

# Shin-ichi Terawaki

## List of Publications by Year in descending order

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Version: 2024-02-01

25  
papers

566  
citations

840119

11  
h-index

676716

22  
g-index

25  
all docs

25  
docs citations

25  
times ranked

697  
citing authors

#	ARTICLE	IF	CITATIONS
1	A direct heterotypic interaction between the DIX domains of Dishevelled and Axin mediates signaling to $\beta$ -catenin. <i>Science Signaling</i> , 2019, 12, .	1.6	15
2	High-resolution structure of a Y27W mutant of the Dishevelled2 DIX domain. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2019, 75, 116-122.	0.4	6
3	Head-to-Tail Complex of Dishevelled and Axin-DIX Domains: Expression, Purification, Crystallographic Studies and Packing Analysis. <i>Protein and Peptide Letters</i> , 2019, 26, 792-797.	0.4	0
4	In-frame Val 216 -Ser 217 deletion of KIT in mild piebaldism causes aberrant secretion and SCF response. <i>Journal of Dermatological Science</i> , 2018, 91, 35-42.	1.0	3
5	Structural basis for Ccd1 auto-inhibition in the Wnt pathway through homomerization of the DIX domain. <i>Scientific Reports</i> , 2017, 7, 7739.	1.6	6
6	Protein stabilizer, NDSB-195, enhances the dynamics of the $\beta$ -catenin loop of ubiquitin. <i>Journal of Peptide Science</i> , 2016, 22, 174-180.	0.8	3
7	MT1-MMP recognition by ERM proteins and its implication in CD44 shedding. <i>Genes To Cells</i> , 2015, 20, 847-859.	0.5	26
8	Biochemical characterization of a heterotrimeric Gi-protein activator peptide designed from the junction between the intracellular third loop and sixth transmembrane helix in the m4 muscarinic acetylcholine receptor. <i>Biochemical and Biophysical Research Communications</i> , 2015, 463, 64-69.	1.0	0
9	Structural basis for cargo binding and autoinhibition of Bicaudal-D1 by a parallel coiled-coil with homotypic registry. <i>Biochemical and Biophysical Research Communications</i> , 2015, 460, 451-456.	1.0	43
10	Refolding Additive, Dimethylbenzylammonium Propane Sulfonate (NDSB- 256), Accelerates Gly-Pro cis-trans Isomerization. <i>Protein and Peptide Letters</i> , 2015, 22, 234-238.	0.4	1
11	Crystallographic characterization of the C-terminal coiled-coil region of mouse Bicaudal-D1 (BICD1). <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 1103-1106.	0.4	4
12	Crystallographic characterization of the DIX domain of the Wnt signalling positive regulator Ccd1. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 758-761.	0.7	1
13	Expression, crystallization and preliminary X-ray crystallographic study of ethanolamine ammonia-lyase from <i>Escherichia coli</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 709-711.	0.7	1
14	The PHCCEX domain of Tiam1/2 is a novel protein- and membrane-binding module. <i>EMBO Journal</i> , 2010, 29, 236-250.	3.5	31
15	Crystal Structures of Ethanolamine Ammonia-lyase Complexed with Coenzyme B12 Analogs and Substrates. <i>Journal of Biological Chemistry</i> , 2010, 285, 26484-26493.	1.6	87
16	Crystallographic characterization of the radixin FERM domain bound to the cytoplasmic tail of membrane-type 1 matrix metalloproteinase (MT1-MMP). <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 911-913.	0.7	9
17	Crystallographic characterization of the membrane-targeting domains of the Rac-specific guanine nucleotide-exchange factors Tiam1 and Tiam2. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 1039-1042.	0.7	2
18	Structural Basis of the Cytoplasmic Tail of Adhesion Molecule CD43 and Its Binding to ERM Proteins. <i>Journal of Molecular Biology</i> , 2008, 381, 634-644.	2.0	30

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19	Structural Basis for CD44 Recognition by ERM Proteins. <i>Journal of Biological Chemistry</i> , 2008, 283, 29602-29612.	1.6	111
20	Structural Basis for Type II Membrane Protein Binding by ERM Proteins Revealed by the Radixin-neutral Endopeptidase 24.11 (NEP) Complex. <i>Journal of Biological Chemistry</i> , 2007, 282, 19854-19862.	1.6	38
21	Crystallographic characterization of the radixin FERM domain bound to the cytoplasmic tails of adhesion molecules CD43 and PSGL-1. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 49-51.	0.7	7
22	Crystallographic characterization of the radixin FERM domain bound to the cytoplasmic tail of adhesion molecule CD44. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 844-847.	0.7	9
23	Structural basis of PSGL-1 binding to ERM proteins. <i>Genes To Cells</i> , 2007, 12, 1329-1338.	0.5	34
24	Structural Basis for NHERF Recognition by ERM Proteins. <i>Structure</i> , 2006, 14, 777-789.	1.6	86
25	Crystallographic characterization of the radixin FERM domain bound to the C-terminal region of the human Na <sup>+</sup> /H <sup>+</sup> -exchanger regulatory factor (NHERF). <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 177-179.	2.5	13