

Hiroshi Hashimoto

List of Publications by Year in descending order

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76
papers

2,803
citations

186265

28
h-index

182427

51
g-index

77
all docs

77
docs citations

77
times ranked

3529
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural basis for Ca ²⁺ -induced activation of human PAD4. <i>Nature Structural and Molecular Biology</i> , 2004, 11, 777-783.	8.2	363
2	Crystal structure of DNA polymerase from hyperthermophilic archaeon <i>Pyrococcus kodakaraensis</i> KOD111 Edited by R. Huber. <i>Journal of Molecular Biology</i> , 2001, 306, 469-477.	4.2	143
3	Structural Basis for Novel Interactions between Human Translesion Synthesis Polymerases and Proliferating Cell Nuclear Antigen. <i>Journal of Biological Chemistry</i> , 2009, 284, 10552-10560.	3.4	134
4	Structure of the N-terminal Regulatory Domain of a Plant NADPH Oxidase and Its Functional Implications. <i>Journal of Biological Chemistry</i> , 2010, 285, 1435-1445.	3.4	129
5	Structural basis for histone N-terminal recognition by human peptidylarginine deiminase 4. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 5291-5296.	7.1	118
6	The Crystal Structure of the Novel Calcium-binding Protein AtCBL2 from <i>Arabidopsis thaliana</i> . <i>Journal of Biological Chemistry</i> , 2003, 278, 42240-42246.	3.4	113
7	Crystal Structure of Human REV7 in Complex with a Human REV3 Fragment and Structural Implication of the Interaction between DNA Polymerase ϵ and REV1. <i>Journal of Biological Chemistry</i> , 2010, 285, 12299-12307.	3.4	110
8	Identification of Small Molecule Proliferating Cell Nuclear Antigen (PCNA) Inhibitor That Disrupts Interactions with PIP-box Proteins and Inhibits DNA Replication. <i>Journal of Biological Chemistry</i> , 2012, 287, 14289-14300.	3.4	109
9	Identification of a novel REV1-interacting motif necessary for DNA polymerase ϵ function. <i>Genes To Cells</i> , 2009, 14, 101-111.	1.2	94
10	Structural Basis of Recruitment of DNA Polymerase ϵ by Interaction between REV1 and REV7 Proteins. <i>Journal of Biological Chemistry</i> , 2012, 287, 33847-33852.	3.4	83
11	The Crystal Structure of Plant-Specific Calcium-Binding Protein AtCBL2 in Complex with the Regulatory Domain of AtCIPK14. <i>Journal of Molecular Biology</i> , 2008, 377, 246-257.	4.2	77
12	The Development of <i>N</i> -(2-Carboxyl)benzoyl- <i>N</i> - ⁵ -(2-fluoro-1-iminoethyl)-ornithine Amide (<i>N</i> -F-amidine) and <i>N</i> -(2-Carboxyl)benzoyl- <i>N</i> - ⁵ -(2-chloro-1-iminoethyl)-ornithine Amide (<i>N</i> -Cl-amidine) As Second Generation Protein Arginine Deiminase (PAD) Inhibitors. <i>Journal of Medicinal Chemistry</i> , 2011, 54, 6919-6935.	6.4	76
13	Structural Basis for Substrate Recognition and Dissociation by Human Transportin 1. <i>Molecular Cell</i> , 2007, 28, 57-67.	9.7	75
14	Synthesis and Olefin Polymerization Catalysis of New Divalent Samarium Complexes with Bridging Bis(cyclopentadienyl) Ligands. <i>Organometallics</i> , 1998, 17, 3945-3956.	2.3	73
15	A Small Molecule Inhibitor of Monoubiquitinated Proliferating Cell Nuclear Antigen (PCNA) Inhibits Repair of Interstrand DNA Cross-link, Enhances DNA Double Strand Break, and Sensitizes Cancer Cells to Cisplatin. <i>Journal of Biological Chemistry</i> , 2014, 289, 7109-7120.	3.4	70
16	Structure of a Novel DNA-binding Domain of Helicase-like Transcription Factor (HLTF) and Its Functional Implication in DNA Damage Tolerance. <i>Journal of Biological Chemistry</i> , 2015, 290, 13215-13223.	3.4	61
17	Structure and Functional Characterization of <i>Vibrio parahaemolyticus</i> Thermostable Direct Hemolysin. <i>Journal of Biological Chemistry</i> , 2010, 285, 16267-16274.	3.4	57
18	En bloc transfer of polyubiquitin chains to PCNA in vitro is mediated by two different human E2-E3 pairs. <i>Nucleic Acids Research</i> , 2012, 40, 10394-10407.	14.5	53

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19	Intrinsic Dynamics of Restriction Endonuclease EcoO109I Studied by Molecular Dynamics Simulations and X-Ray Scattering Data Analysis. <i>Biophysical Journal</i> , 2009, 96, 2808-2822.	0.5	52
20	Structural Basis for Matrix Metalloproteinase-2 (MMP-2)-selective Inhibitory Action of Î²-Amyloid Precursor Protein-derived Inhibitor. <i>Journal of Biological Chemistry</i> , 2011, 286, 33236-33243.	3.4	49
21	Structural Basis for Inhibition of Xyloglucan-specific Endo-Î²-1,4-glucanase (XEG) by XEG-Protein Inhibitor. <i>Journal of Biological Chemistry</i> , 2012, 287, 18710-18716.	3.4	49
22	Crystal structure of basic 7S globulin, a xyloglucan-specific endo-Î²-1,4-glucanase inhibitor protein-like protein from soybean lacking inhibitory activity against endo-Î²-1,4-glucanase. <i>FEBS Journal</i> , 2011, 278, 1944-1954.	4.7	47
23	Structural Basis of New Allosteric Inhibition in Kinesin Spindle Protein Eg5. <i>ACS Chemical Biology</i> , 2015, 10, 1128-1136.	3.4	39
24	Mechanistic Insights into the Activation of Rad51-Mediated Strand Exchange from the Structure of a Recombination Activator, the Swi5-Sfr1 Complex. <i>Structure</i> , 2012, 20, 440-449.	3.3	35
25	Crystal structure of zinc-finger domain of Nanos and its functional implications. <i>EMBO Reports</i> , 2010, 11, 848-853.	4.5	33
26	Identification of the first small-molecule inhibitor of the REV7 DNA repair protein interaction. <i>Bioorganic and Medicinal Chemistry</i> , 2016, 24, 4339-4346.	3.0	33
27	Structural Mechanism for Coordination of Proofreading and Polymerase Activities in Archaeal DNA Polymerases. <i>Journal of Molecular Biology</i> , 2005, 351, 291-298.	4.2	32
28	Dynamic feature of mitotic arrest deficient 2-like protein 2 (MAD2L2) and structural basis for its interaction with chromosome alignment-maintaining phosphoprotein (CAMP). <i>Journal of Biological Chemistry</i> , 2017, 292, 17658-17667.	3.4	32
29	Crystal Structures of Type II Restriction Endonuclease EcoO109I and Its Complex with Cognate DNA. <i>Journal of Biological Chemistry</i> , 2005, 280, 5605-5610.	3.4	25
30	Purification, crystallization and initial X-ray diffraction study of human REV7 in complex with a REV3 fragment. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 1302-1305.	0.7	24
31	A Missense Mutation in Rev7 Disrupts Formation of PolÎ¶, Impairing Mouse Development and Repair of Genotoxic Agent-induced DNA Lesions. <i>Journal of Biological Chemistry</i> , 2014, 289, 3811-3824.	3.4	24
32	Oxidative <i>trans</i> to <i>cis</i> Isomerization of Olefins in Polyketide Biosynthesis. <i>Angewandte Chemie - International Edition</i> , 2016, 55, 6207-6210.	13.8	23
33	Structural Characterization of Calcineurin B Homologous Protein 1. <i>Journal of Biological Chemistry</i> , 2005, 280, 32372-32378.	3.4	22
34	Fission Yeast Swi5-Sfr1 Protein Complex, an Activator of Rad51 Recombinase, Forms an Extremely Elongated Dogleg-shaped Structure. <i>Journal of Biological Chemistry</i> , 2011, 286, 43569-43576.	3.4	22
35	Crystal structure of intein homing endonuclease II encoded in DNA polymerase gene from hyperthermophilic archaeon <i>Thermococcus kodakaraensis</i> strain KOD1. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 63, 711-715.	2.6	21
36	Relationship between heat-induced fibrillogenicity and hemolytic activity of thermostable direct hemolysin and a related hemolysin of <i>Vibrio parahaemolyticus</i> . <i>FEMS Microbiology Letters</i> , 2011, 318, 10-17.	1.8	20

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37	Mechanistic Insight into Weak Baseâ€Catalyzed Generation of Carbon Monoxide from Phenyl Formate and Its Application to Catalytic Carbonylation at Room Temperature without Use of External Carbon Monoxide Gas. <i>Advanced Synthesis and Catalysis</i> , 2017, 359, 3592-3601.	4.3	19
38	Structural basis of <sc>HEAT</sc> â€Cklesin interactions in the human condensin I subcomplex. <i>EMBO Reports</i> , 2019, 20, .	4.5	19
39	Enzymatic one-step ring contraction for quinolone biosynthesis. <i>Nature Communications</i> , 2018, 9, 2826.	12.8	18
40	Structure of proliferating cell nuclear antigen (PCNA) bound to an APIM peptide reveals the universality of PCNA interaction. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2018, 74, 214-221.	0.8	16
41	Regulation of HLTf-mediated PCNA polyubiquitination by RFC and PCNA monoubiquitination levels determines choice of damage tolerance pathway. <i>Nucleic Acids Research</i> , 2018, 46, 11340-11356.	14.5	16
42	Crystallization and preliminary X-ray crystallographic analysis of human peptidylarginine deiminase V. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 2332-2333.	2.5	15
43	The first crystal structure of a family 31 carbohydrate-binding module with affinity to β -1,3-xylan. <i>FEBS Letters</i> , 2005, 579, 4324-4328.	2.8	15
44	Conserved aromatic and basic amino acid residues in the pore region of <i>Caenorhabditis elegans</i> spastin play critical roles in microtubule severing. <i>Genes To Cells</i> , 2009, 14, 925-940.	1.2	13
45	A novel heterotetrameric structure of the crenarchaeal PCNA2â€PCNA3 complex. <i>Journal of Structural Biology</i> , 2011, 174, 443-450.	2.8	13
46	Development of a DNA aptamer that binds to the complementarity-determining region of therapeutic monoclonal antibody and affinity improvement induced by pH-change for sensitive detection. <i>Biosensors and Bioelectronics</i> , 2022, 203, 114027.	10.1	13
47	Expression, purification and crystallization of Swi5 and the Swi5â€Sfr1 complex from fission yeast. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1124-1126.	0.7	11
48	Structural basis of autoinhibition and activation of the DNA-targeting ADP-ribosyltransferase pierisin-1. <i>Journal of Biological Chemistry</i> , 2017, 292, 15445-15455.	3.4	11
49	Functional and Structural Analyses of <i>trans C</i>-Methyltransferase in Fungal Polyketide Biosynthesis. <i>Biochemistry</i> , 2019, 58, 3933-3937.	2.5	11
50	Crystallization and preliminary X-ray crystallographic analysis of archaeal O 6-methylguanineâ€DNA methyltransferase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998, 54, 1395-1396.	2.5	8
51	Crystallographic study of G178S mutant of human proliferating cell nuclear antigen. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 819-821.	0.7	7
52	Crystallographic characterization of the N-terminal domain of a plant NADPH oxidase. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 867-869.	0.7	7
53	Structural and Thermodynamic Basis of the Enhanced Interaction between Kinesin Spindle Protein Eg5 and STLC-type Inhibitors. <i>ACS Omega</i> , 2018, 3, 12284-12294.	3.5	7
54	Structure of HIRAN domain of human HLTf bound to duplex DNA provides structural basis for DNA unwinding to initiate replication fork regression. <i>Journal of Biochemistry</i> , 2020, 167, 597-602.	1.7	7

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55	Structure of the RAD9-RAD1-HUS1 checkpoint clamp bound to RHINO sheds light on the other side of the DNA clamp. <i>Journal of Biological Chemistry</i> , 2020, 295, 899-904.	3.4	7
56	Crystallization and X-ray diffraction analysis of the ternary complex of the C-terminal domain of human REV1 in complex with REV7 bound to a REV3 fragment involved in translesion DNA synthesis. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 962-964.	0.7	6
57	Crystallization and preliminary X-ray characterization of a novel calcium-binding protein AtCBL2 from <i>Arabidopsis thaliana</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 1079-1080.	2.5	4
58	Crystallization and preliminary X-ray crystallographic analyses of EcoO109I and its complex with DNA. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1165-1166.	2.5	4
59	Initial crystallographic study of human PCNA in complex with a peptide containing the noncanonical PIP-box sequence of human DNA polymerase η . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 954-956.	0.7	4
60	Purification, crystallization and initial X-ray diffraction study of the zinc-finger domain of zebrafish Nanos. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 959-961.	0.7	4
61	Purification, crystallization and X-ray diffraction study of basic 7S globulin from soybean. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 87-89.	0.7	4
62	Structure of the RAD9-RAD1-HUS1 checkpoint clamp bound to RHINO sheds light on the other side of the DNA clamp. <i>Journal of Biological Chemistry</i> , 2020, 295, 899-904.	3.4	4
63	Syntheses, Structures and Solution Dynamics of Anionic 5-Coordinate Pt(II) Complexes with Halide. <i>Chemistry Letters</i> , 1998, 27, 541-542.	1.3	3
64	Purification, crystallization and X-ray diffraction study of extracellular dermal glycoprotein from carrot and the inhibition complex that it forms with an endo- β -glucanase from <i>Aspergillus aculeatus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 830-832.	0.7	3
65	Crystallographic study of a novel DNA-binding domain of human HLTf involved in the template-switching pathway to avoid the replication arrest caused by DNA damage. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 668-670.	0.8	3
66	Structural basis for the molecular interactions in DNA damage tolerances. <i>Biophysics and Physicobiology</i> , 2017, 14, 199-205.	1.0	3
67	Substituent Effects on the Second Hyperpolarizability of Thioxanthene and Its Derivatives. <i>Main Group Chemistry</i> , 1996, 1, 325-330.	0.8	2
68	Crystallization and preliminary X-ray crystallographic analysis of rat calcineurin B homologous protein 1. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 612-613.	0.7	2
69	Structural basis for molecular interactions on the eukaryotic DNA sliding clamps PCNA and RAD9-RAD1-HUS1. <i>Journal of Biochemistry</i> , 2022, 172, 189-196.	1.7	2
70	Crystallization and preliminary X-ray crystallographic studies of transportin 1 in complex with nucleocytoplasmic shuttling and nuclear localization fragments. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 785-787.	0.7	1
71	Structure of the HLTf HIRAN domain and its functional implications in regression of a stalled replication fork. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 729-735.	2.3	1
72	Crystallization and X-ray diffraction studies of DNA-free and DNA-bound forms of EcoO109I DNA methyltransferase. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1528-1530.	0.7	0

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73	Title is missing!. Kagaku To Seibutsu, 2011, 49, 662-663.	0.0	0
74	3H1024 P24 Analysis on dynamical structure of intrinsically disordered protein Hef, using MD-SAXS method(3H Protein: Property 4,The 49th Annual Meeting of the Biophysical Society of Japan). Seibutsu Butsuri, 2011, 51, S133.	0.1	0
75	Inactive dimeric structure of the protease domain of stomatin operon partner protein. Acta Crystallographica Section D: Structural Biology, 2020, 76, 515-520.	2.3	0
76	Integrated Structural Biology in Combination with SAXS Analysis for Biological Macromolecules. Nihon Kessho Gakkaishi, 2014, 56, 247-252.	0.0	0