

# Kunio Hirata

## List of Publications by Year in descending order

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93  
papers

6,321  
citations

76196

40  
h-index

71532

76  
g-index

103  
all docs

103  
docs citations

103  
times ranked

7977  
citing authors

#	ARTICLE	IF	CITATIONS
1	Native structure of photosystem II at 1.95Å... resolution viewed by femtosecond X-ray pulses. <i>Nature</i> , 2015, 517, 99-103.	13.7	1,050
2	Crystal structure of the channelrhodopsin light-gated cation channel. <i>Nature</i> , 2012, 482, 369-374.	13.7	503
3	Molecular basis of ligand recognition and transport by glucose transporters. <i>Nature</i> , 2015, 526, 391-396.	13.7	305
4	An oxyl/oxo mechanism for oxygen-oxygen coupling in PSII revealed by an x-ray free-electron laser. <i>Science</i> , 2019, 366, 334-338.	6.0	248
5	Determination of damage-free crystal structure of an X-ray-sensitive protein using an XFEL. <i>Nature Methods</i> , 2014, 11, 734-736.	9.0	237
6	Structural basis of Sec-independent membrane protein insertion by YidC. <i>Nature</i> , 2014, 509, 516-520.	13.7	203
7	<i>KAMO</i> : towards automated data processing for microcrystals. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 441-449.	1.1	198
8	Crystal structures of the human adiponectin receptors. <i>Nature</i> , 2015, 520, 312-316.	13.7	176
9	Polymerization of Phenylacetylene by Rhodium Complexes within a Discrete Space of apo-Ferritin. <i>Journal of the American Chemical Society</i> , 2009, 131, 6958-6960.	6.6	165
10	Determination of Damage-free Crystal Structure of an X-ray Sensitive Protein Using XFEL. <i>Nihon Kessho Gakkaishi</i> , 2015, 57, 122-128.	0.0	158
11	<i>ZOO</i> : an automatic data-collection system for high-throughput structure analysis in protein microcrystallography. <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 138-150.	1.1	156
12	Structures of the 5-HT <sub>2A</sub> receptor in complex with the antipsychotics risperidone and zotepine. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 121-128.	3.6	133
13	A peroxide bridge between Fe and Cu ions in the O <sub>2</sub> reduction site of fully oxidized cytochrome <i>c</i> oxidase could suppress the proton pump. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 2165-2169.	3.3	132
14	Structural insights into ligand recognition by the lysophosphatidic acid receptor LPA6. <i>Nature</i> , 2017, 548, 356-360.	13.7	101
15	Process of Accumulation of Metal Ions on the Interior Surface of apo-Ferritin: Crystal Structures of a Series of apo-Ferritins Containing Variable Quantities of Pd(II) Ions. <i>Journal of the American Chemical Society</i> , 2009, 131, 5094-5100.	6.6	88
16	Ribosomal synthesis and de novo discovery of bioactive foldamer peptides containing cyclic Î <sup>2</sup> -amino acids. <i>Nature Chemistry</i> , 2020, 12, 1081-1088.	6.6	86
17	Structural basis for disruption of claudin assembly in tight junctions by an enterotoxin. <i>Scientific Reports</i> , 2016, 6, 33632.	1.6	85
18	Ligand binding to human prostaglandin E receptor EP4 at the lipid-bilayer interface. <i>Nature Chemical Biology</i> , 2019, 15, 18-26.	3.9	85

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19	Mechanism of $\beta^2$ AR regulation by an intracellular positive allosteric modulator. <i>Science</i> , 2019, 364, 1283-1287.	6.0	82
20	Na <sup>+</sup> -mimicking ligands stabilize the inactive state of leukotriene B4 receptor BLT1. <i>Nature Chemical Biology</i> , 2018, 14, 262-269.	3.9	80
21	X-ray structures of endothelin ETB receptor bound to clinical antagonist bosentan and its analog. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 758-764.	3.6	79
22	Atomistic design of microbial opsin-based blue-shifted optogenetics tools. <i>Nature Communications</i> , 2015, 6, 7177.	5.8	78
23	Capturing an initial intermediate during the P450 <sub>nor</sub> enzymatic reaction using time-resolved XFEL crystallography and caged-substrate. <i>Nature Communications</i> , 2017, 8, 1585.	5.8	74
24	Structural Basis for the Counter-Transport Mechanism of a H <sup>+</sup> /Ca <sup>2+</sup> Exchanger. <i>Science</i> , 2013, 341, 168-172.	6.0	73
25	Achievement of protein micro-crystallography at SPring-8 beamline BL32XU. <i>Journal of Physics: Conference Series</i> , 2013, 425, 012002.	0.3	72
26	Crystal structure of a bacterial homologue of SWEET transporters. <i>Cell Research</i> , 2014, 24, 1486-1489.	5.7	71
27	Structural basis for xenobiotic extrusion by eukaryotic MATE transporter. <i>Nature Communications</i> , 2017, 8, 1633.	5.8	69
28	A nanosecond time-resolved XFEL analysis of structural changes associated with CO release from cytochrome c oxidase. <i>Science Advances</i> , 2017, 3, e1603042.	4.7	68
29	Binding pathway determines norepinephrine selectivity for the human $\beta^1$ AR over $\beta^2$ AR. <i>Cell Research</i> , 2021, 31, 569-579.	5.7	65
30	Dose dependence of radiation damage for protein crystals studied at various X-ray energies. <i>Journal of Synchrotron Radiation</i> , 2007, 14, 4-10.	1.0	64
31	Structure-guided development of selective M3 muscarinic acetylcholine receptor antagonists. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 12046-12050.	3.3	64
32	Isoform-selective regulation of mammalian cryptochromes. <i>Nature Chemical Biology</i> , 2020, 16, 676-685.	3.9	61
33	Crystal structures of human ETB receptor provide mechanistic insight into receptor activation and partial activation. <i>Nature Communications</i> , 2018, 9, 4711.	5.8	60
34	Structural insights into the subtype-selective antagonist binding to the M2 muscarinic receptor. <i>Nature Chemical Biology</i> , 2018, 14, 1150-1158.	3.9	59
35	Crystal structure of the human angiotensin II type 2 receptor bound to an angiotensin II analog. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 570-576.	3.6	58
36	Cell-free methods to produce structurally intact mammalian membrane proteins. <i>Scientific Reports</i> , 2016, 6, 30442.	1.6	56

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37	Protein microcrystallography using synchrotron radiation. <i>IUCr</i> , 2017, 4, 529-539.	1.0	56
38	Structure of an antagonist-bound ghrelin receptor reveals possible ghrelin recognition mode. <i>Nature Communications</i> , 2020, 11, 4160.	5.8	55
39	Crystal Engineering of Self-Assembled Porous Protein Materials in Living Cells. <i>ACS Nano</i> , 2017, 11, 2410-2419.	7.3	53
40	An allosteric modulator binds to a conformational hub in the $\beta_2$ adrenergic receptor. <i>Nature Chemical Biology</i> , 2020, 16, 749-755.	3.9	51
41	Crystal structure of the endogenous agonist-bound prostanoid receptor EP3. <i>Nature Chemical Biology</i> , 2019, 15, 8-10.	3.9	49
42	Crystal structure of the M <sub>5</sub> muscarinic acetylcholine receptor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 26001-26007.	3.3	48
43	Structural Basis for Blocking Sugar Uptake into the Malaria Parasite <i>Plasmodium falciparum</i> . <i>Cell</i> , 2020, 183, 258-268.e12.	13.5	42
44	A magnetic anti-cancer compound for magnet-guided delivery and magnetic resonance imaging. <i>Scientific Reports</i> , 2015, 5, 9194.	1.6	40
45	The Crystal Structure of Angiotensin II Type 2 Receptor with Endogenous Peptide Hormone. <i>Structure</i> , 2020, 28, 418-425.e4.	1.6	40
46	Development of a dose-limiting data collection strategy for serial synchrotron rotation crystallography. <i>Journal of Synchrotron Radiation</i> , 2017, 24, 29-41.	1.0	39
47	Design of Enzyme-Encapsulated Protein Containers by In Vivo Crystal Engineering. <i>Advanced Materials</i> , 2015, 27, 7951-7956.	11.1	32
48	Endogenous agonist-bound S1PR3 structure reveals determinants of G protein subtype bias. <i>Science Advances</i> , 2021, 7, .	4.7	31
49	Structural basis for promotion of duodenal iron absorption by enteric ferric reductase with ascorbate. <i>Communications Biology</i> , 2018, 1, 120.	2.0	30
50	An unprecedented dioxygen species revealed by serial femtosecond rotation crystallography in copper nitrite reductase. <i>IUCr</i> , 2018, 5, 22-31.	1.0	27
51	Redox-coupled structural changes in nitrite reductase revealed by serial femtosecond and microfocus crystallography. <i>Journal of Biochemistry</i> , 2016, 159, 527-538.	0.9	26
52	SPring-8 BL41XU, a high-flux macromolecular crystallography beamline. <i>Journal of Synchrotron Radiation</i> , 2013, 20, 910-913.	1.0	25
53	An unprecedented insight into the catalytic mechanism of copper nitrite reductase from atomic-resolution and damage-free structures. <i>Science Advances</i> , 2021, 7, .	4.7	25
54	Catalytically important damage-free structures of a copper nitrite reductase obtained by femtosecond X-ray laser and room-temperature neutron crystallography. <i>IUCr</i> , 2019, 6, 761-772.	1.0	24

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55	Remote access and automation of SPring-8 MX beamlines. AIP Conference Proceedings, 2016, , .	0.3	23
56	<i>In-Cell</i> Engineering of Protein Crystals with Nanoporous Structures for Promoting Cascade Reactions. ACS Applied Nano Materials, 2021, 4, 1672-1681.	2.4	21
57	Short-lived intermediate in N <sub>2</sub> O generation by P450 NO reductase captured by time-resolved IR spectroscopy and XFEL crystallography. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	21
58	Development of a shutterless continuous rotation method using an X-ray CMOS detector for protein crystallography. Journal of Applied Crystallography, 2009, 42, 1165-1175.	1.9	19
59	New micro-beam beamline at SPring-8, targeting at protein micro-crystallography. AIP Conference Proceedings, 2010, , .	0.3	18
60	XFEL Crystal Structures of Peroxidase Compound II. Angewandte Chemie - International Edition, 2021, 60, 14578-14585.	7.2	18
61	Molecular mechanism of agonism and inverse agonism in ghrelin receptor. Nature Communications, 2022, 13, 300.	5.8	18
62	Isoprenoid-chained lipid EROCO17+4: a new matrix for membrane protein crystallization and a crystal delivery medium in serial femtosecond crystallography. Scientific Reports, 2020, 10, 19305.	1.6	16
63	Design optimization of highly accurate elliptical mirrors for hard-x-ray microfocusing probes at SPring-8. , 2009, , .		14
64	Expression, purification, crystallization, and preliminary X-ray crystallographic studies of the human adiponectin receptors, AdipoR1 and AdipoR2. Journal of Structural and Functional Genomics, 2015, 16, 11-23.	1.2	14
65	Design of an In-Cell Protein Crystal for the Environmentally Responsive Construction of a Supramolecular Filament. Angewandte Chemie - International Edition, 2021, 60, 12341-12345.	7.2	13
66	Crystallization and preliminary X-ray diffraction analysis of YidC, a membrane-protein chaperone and insertase from <i>Bacillus halodurans</i> . Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 1056-1060.	0.4	11
67	Supramolecular protein cages constructed from a crystalline protein matrix. Chemical Communications, 2018, 54, 1988-1991.	2.2	10
68	Structural Biology with Microfocus Beamlines. Springer Protocols, 2016, , 241-273.	0.1	7
69	Guidelines for <i>de novo</i> phasing using multiple small-wedge data collection. Journal of Synchrotron Radiation, 2021, 28, 1284-1295.	1.0	7
70	Crystallization and X-ray diffraction analysis of a catalytic domain of hyperthermophilic chitinase from <i>Pyrococcus furiosus</i> . Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 791-793.	0.7	6
71	Present status of SPring-8 macromolecular crystallography beamlines. AIP Conference Proceedings, 2010, , .	0.3	6
72	Structure of in cell protein crystals containing organometallic complexes. Physical Chemistry Chemical Physics, 2018, 20, 2986-2989.	1.3	5

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73	Computer-controlled liquid-nitrogen drizzling device for removing frost from cryopreserved crystals. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2020, 76, 616-622.	0.4	5
74	Expression, purification and preliminary X-ray crystallographic analysis of cyanobacterial biliverdin reductase. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 313-317.	0.7	4
75	The structure of an archaeal oligosaccharyltransferase provides insight into the strict exclusion of proline from the N-glycosylation sequon. <i>Communications Biology</i> , 2021, 4, 941.	2.0	4
76	The structure of NLRP9 reveals a unique C-terminal region with putative regulatory function. <i>FEBS Letters</i> , 2022, 596, 876-885.	1.3	4
77	Fine-needle capillary mounting for protein microcrystals. <i>Journal of Applied Crystallography</i> , 2012, 45, 785-788.	1.9	3
78	Scaling of one-shot oscillation images with a reference data set. <i>Journal of Synchrotron Radiation</i> , 2004, 11, 60-63.	1.0	2
79	Radiation Damage of Protein Crystal in Various X-ray Energies. <i>AIP Conference Proceedings</i> , 2007, , .	0.3	1
80	S11.17 A peroxide bridge between the two metals in the dinuclear center of the fully oxidized cytochrome c oxidase. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2008, 1777, S69.	0.5	1
81	Crystallization and preliminary X-ray analysis of the stress-response PPM phosphatase RsbX from <i>Bacillus subtilis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 1128-1130.	0.7	1
82	Determination of Radiation Damage-free Crystal Structure of Cytochrome <i>c</i> Oxidase Using XFEL. <i>Seibutsu Butsuri</i> , 2015, 55, 084-086.	0.0	1
83	Crystal structure of Tam41 cytidine diphosphate diacylglycerol synthase from a Firmicutes bacterium. <i>Journal of Biochemistry</i> , 2022, 171, 429-441.	0.9	1
84	2P026 Current Status of Public Beamlines for Protein Crystallography at SPring-8(29. Protein) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 307 Butsuri, 2006, 46, S302.	0.0	0
85	1P067 The micro-focus beamline to open the new field of protein micro-crystallography(Proteins-functions, methodology, and protein engineering,Oral) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 2	0.0	0
86	1P034 Structural Basis for the Counter-Transport Mechanism of a H <sup>+</sup> /Ca <sup>2+</sup> Exchanger(01B.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 .	0.0	0
87	Automated system for data collection and data processing using microcrystals. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2015, 71, s187-s187.	0.0	0
88	High-resolution native structure analyses of supramacromolecular complexes susceptible to radiation damage. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2015, 71, s15-s15.	0.0	0
89	Design of an In-cell Protein Crystal for the Environmentally Responsive Construction of a Supramolecular Filament. <i>Angewandte Chemie</i> , 2021, 133, 12449-12453.	1.6	0
90	XFEL Crystal Structures of Peroxidase Compound II. <i>Angewandte Chemie</i> , 2021, 133, 14699-14706.	1.6	0

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91	Data Collection Strategy in Protein Micro-crystallography at Synchrotron Facility. Seibutsu Butsuri, 2019, 59, 215-218.	0.0	0
92	Remodeling of the optics for a micro-focusing protein crystallography beamline at SPring-8. , 2019, , .		0
93	Macromolecular Crystallography at SPring-8. Nihon Kessho Gakkaishi, 2022, 64, 2-9.	0.0	0