

# Satoru S Watanabe

## List of Publications by Year in descending order

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48  
papers

1,244  
citations

361296

20  
h-index

377752

34  
g-index

49  
all docs

49  
docs citations

49  
times ranked

2266  
citing authors

#	ARTICLE	IF	CITATIONS
1	Phosphatidylinositol monophosphate-binding interface in the oomycete RXLR effector AVR3a is required for its stability in host cells to modulate plant immunity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 14682-14687.	3.3	141
2	Structural Insight into the Zinc Finger CW Domain as a Histone Modification Reader. <i>Structure</i> , 2010, 18, 1127-1139.	1.6	103
3	Structural Basis for Sequence-specific DNA Recognition by an Arabidopsis WRKY Transcription Factor. <i>Journal of Biological Chemistry</i> , 2012, 287, 7683-7691.	1.6	95
4	Structures and evolutionary origins of plant-specific transcription factor DNA-binding domains. <i>Plant Physiology and Biochemistry</i> , 2008, 46, 394-401.	2.8	80
5	RING Domain Mutations Uncouple TRIM5 $\hat{\pm}$ Restriction of HIV-1 from Inhibition of Reverse Transcription and Acceleration of Uncoating. <i>Journal of Virology</i> , 2012, 86, 1717-1727.	1.5	78
6	Structural basis for the dual RNA-recognition modes of human Tra2- $\hat{1}^2$ RRM. <i>Nucleic Acids Research</i> , 2011, 39, 1538-1553.	6.5	62
7	Intracellular Delivery of Proteins via Fusion Peptides in Intact Plants. <i>PLoS ONE</i> , 2016, 11, e0154081.	1.1	62
8	Solution Structure of the SWIRM Domain of Human Histone Demethylase LSD1. <i>Structure</i> , 2006, 14, 457-468.	1.6	59
9	Structural insight into the interaction of ADP $\hat{\text{r}}\text{ibose}$ with the PARP WWE domains. <i>FEBS Letters</i> , 2012, 586, 3858-3864.	1.3	47
10	NMR solution structures of actin depolymerizing factor homology domains. <i>Protein Science</i> , 2009, 18, 2384-2392.	3.1	43
11	Structural and Functional Differences of SWIRM Domain Subtypes. <i>Journal of Molecular Biology</i> , 2007, 369, 222-238.	2.0	41
12	Crystal Structure of the RUN Domain of the RAP2-interacting Protein x. <i>Journal of Biological Chemistry</i> , 2006, 281, 31843-31853.	1.6	36
13	Solution structure of an atypical WW domain in a novel $\hat{1}^2$ -clam-like dimeric form. <i>FEBS Letters</i> , 2007, 581, 462-468.	1.3	33
14	Structural and Functional Characterization of the NHR1 Domain of the Drosophila Neuralized E3 Ligase in the Notch Signaling Pathway. <i>Journal of Molecular Biology</i> , 2009, 393, 478-495.	2.0	27
15	Solution structure of the cysteine $\hat{\text{r}}\text{ich}$ domain in Fn14, a member of the tumor necrosis factor receptor superfamily. <i>Protein Science</i> , 2009, 18, 650-656.	3.1	26
16	Structure of the C-terminal Phosphotyrosine Interaction Domain of Fe65L1 Complexed with the Cytoplasmic Tail of Amyloid Precursor Protein Reveals a Novel Peptide Binding Mode. <i>Journal of Biological Chemistry</i> , 2008, 283, 27165-27178.	1.6	25
17	Cell-free synthesis system suitable for disulfide-containing proteins. <i>Biochemical and Biophysical Research Communications</i> , 2013, 431, 296-301.	1.0	24
18	NMR Studies of the Effects of the 5 $\hat{\text{r}}\text{-Phosphate}$ Group on Conformational Properties of 5-Methylaminomethyluridine Found in the First Position of the Anticodon of <i>Escherichia coli</i> tRNA $\hat{4}\text{Arg}$ . <i>Biochemistry</i> , 1996, 35, 6533-6538.	1.2	23

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19	Co-expression of Two Polyhydroxyalkanoate Synthase Subunits from <i>Synechocystis</i> sp. PCC 6803 by Cell-Free Synthesis and Their Specific Activity for Polymerization of 3-Hydroxybutyryl-Coenzyme A. <i>Biochemistry</i> , 2015, 54, 1401-1407.	1.2	22
20	Active Intermediates of Polyhydroxyalkanoate Synthase from <i>Aeromonas caviae</i> in Polymerization Reaction. <i>Biomacromolecules</i> , 2012, 13, 3450-3455.	2.6	21
21	Solution structure of the RNA binding domain in the human muscleblind-like protein 2. <i>Protein Science</i> , 2009, 18, 80-91.	3.1	20
22	Solution structure of an RNA fragment with the P7/P9.0 region and the 3'-terminal guanosine of the <i>Tetrahymena</i> group I intron. <i>Rna</i> , 2002, 8, 440-451.	1.6	17
23	Solution structures of the DNA-binding domains of immune-related zinc-finger protein ZFAT. <i>Journal of Structural and Functional Genomics</i> , 2015, 16, 55-65.	1.2	17
24	The NMR solution structures of the five constituent cold-shock domains (CSD) of the human UNR (upstream of N-ras) protein. <i>Journal of Structural and Functional Genomics</i> , 2010, 11, 181-188.	1.2	14
25	ZF21 Protein, a Regulator of the Disassembly of Focal Adhesions and Cancer Metastasis, Contains a Novel Noncanonical Pleckstrin Homology Domain. <i>Journal of Biological Chemistry</i> , 2011, 286, 31598-31609.	1.6	14
26	Direct introduction of neomycin phosphotransferase II protein into apple leaves to confer kanamycin resistance. <i>Plant Biotechnology</i> , 2016, 33, 403-407.	0.5	14
27	Molecular cloning of the Lon protease gene from <i>Thermus thermophilus</i> HB8 and characterization of its gene product. <i>FEBS Journal</i> , 1999, 266, 811-819.	0.2	12
28	Solution structure of the GUCT domain from human RNA helicase II/Gu <sup>1</sup> reveals the RRM fold, but implausible RNA interactions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 74, 133-144.	1.5	11
29	NMR Analysis of the Hydrogen Bonding Interactions of the RNA-Binding Domains of the <i>Drosophila</i> Sex-Lethal Protein with Target RNA Fragments with Site-Specific [ <sup>3</sup> - <sup>15</sup> N]Uridine Substitutions. <i>Nucleic Acids Research</i> , 1997, 25, 1565-1569.	6.5	10
30	Structural basis for controlling the dimerization and stability of the WW domains of an atypical subfamily. <i>Protein Science</i> , 2008, 17, 1531-1541.	3.1	8
31	An RNA Fragment Consisting of the P7 and P9.0 Stems and the 3'-Terminal Guanosine of the <i>Tetrahymena</i> Group I Intron. <i>Nucleic Acids Research</i> , 1996, 24, 1337-1344.	6.5	7
32	The Use of the <i>Escherichia coli</i> Cell-Free Protein Synthesis for Structural Biology and Structural Proteomics. , 0, , 99-109.		6
33	Flexible and rigid structures in HIV-1 p17 matrix protein monitored by relaxation and amide proton exchange with NMR. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 520-526.	1.1	6
34	Identification of a Proline-Kinked Amphipathic $\alpha$ -Helix Downstream from the Methyltransferase Domain of a Potexvirus Replicase and Its Role in Virus Replication and Perinuclear Complex Formation. <i>Journal of Virology</i> , 2021, 95, e0190620.	1.5	6
35	Structural basis for the recognition of nucleophosmin-anaplastic lymphoma kinase oncoprotein by the phosphotyrosine binding domain of Suc1-associated neurotrophic factor-induced tyrosine-phosphorylated target-2. <i>Journal of Structural and Functional Genomics</i> , 2010, 11, 125-141.	1.2	5
36	DiRect: Site-directed mutagenesis method for protein engineering by rational design. <i>Biochemical and Biophysical Research Communications</i> , 2021, 551, 107-113.	1.0	5

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37	Hairpin Structure of an RNA 28-mer, Which Contains a Sequence of the Enzyme Component of a Hammerhead Ribozyme System: Evidence for Tandem G: A Pairs That Are Not of Side-by-Side Type. <i>Journal of Biochemistry</i> , 1997, 122, 556-562.	0.9	4
38	Interactions of a didomain fragment of the <i>Drosophila</i> sex-lethal protein with single-stranded uridine-rich oligoribonucleotides derived from the transformer and Sex-lethal messenger RNA precursors: NMR with residue-selective [5-2H]uridine substitutions. <i>Journal of Biomolecular NMR</i> , 2000, 17, 153-165.	1.6	4
39	Comparison of residual alpha- and beta-structures between two intrinsically disordered proteins by using NMR. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2015, 1854, 229-238.	1.1	4
40	<sup>1</sup> H, <sup>13</sup> C and <sup>15</sup> N resonance assignments and solution structures of the two RRM domains of Matrin-3. <i>Biomolecular NMR Assignments</i> , 2022, 16, 41-49.	0.4	3
41	A new modeling method in feature construction for the HSQC spectra screening problem. <i>Bioinformatics</i> , 2009, 25, 948-953.	1.8	2
42	<sup>1</sup> H, <sup>13</sup> C and <sup>15</sup> N resonance assignment of the YTH domain of YTHDC2. <i>Biomolecular NMR Assignments</i> , 2021, 15, 1-7.	0.4	2
43	Effect of Glu12-His89 Interaction on Dynamic Structures in HIV-1 p17 Matrix Protein Elucidated by NMR. <i>PLoS ONE</i> , 2016, 11, e0167176.	1.1	2
44	The guanosine binding mechanism of the <i>Tetrahymena</i> group I intron. <i>Nucleic Acids Symposium Series</i> , 1999, 42, 191-192.	0.3	1
45	Changes in dynamic and static structures of the HIV-1 p24 capsid protein N-terminal domain caused by amino acid substitution are associated with its viral viability. <i>Protein Science</i> , 2021, 30, 2233-2245.	3.1	1
46	<sup>1</sup> H, <sup>13</sup> C, and <sup>15</sup> N resonance assignments and solution structures of the KH domain of human ribosome binding factor A, mtRbfA, involved in mitochondrial ribosome biogenesis. <i>Biomolecular NMR Assignments</i> , 0, , .	0.4	1
47	NMR signal assignment of the polyuridine tract of the single-stranded RNA complexed with Sxl RBD1-RBD2 by using residue selective [5-2H]uridine substitutions. <i>Nucleic Acids Symposium Series</i> , 1999, 42, 203-204.	0.3	0
48	Long-range effects of tag sequence on marginally stabilized structure in HIV-1 p24 capsid protein monitored using NMR. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 1638-1647.	1.1	0