

Kunio Hirata

List of Publications by Year in descending order

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Version: 2024-02-01

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 | The structure of NLRP9 reveals a unique C-terminal region with putative regulatory function. FEBS Letters, 2022, 596, 876-885. | 1.3 | 4 |
| 2 | Molecular mechanism of agonism and inverse agonism in ghrelin receptor. Nature Communications, 2022, 13, 300. | 5.8 | 18 |
| 3 | Macromolecular Crystallography at SPring-8. Nihon Kessho Gakkaishi, 2022, 64, 2-9. | 0.0 | 0 |
| 4 | Crystal structure of Tam41 cytidine diphosphate diacylglycerol synthase from a Firmicutes bacterium. Journal of Biochemistry, 2022, 171, 429-441. | 0.9 | 1 |
| 5 | Binding pathway determines norepinephrine selectivity for the human β^2 1AR over β^2 2AR. Cell Research, 2021, 31, 569-579. | 5.7 | 65 |
| 6 | An unprecedented insight into the catalytic mechanism of copper nitrite reductase from atomic-resolution and damage-free structures. Science Advances, 2021, 7, . | 4.7 | 25 |
| 7 | <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 |
| 8 | Design of an <i>In-Cell</i> Protein Crystal for the Environmentally Responsive Construction of a Supramolecular Filament. Angewandte Chemie - International Edition, 2021, 60, 12341-12345. | 7.2 | 13 |
| 9 | Design of an <i>In-Cell</i> Protein Crystal for the Environmentally Responsive Construction of a Supramolecular Filament. Angewandte Chemie, 2021, 133, 12449-12453. | 1.6 | 0 |
| 10 | XFEL Crystal Structures of Peroxidase Compound II. Angewandte Chemie - International Edition, 2021, 60, 14578-14585. | 7.2 | 18 |
| 11 | XFEL Crystal Structures of Peroxidase Compound II. Angewandte Chemie, 2021, 133, 14699-14706. | 1.6 | 0 |
| 12 | Short-lived intermediate in N ₂ 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 |
| 13 | Endogenous agonist-bound S1PR3 structure reveals determinants of G protein subtype bias. Science Advances, 2021, 7, . | 4.7 | 31 |
| 14 | Guidelines for <i>de novo</i> phasing using multiple small-wedge data collection. Journal of Synchrotron Radiation, 2021, 28, 1284-1295. | 1.0 | 7 |
| 15 | The structure of an archaeal oligosaccharyltransferase provides insight into the strict exclusion of proline from the N-glycosylation sequon. Communications Biology, 2021, 4, 941. | 2.0 | 4 |
| 16 | The Crystal Structure of Angiotensin II Type 2 Receptor with Endogenous Peptide Hormone. Structure, 2020, 28, 418-425.e4. | 1.6 | 40 |
| 17 | Structural Basis for Blocking Sugar Uptake into the Malaria Parasite Plasmodium falciparum. Cell, 2020, 183, 258-268.e12. | 13.5 | 42 |
| 18 | Ribosomal synthesis and <i>de novo</i> discovery of bioactive foldamer peptides containing cyclic β -amino acids. Nature Chemistry, 2020, 12, 1081-1088. | 6.6 | 86 |

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|----|---|-----|-----------|
| 19 | Structure of an antagonist-bound ghrelin receptor reveals possible ghrelin recognition mode. <i>Nature Communications</i> , 2020, 11, 4160. | 5.8 | 55 |
| 20 | Isoprenoid-chained lipid EROCO17+4: a new matrix for membrane protein crystallization and a crystal delivery medium in serial femtosecond crystallography. <i>Scientific Reports</i> , 2020, 10, 19305. | 1.6 | 16 |
| 21 | An allosteric modulator binds to a conformational hub in the β_2 adrenergic receptor. <i>Nature Chemical Biology</i> , 2020, 16, 749-755. | 3.9 | 51 |
| 22 | Isoform-selective regulation of mammalian cryptochromes. <i>Nature Chemical Biology</i> , 2020, 16, 676-685. | 3.9 | 61 |
| 23 | 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 |
| 24 | 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 |
| 25 | Mechanism of β_2 AR regulation by an intracellular positive allosteric modulator. <i>Science</i> , 2019, 364, 1283-1287. | 6.0 | 82 |
| 26 | An oxy/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 |
| 27 | Structures of the 5-HT _{2A} receptor in complex with the antipsychotics risperidone and zotepine. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 121-128. | 3.6 | 133 |
| 28 | Crystal structure of the M ₅ 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 |
| 29 | 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 |
| 30 | Crystal structure of the endogenous agonist-bound prostanoid receptor EP3. <i>Nature Chemical Biology</i> , 2019, 15, 8-10. | 3.9 | 49 |
| 31 | <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 |
| 32 | Data Collection Strategy in Protein Micro-crystallography at Synchrotron Facility. <i>Seibutsu Butsuri</i> , 2019, 59, 215-218. | 0.0 | 0 |
| 33 | Remodeling of the optics for a micro-focusing protein crystallography beamline at SPring-8. , 2019, , . | | 0 |
| 34 | Supramolecular protein cages constructed from a crystalline protein matrix. <i>Chemical Communications</i> , 2018, 54, 1988-1991. | 2.2 | 10 |
| 35 | Na ⁺ -mimicking ligands stabilize the inactive state of leukotriene B ₄ receptor BLT1. <i>Nature Chemical Biology</i> , 2018, 14, 262-269. | 3.9 | 80 |
| 36 | Structure of in cell protein crystals containing organometallic complexes. <i>Physical Chemistry Chemical Physics</i> , 2018, 20, 2986-2989. | 1.3 | 5 |

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|----|--|------|-----------|
| 37 | 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 |
| 38 | 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 |
| 39 | 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 |
| 40 | 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 |
| 41 | Structural basis for promotion of duodenal iron absorption by enteric ferric reductase with ascorbate. <i>Communications Biology</i> , 2018, 1, 120. | 2.0 | 30 |
| 42 | An unprecedented dioxygen species revealed by serial femtosecond rotation crystallography in copper nitrite reductase. <i>IUCr</i> , 2018, 5, 22-31. | 1.0 | 27 |
| 43 | <i>KAMO</i> : towards automated data processing for microcrystals. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 441-449. | 1.1 | 198 |
| 44 | Crystal Engineering of Self-Assembled Porous Protein Materials in Living Cells. <i>ACS Nano</i> , 2017, 11, 2410-2419. | 7.3 | 53 |
| 45 | 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 |
| 46 | 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 |
| 47 | Structural insights into ligand recognition by the lysophosphatidic acid receptor LPA6. <i>Nature</i> , 2017, 548, 356-360. | 13.7 | 101 |
| 48 | 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 |
| 49 | Structural basis for xenobiotic extrusion by eukaryotic MATE transporter. <i>Nature Communications</i> , 2017, 8, 1633. | 5.8 | 69 |
| 50 | Capturing an initial intermediate during the P450nor enzymatic reaction using time-resolved XFEL crystallography and caged-substrate. <i>Nature Communications</i> , 2017, 8, 1585. | 5.8 | 74 |
| 51 | Protein microcrystallography using synchrotron radiation. <i>IUCr</i> , 2017, 4, 529-539. | 1.0 | 56 |
| 52 | Remote access and automation of SPring-8 MX beamlines. <i>AIP Conference Proceedings</i> , 2016, , . | 0.3 | 23 |
| 53 | Structural Biology with Microfocus Beamlines. <i>Springer Protocols</i> , 2016, , 241-273. | 0.1 | 7 |
| 54 | Cell-free methods to produce structurally intact mammalian membrane proteins. <i>Scientific Reports</i> , 2016, 6, 30442. | 1.6 | 56 |

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|----|--|------|-----------|
| 55 | Structural basis for disruption of claudin assembly in tight junctions by an enterotoxin. <i>Scientific Reports</i> , 2016, 6, 33632. | 1.6 | 85 |
| 56 | 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 |
| 57 | 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 |
| 58 | 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 |
| 59 | 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 |
| 60 | 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 |
| 61 | Design of Enzyme-Encapsulated Protein Containers by In Vivo Crystal Engineering. <i>Advanced Materials</i> , 2015, 27, 7951-7956. | 11.1 | 32 |
| 62 | Atomistic design of microbial opsin-based blue-shifted optogenetics tools. <i>Nature Communications</i> , 2015, 6, 7177. | 5.8 | 78 |
| 63 | Expression, purification, crystallization, and preliminary X-ray crystallographic studies of the human adiponectin receptors, AdipoR1 and AdipoR2. <i>Journal of Structural and Functional Genomics</i> , 2015, 16, 11-23. | 1.2 | 14 |
| 64 | Molecular basis of ligand recognition and transport by glucose transporters. <i>Nature</i> , 2015, 526, 391-396. | 13.7 | 305 |
| 65 | A magnetic anti-cancer compound for magnet-guided delivery and magnetic resonance imaging. <i>Scientific Reports</i> , 2015, 5, 9194. | 1.6 | 40 |
| 66 | Crystal structures of the human adiponectin receptors. <i>Nature</i> , 2015, 520, 312-316. | 13.7 | 176 |
| 67 | Native structure of photosystem II at 1.95 Å resolution viewed by femtosecond X-ray pulses. <i>Nature</i> , 2015, 517, 99-103. | 13.7 | 1,050 |
| 68 | Crystal structure of a bacterial homologue of SWEET transporters. <i>Cell Research</i> , 2014, 24, 1486-1489. | 5.7 | 71 |
| 69 | Crystallization and preliminary X-ray diffraction analysis of YidC, a membrane-protein chaperone and insertase from <i>Bacillus halodurans</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 1056-1060. | 0.4 | 11 |
| 70 | Structural basis of Sec-independent membrane protein insertion by YidC. <i>Nature</i> , 2014, 509, 516-520. | 13.7 | 203 |
| 71 | 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 |
| 72 | Structural Basis for the Counter-Transport Mechanism of a H ⁺ /Ca ²⁺ Exchanger. <i>Science</i> , 2013, 341, 168-172. | 6.0 | 73 |

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|----|---|------|-----------|
| 73 | Achievement of protein micro-crystallography at SPring-8 beamline BL32XU. Journal of Physics: Conference Series, 2013, 425, 012002. | 0.3 | 72 |
| 74 | SPring-8 BL41XU, a high-flux macromolecular crystallography beamline. Journal of Synchrotron Radiation, 2013, 20, 910-913. | 1.0 | 25 |
| 75 | 1P034 Structural Basis for the Counter-Transport Mechanism of a H ⁺ /Ca ²⁺ Exchanger(01B.) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 97 | 0.0 | 0 |
| 76 | Crystal structure of the channelrhodopsin light-gated cation channel. Nature, 2012, 482, 369-374. | 13.7 | 503 |
| 77 | Fine-needle capillary mounting for protein microcrystals. Journal of Applied Crystallography, 2012, 45, 785-788. | 1.9 | 3 |
| 78 | Expression, purification and preliminary X-ray crystallographic analysis of cyanobacterial biliverdin reductase. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 313-317. | 0.7 | 4 |
| 79 | Present status of SPring-8 macromolecular crystallography beamlines. AIP Conference Proceedings, 2010, , . | 0.3 | 6 |
| 80 | New micro-beam beamline at SPring-8, targeting at protein micro-crystallography. AIP Conference Proceedings, 2010, , . | 0.3 | 18 |
| 81 | A peroxide bridge between Fe and Cu ions in the O ₂ reduction site of fully oxidized cytochrome c oxidase could suppress the proton pump. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 2165-2169. | 3.3 | 132 |
| 82 | Design optimization of highly accurate elliptical mirrors for hard-x-ray microfocusing probes at SPring-8. , 2009, , . | | 14 |
| 83 | Crystallization and preliminary X-ray analysis of the stress-response PPM phosphatase RsbX from Bacillus subtilis. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 1128-1130. | 0.7 | 1 |
| 84 | 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 |
| 85 | 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. Journal of the American Chemical Society, 2009, 131, 5094-5100. | 6.6 | 88 |
| 86 | Polymerization of Phenylacetylene by Rhodium Complexes within a Discrete Space of apo-Ferritin. Journal of the American Chemical Society, 2009, 131, 6958-6960. | 6.6 | 165 |
| 87 | S11.17 A peroxide bridge between the two metals in the dinuclear center of the fully oxidized cytochrome c oxidase. Biochimica Et Biophysica Acta - Bioenergetics, 2008, 1777, S69. | 0.5 | 1 |
| 88 | Radiation Damage of Protein Crystal in Various X-ray Energies. AIP Conference Proceedings, 2007, , . | 0.3 | 1 |
| 89 | 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 97 | 0.0 | 0 |
| 90 | Dose dependence of radiation damage for protein crystals studied at various X-ray energies. Journal of Synchrotron Radiation, 2007, 14, 4-10. | 1.0 | 64 |

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|----|---|-----|-----------|
| 91 | 2P026 Current Status of Public Beamlines for Protein Crystallography at SPring-8(29. Protein) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T Butsuri, 2006, 46, S302. | 0.0 | 0 |
| 92 | 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 |
| 93 | Scaling of one-shot oscillation images with a reference data set. Journal of Synchrotron Radiation, 2004, 11, 60-63. | 1.0 | 2 |