

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	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
2	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
3	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
4	Inactive dimeric structure of the protease domain of stomatin operon partner protein. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 515-520.	2.3	0
5	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
6	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
7	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
8	Functional and Structural Analyses of <i>trans</i> -C-Methyltransferase in Fungal Polyketide Biosynthesis. <i>Biochemistry</i> , 2019, 58, 3933-3937.	2.5	11
9	Structural basis of HEAT- κ kleisin interactions in the human condensin I subcomplex. <i>EMBO Reports</i> , 2019, 20, .	4.5	19
10	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
11	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
12	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
13	Enzymatic one-step ring contraction for quinolone biosynthesis. <i>Nature Communications</i> , 2018, 9, 2826.	12.8	18
14	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
15	Mechanistic Insight into Weak Base-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
16	Structural basis of autoinhibition and activation of the DNA-targeting ADP-ribosyltransferase pterisin-1. <i>Journal of Biological Chemistry</i> , 2017, 292, 15445-15455.	3.4	11
17	Structural basis for the molecular interactions in DNA damage tolerances. <i>Biophysics and Physicobiology</i> , 2017, 14, 199-205.	1.0	3
18	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

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19	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
20	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
21	Structural Basis of New Allosteric Inhibition in Kinesin Spindle Protein Eg5. <i>ACS Chemical Biology</i> , 2015, 10, 1128-1136.	3.4	39
22	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
23	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
24	A Missense Mutation in Rev7 Disrupts Formation of Pol η , Impairing Mouse Development and Repair of Genotoxic Agent-induced DNA Lesions. <i>Journal of Biological Chemistry</i> , 2014, 289, 3811-3824.	3.4	24
25	Integrated Structural Biology in Combination with SAXS Analysis for Biological Macromolecules. <i>Nihon Kessho Gakkaishi</i> , 2014, 56, 247-252.	0.0	0
26	Structural Basis for Inhibition of Xyloglucan-specific Endo- β -1,4-glucanase (XEG) by XEG-Protein Inhibitor. <i>Journal of Biological Chemistry</i> , 2012, 287, 18710-18716.	3.4	49
27	Structural Basis of Recruitment of DNA Polymerase η by Interaction between REV1 and REV7 Proteins. <i>Journal of Biological Chemistry</i> , 2012, 287, 33847-33852.	3.4	83
28	En bloc transfer of polyubiquitin chains to PCNA in vitro is mediated by two different human E2 \rightarrow E3 pairs. <i>Nucleic Acids Research</i> , 2012, 40, 10394-10407.	14.5	53
29	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
30	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
31	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
32	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
33	A novel heterotetrameric structure of the crenarchaeal PCNA \rightarrow PCNA3 complex. <i>Journal of Structural Biology</i> , 2011, 174, 443-450.	2.8	13
34	Title is missing!. <i>Kagaku To Seibutsu</i> , 2011, 49, 662-663.	0.0	0
35	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). <i>Seibutsu Butsuri</i> , 2011, 51, S133.	0.1	0
36	Crystal structure of basic 7S globulin, a xyloglucan-specific endo- β -1,4-glucanase inhibitor protein-like protein from soybean lacking inhibitory activity against endo- β -glucanase. <i>FEBS Journal</i> , 2011, 278, 1944-1954.	4.7	47

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37	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
38	Structural Basis for Matrix Metalloproteinase-2 (MMP-2)-selective Inhibitory Action of β -Amyloid Precursor Protein-derived Inhibitor. <i>Journal of Biological Chemistry</i> , 2011, 286, 33236-33243.	3.4	49
39	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
40	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
41	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
42	Expression, purification and crystallization of Swi5 and the Swi5-Sfr1 complex from fission yeast. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1124-1126.	0.7	11
43	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
44	Crystal structure of zinc-finger domain of Nanos and its functional implications. <i>EMBO Reports</i> , 2010, 11, 848-853.	4.5	33
45	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
46	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
47	Crystal Structure of Human REV7 in Complex with a Human REV3 Fragment and Structural Implication of the Interaction between DNA Polymerase η and REV1. <i>Journal of Biological Chemistry</i> , 2010, 285, 12299-12307.	3.4	110
48	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
49	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
50	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
51	Identification of a novel REV1-interacting motif necessary for DNA polymerase η function. <i>Genes To Cells</i> , 2009, 14, 101-111.	1.2	94
52	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
53	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
54	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

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55	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
56	Initial crystallographic study of human PCNA in complex with a peptide containing the noncanonical PIP-box sequence of human DNA polymerase β . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 954-956.	0.7	4
57	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
58	Structural Basis for Substrate Recognition and Dissociation by Human Transportin 1. <i>Molecular Cell</i> , 2007, 28, 57-67.	9.7	75
59	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
60	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
61	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
62	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
63	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
64	Structural Characterization of Calcineurin B Homologous Protein 1. <i>Journal of Biological Chemistry</i> , 2005, 280, 32372-32378.	3.4	22
65	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
66	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
67	Structural basis for Ca ²⁺ -induced activation of human PAD4. <i>Nature Structural and Molecular Biology</i> , 2004, 11, 777-783.	8.2	363
68	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
69	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
70	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
71	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
72	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

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73	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
74	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
75	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
76	Substituent Effects on the Second Hyperpolarizability of Thioxanthenâ€“9â€“one and Its Derivatives. <i>Main Group Chemistry</i> , 1996, 1, 325-330.	0.8	2