

Keitaro Yamashita

List of Publications by Year in descending order

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83
papers

5,754
citations

94269

37
h-index

82410

72
g-index

95
all docs

95
docs citations

95
times ranked

6792
citing authors

#	ARTICLE	IF	CITATIONS
1	Native structure of photosystem II at 1.95Å... resolution viewed by femtosecond X-ray pulses. Nature, 2015, 517, 99-103.	13.7	1,050
2	Light-induced structural changes and the site of O=O bond formation in PSII caught by XFEL. Nature, 2017, 543, 131-135.	13.7	515
3	An oxyl/oxo mechanism for oxygen-oxygen coupling in PSII revealed by an x-ray free-electron laser. Science, 2019, 366, 334-338.	6.0	248
4	Structural basis for Na ⁺ transport mechanism by a light-driven Na ⁺ pump. Nature, 2015, 521, 48-53.	13.7	224
5	Recent developments in <i>CrystFEL</i> . Journal of Applied Crystallography, 2016, 49, 680-689.	1.9	222
6	<i>KAMO</i> : towards automated data processing for microcrystals. Acta Crystallographica Section D: Structural Biology, 2018, 74, 441-449.	1.1	198
7	<i>ZOO</i> : an automatic data-collection system for high-throughput structure analysis in protein microcrystallography. Acta Crystallographica Section D: Structural Biology, 2019, 75, 138-150.	1.1	156
8	Crystal structure of the octameric pore of staphylococcal β -hemolysin reveals the β -barrel pore formation mechanism by two components. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 17314-17319.	3.3	152
9	Cryo-EM structures capture the transport cycle of the P4-ATPase flippase. Science, 2019, 365, 1149-1155.	6.0	143
10	Cryo-EM single-particle structure refinement and map calculation using <i>Servalcat</i> . Acta Crystallographica Section D: Structural Biology, 2021, 77, 1282-1291.	1.1	117
11	Crystal structure of the red light-activated channelrhodopsin Chrimson. Nature Communications, 2018, 9, 3949.	5.8	112
12	Structural insights into ligand recognition by the lysophosphatidic acid receptor LPA6. Nature, 2017, 548, 356-360.	13.7	101
13	Structure of the miniature type V-F CRISPR-Cas effector enzyme. Molecular Cell, 2021, 81, 558-570.e3.	4.5	95
14	Crystal structure of the natural anion-conducting channelrhodopsin GtACR1. Nature, 2018, 561, 343-348.	13.7	93
15	Ligand binding to human prostaglandin E receptor EP4 at the lipid-bilayer interface. Nature Chemical Biology, 2019, 15, 18-26.	3.9	85
16	Molecular Basis for the Recognition of Long-chain Substrates by Plant β -Glucosidases. Journal of Biological Chemistry, 2013, 288, 19296-19303.	1.6	83
17	Na ⁺ -mimicking ligands stabilize the inactive state of leukotriene B4 receptor BLT1. Nature Chemical Biology, 2018, 14, 262-269.	3.9	80
18	X-ray structures of endothelin ETB receptor bound to clinical antagonist bosentan and its analog. Nature Structural and Molecular Biology, 2017, 24, 758-764.	3.6	79

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19	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
20	Structural basis for channel conduction in the pump-like channelrhodopsin ChRmine. <i>Cell</i> , 2022, 185, 672-689.e23.	13.5	72
21	Crystal structure of heliorhodopsin. <i>Nature</i> , 2019, 574, 132-136.	13.7	71
22	Structural basis for xenobiotic extrusion by eukaryotic MATE transporter. <i>Nature Communications</i> , 2017, 8, 1633.	5.8	69
23	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
24	Structural basis for the facilitative diffusion mechanism by SemiSWEET transporter. <i>Nature Communications</i> , 2015, 6, 6112.	5.8	67
25	Structural mechanisms of selectivity and gating in anion channelrhodopsins. <i>Nature</i> , 2018, 561, 349-354.	13.7	67
26	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
27	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
28	Molecular basis of dihydrouridine formation on tRNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 19593-19598.	3.3	58
29	Protein microcrystallography using synchrotron radiation. <i>IUCr</i> , 2017, 4, 529-539.	1.0	56
30	Crystal Structures of Human Orexin 2 Receptor Bound to the Subtype-Selective Antagonist EMPA. <i>Structure</i> , 2018, 26, 7-19.e5.	1.6	55
31	An isomorphous replacement method for efficient de novo phasing for serial femtosecond crystallography. <i>Scientific Reports</i> , 2015, 5, 14017.	1.6	54
32	Crystal Engineering of Self-Assembled Porous Protein Materials in Living Cells. <i>ACS Nano</i> , 2017, 11, 2410-2419.	7.3	53
33	Structure of the triose-phosphate/phosphate translocator reveals the basis of substrate specificity. <i>Nature Plants</i> , 2017, 3, 825-832.	4.7	51
34	Crystal structure of plant vacuolar iron transporter VIT1. <i>Nature Plants</i> , 2019, 5, 308-315.	4.7	51
35	Crystal structure of the endogenous agonist-bound prostanoid receptor EP3. <i>Nature Chemical Biology</i> , 2019, 15, 8-10.	3.9	49
36	Crystal structure of <i>Drosophila</i> Piwi. <i>Nature Communications</i> , 2020, 11, 858.	5.8	42

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37	Structural basis for ion selectivity revealed by high-resolution crystal structure of Mg ²⁺ channel MgtE. <i>Nature Communications</i> , 2014, 5, 5374.	5.8	41
38	Time-resolved serial femtosecond crystallography reveals early structural changes in channelrhodopsin. <i>ELife</i> , 2021, 10, .	2.8	41
39	Alternating Heterochiral Supramolecular Copolymerization. <i>Journal of the American Chemical Society</i> , 2021, 143, 5121-5126.	6.6	40
40	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
41	X-ray Crystallographic Structure of Thermophilic Rhodopsin. <i>Journal of Biological Chemistry</i> , 2016, 291, 12223-12232.	1.6	38
42	B/N-Doped <i>p</i> -Arylenevinylene Chromophores: Synthesis, Properties, and Microcrystal Electron Crystallographic Study. <i>Journal of the American Chemical Society</i> , 2020, 142, 18990-18996.	6.6	37
43	Cryo-EM structures of calcium homeostasis modulator channels in diverse oligomeric assemblies. <i>Science Advances</i> , 2020, 6, eaba8105.	4.7	32
44	Cryo-EM structure of the human MT1 α -Gi signaling complex. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 694-701.	3.6	31
45	Structural basis for promotion of duodenal iron absorption by enteric ferric reductase with ascorbate. <i>Communications Biology</i> , 2018, 1, 120.	2.0	30
46	Structural insights into the mechanism of rhodopsin phosphodiesterase. <i>Nature Communications</i> , 2020, 11, 5605.	5.8	30
47	An unprecedented dioxygen species revealed by serial femtosecond rotation crystallography in copper nitrite reductase. <i>IUCr</i> , 2018, 5, 22-31.	1.0	27
48	Structural basis for ligand capture and release by the endocytic receptor Apo ER 2. <i>EMBO Reports</i> , 2017, 18, 982-999.	2.0	26
49	Asymmetric Trimeric Ring Structure of the Nucleocapsid Protein of Tosopvirus. <i>Journal of Virology</i> , 2017, 91, .	1.5	26
50	Structural basis of reverse nucleotide polymerization. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 20970-20975.	3.3	25
51	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
52	The loop structure of <i>Actinomycete</i> glycoside hydrolase family 5 mannanases governs substrate recognition. <i>FEBS Journal</i> , 2015, 282, 4001-4014.	2.2	24
53	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
54	Experimental phase determination with selenomethionine or mercury-derivatization in serial femtosecond crystallography. <i>IUCr</i> , 2017, 4, 639-647.	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	Cryo-EM reveals mechanistic insights into lipid-facilitated polyamine export by human ATP13A2. Molecular Cell, 2021, 81, 4799-4809.e5.	4.5	22
57	EMDA: A Python package for Electron Microscopy Data Analysis. Journal of Structural Biology, 2022, 214, 107826.	1.3	22
58	Crystal structures of the TRIC trimeric intracellular cation channel orthologues. Cell Research, 2016, 26, 1288-1301.	5.7	21
59	<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
60	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
61	Cryo-EM structure of the Î ² 3-adrenergic receptor reveals the molecular basis of subtype selectivity. Molecular Cell, 2021, 81, 3205-3215.e5.	4.5	21
62	Efficient synthesis of Î±-galactosyl oligosaccharides using a mutant <i>Bacteroides thetaiotaomicron</i> retaining Î±-galactosidase (<i>BtGH</i> _{97b}). FEBS Journal, 2017, 284, 766-783.	2.2	19
63	Consensus mutagenesis approach improves the thermal stability of system x _c [±] transporter, xCT, and enables cryo-EM analyses. Protein Science, 2020, 29, 2398-2407.	3.1	19
64	XFEL Crystal Structures of Peroxidase Compound II. Angewandte Chemie - International Edition, 2021, 60, 14578-14585.	7.2	18
65	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
66	B ₂ N ₂ -Doped Dibenzo[<i>a,m</i>]Rubicene: Modular Synthesis, Properties, and Coordination-Induced Color Tunability. Chemistry of Materials, 2021, 33, 5337-5344.	3.2	16
67	Structural basis for unique color tuning mechanism in heliorhodopsin. Biochemical and Biophysical Research Communications, 2020, 533, 262-267.	1.0	14
68	Spiro-Conjugated Carbon/Heteroatom-Bridged <i>p</i> -Phenylenevinylenes: Synthesis, Properties, and Microcrystal Electron Crystallographic Analysis of Racemic Solid Solutions. Bulletin of the Chemical Society of Japan, 2020, 93, 776-782.	2.0	13
69	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
70	Structure of the type V-C CRISPR-Cas effector enzyme. Molecular Cell, 2022, 82, 1865-1877.e4.	4.5	12
71	Structural Advantage of Sugar Beet Î±-Glucosidase to Stabilize the Michaelis Complex with Long-chain Substrate. Journal of Biological Chemistry, 2015, 290, 1796-1803.	1.6	11
72	Supramolecular protein cages constructed from a crystalline protein matrix. Chemical Communications, 2018, 54, 1988-1991.	2.2	10

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73	New model-fitting and model-completion programs for automated iterative nucleic acid refinement. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 1171-1179.	2.5	7
74	Structure of in cell protein crystals containing organometallic complexes. <i>Physical Chemistry Chemical Physics</i> , 2018, 20, 2986-2989.	1.3	5
75	Bipartite binding and partial inhibition links DEPTOR and mTOR in a mutually antagonistic embrace. <i>ELife</i> , 2021, 10, .	2.8	5
76	Cryo-EM structures of thylakoid-located voltage-dependent chloride channel VCCN1. <i>Nature Communications</i> , 2022, 13, 2505.	5.8	5
77	Crystallization and preliminary X-ray crystallographic analysis of a bacterial Asn-transamidosome. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 790-793.	0.4	3
78	Crystal structure of the <i>Agrobacterium tumefaciens</i> type VI effector- ϵ immunity complex. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2018, 74, 810-816.	0.4	3
79	KAMO: Automated Data Processing System for Microcrystals. <i>Nihon Kessho Gakkaishi</i> , 2017, 59, 207-208.	0.0	2
80	Development of X-ray Data Processing System for Protein Microcrystals. <i>Nihon Kessho Gakkaishi</i> , 2018, 60, 104-112.	0.0	0
81	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
82	XFEL Crystal Structures of Peroxidase Compound II. <i>Angewandte Chemie</i> , 2021, 133, 14699-14706.	1.6	0
83	Structure Refinement and Map Calculation for Single Particle Analysis Using Servalcat. <i>Nihon Kessho Gakkaishi</i> , 2022, 64, 118-124.	0.0	0