005, 13, 521-532.  | 3.3  | 126       |
| 15 | 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       |
| 16 | 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       |
| 17 | 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       |
| 18 | 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       |

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|----|---|------|-----------|
| 19 | The structural basis for receptor recognition of human interleukin-18. <i>Nature Communications</i> , 2014, 5, 5340.  | 12.8 | 107       |
| 20 | 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       |
| 21 | 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       |
| 22 | 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        |
| 23 | 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        |
| 24 | 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        |
| 25 | The unexpected role of polyubiquitin chains in the formation of fibrillar aggregates. <i>Nature Communications</i> , 2015, 6, 6116.   | 12.8 | 75        |
| 26 | 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        |
| 27 | A Structured Monodisperse PEG for the Effective Suppression of Protein Aggregation. <i>Angewandte Chemie - International Edition</i> , 2013, 52, 2430-2434.   | 13.8 | 66        |
| 28 | 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        |
| 29 | Crystal Structure of SUMO-3-modified Thymine-DNA Glycosylase. <i>Journal of Molecular Biology</i> , 2006, 359, 137-147.   | 4.2  | 51        |
| 30 | Solution structure of a protein inhibitor of neuronal nitric oxide synthase. <i>Nature Structural Biology</i> , 1998, 5, 965-969.   | 9.7  | 49        |
| 31 | Quantitative comparison of protein dynamics in live cells and in vitro by in-cell 19F-NMR. <i>Chemical Communications</i> , 2013, 49, 2801.   | 4.1  | 47        |
| 32 | 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        |
| 33 | 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        |
| 34 | Structural characterization of the MIT domain from human Vps4b. <i>Biochemical and Biophysical Research Communications</i> , 2005, 334, 460-465.  | 2.1  | 35        |
| 35 | 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        |
| 36 | Tracking the 3D Rotational Dynamics in Nanoscopic Biological Systems. <i>Journal of the American Chemical Society</i> , 2020, 142, 7542-7554.   | 13.7 | 34        |

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|----|--|------|-----------|
| 37 | Assignment of Backbone Resonances for Larger Proteins Using the $^{13}\text{C}$ - $^1\text{H}$ Coherence of a $^1\text{H}$ - $^2\text{H}$ , $^{13}\text{C}$ - and $^{15}\text{N}$ -Labeled Sample. <i>Journal of the American Chemical Society</i> , 1997, 119, 872-880. | 13.7 | 33        |
| 38 | 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        |
| 39 | Structural basis for regulation of poly-SUMO chain by a SUMO-like domain of Nip45. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 1491-1502.  | 2.6  | 28        |
| 40 | Suppression of Nonspecific Protein-Nanodiamond Adsorption Enabling Specific Targeting of Nanodiamonds to Biomolecules of Interest. <i>Chemistry Letters</i> , 2015, 44, 354-356.   | 1.3  | 27        |
| 41 | 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        |
| 42 | 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        |
| 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 | 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        |
| 45 | Functional assessment of the mutational effects of human IRAK4 and MyD88 genes. <i>Molecular Immunology</i> , 2014, 58, 66-76.   | 2.2  | 24        |
| 46 | Selective Labeling of Proteins on Living Cell Membranes Using Fluorescent Nanodiamond Probes. <i>Nanomaterials</i> , 2016, 6, 56.  | 4.1  | 24        |
| 47 | Contribution of Coiled-Coil Assembly to $\text{Ca}^{2+}$ /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        |
| 48 | 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        |
| 49 | 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        |
| 50 | 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        |
| 51 | In-Cell NMR Spectroscopy in Protein Chemistry and Drug Discovery. <i>Current Topics in Medicinal Chemistry</i> , 2011, 11, 68-73.  | 2.1  | 18        |
| 52 | 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        |
| 53 | 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        |
| 54 | 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        |

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|----|---|------|-----------|
| 55 | 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        |
| 56 | 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        |
| 57 | 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        |
| 58 | Molecular Mechanism of a Temperature-Sensitive Phenotype in Peroxisomal Biogenesis Disorder. <i>Pediatric Research</i> , 2005, 58, 263-269.   | 2.3  | 15        |
| 59 | An innate interaction between IL-18 and the propeptide that inactivates its precursor form. <i>Scientific Reports</i> , 2019, 9, 6160.  | 3.3  | 15        |
| 60 | 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        |
| 61 | 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        |
| 62 | 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        |
| 63 | [21] Induced structural changes in protein-DNA complexes. <i>Methods in Enzymology</i> , 1995, 261, 524-541.  | 1.0  | 13        |
| 64 | 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        |
| 65 | 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        |
| 66 | 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        |
| 67 | 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         |
| 68 | 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         |
| 69 | Selective autophagic receptor p62 regulates the abundance of transcriptional coregulator ARIP4 during nutrient starvation. <i>Scientific Reports</i> , 2015, 5, 14498.  | 3.3  | 8         |
| 70 | 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         |
| 71 | 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         |
| 72 | 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         |

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|----|--|-----|-----------|
| 73 | Structural analysis of the TKB domain of ubiquitin ligase Cbl-b complexed with its small inhibitory peptide, Cblin. Archives of Biochemistry and Biophysics, 2016, 594, 1-7.   | 3.0 | 7         |
| 74 | <sup>1</sup> H, <sup>13</sup> C, and <sup>15</sup> N resonance assignment of the TIR domain of human MyD88. Biomolecular NMR Assignments, 2010, 4, 123-125.  | 0.8 | 6         |
| 75 | Fine-tuning of protein domain boundary by minimizing potential coiled coil regions. Journal of Biomolecular NMR, 2006, 37, 53-63.  | 2.8 | 5         |
| 76 | Purification, crystallization and preliminary crystallographic studies of Lys48-linked polyubiquitin chains. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 834-837.                                     | 0.7 | 4         |
| 77 | Intramolecular interaction suggests an autosuppression mechanism for the innate immune adaptor protein MyD88. Chemical Communications, 2018, 54, 12318-12321.  | 4.1 | 3         |
| 78 | Cytokine-inducing glycolipids in the lipoteichoic acid fraction from Enterococcus hirae ATCC 9790. FEMS Immunology and Medical Microbiology, 1995, 12, 97-112.   | 2.7 | 2         |
| 79 | Characterizing conformational ensembles of multi-domain proteins using anisotropic paramagnetic NMR restraints. Biophysical Reviews, 2022, 14, 55-66.  | 3.2 | 2         |
| 80 | 2P127 SUMO-3 (Small Ubiquitin-like Modifier) Recognition by a SUMO Binding Motif(31. Protein folding) Tj ETQq0 0 0 rgBT /Overlock 10 T<br>2006, 46, S327.  | 0.1 | 0         |
| 81 | S1f2-3 In vitro and in cell NMR studies of modifier proteins(S1-f2: "Functions and dynamics of protein) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T<br>Butsuri, 2006, 46, S119.  | 0.1 | 0         |
| 82 | 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). Seibutsu Butsuri, 2008, 48, S27.                                      | 0.1 | 0         |
| 83 | 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). Seibutsu Butsuri, 2008, 48, S27.                                       | 0.1 | 0         |
| 84 | 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). Seibutsu Butsuri, 2009, 49, S166. | 0.1 | 0         |
| 85 | 3P019 Structural and thermodynamic analyses of histone H3 recognition by UHRF1(Protein:) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T<br>S148.  | 0.1 | 0         |
| 86 | 2SB-02 Protein NMR spectroscopy in the cellular environment(2SB Symposium organized by younger) Tj ETQq0 0 0 rgBT /Overlock 10 T<br>0.1 0  | 0.1 | 0         |
| 87 | 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 ETQq1 d.0.784314 rgBT /Overlock 10 T    | 0.1 | 0         |
| 88 | Impairment of Calcium-dependent inactivation of TRPC6 Mediated by Calmodulin Underlies Renal Channelopathy. Proceedings for Annual Meeting of the Japanese Pharmacological Society, 2018, WCP2018, PO1-3-25.                             | 0.0 | 0         |