

Keitaro Yamashita

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

88

papers

3,791

citations

31

h-index

61

g-index

95

ext. papers

4,896

ext. citations

14.5

avg, IF

5.38

L-index

#	Paper	IF	Citations
88	Native structure of photosystem II at 1.95 Å resolution viewed by femtosecond X-ray pulses. <i>Nature</i> , 2015 , 517, 99-103	50.4	887
87	Light-induced structural changes and the site of O=O bond formation in PSII caught by XFEL. <i>Nature</i> , 2017 , 543, 131-135	50.4	400
86	Structural basis for Na(+) transport mechanism by a light-driven Na(+) pump. <i>Nature</i> , 2015 , 521, 48-53	50.4	167
85	Recent developments in. <i>Journal of Applied Crystallography</i> , 2016 , 49, 680-689	3.8	166
84	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	33.3	143
83	Crystal structure of the octameric pore of staphylococcal β hemolysin reveals the β barrel pore formation mechanism by two components. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 17314-9	11.5	125
82	KAMO: towards automated data processing for microcrystals. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018 , 74, 441-449	5.5	110
81	Cryo-EM structures capture the transport cycle of the P4-ATPase flippase. <i>Science</i> , 2019 , 365, 1149-1155	33.3	88
80	ZOO: 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	5.5	77
79	Structural insights into ligand recognition by the lysophosphatidic acid receptor LPA. <i>Nature</i> , 2017 , 548, 356-360	50.4	66
78	Na-mimicking ligands stabilize the inactive state of leukotriene B receptor BLT1. <i>Nature Chemical Biology</i> , 2018 , 14, 262-269	11.7	60
77	Ligand binding to human prostaglandin E receptor EP at the lipid-bilayer interface. <i>Nature Chemical Biology</i> , 2019 , 15, 18-26	11.7	58
76	Crystal structure of the red light-activated channelrhodopsin Chrimson. <i>Nature Communications</i> , 2018 , 9, 3949	17.4	58
75	Molecular basis for the recognition of long-chain substrates by plant β glucosidases. <i>Journal of Biological Chemistry</i> , 2013 , 288, 19296-303	5.4	57
74	Crystal structure of the natural anion-conducting channelrhodopsin GtACR1. <i>Nature</i> , 2018 , 561, 343-348	50.4	55
73	A nanosecond time-resolved XFEL analysis of structural changes associated with CO release from cytochrome c oxidase. <i>Science Advances</i> , 2017 , 3, e1603042	14.3	52
72	Capturing an initial intermediate during the P450nor enzymatic reaction using time-resolved XFEL crystallography and caged-substrate. <i>Nature Communications</i> , 2017 , 8, 1585	17.4	52

71	An isomorphous replacement method for efficient de novo phasing for serial femtosecond crystallography. <i>Scientific Reports</i> , 2015 , 5, 14017	4.9	49
70	Structural mechanisms of selectivity and gating in anion channelrhodopsins. <i>Nature</i> , 2018 , 561, 349-354	50.4	48
69	Structural basis for xenobiotic extrusion by eukaryotic MATE transporter. <i>Nature Communications</i> , 2017 , 8, 1633	17.4	47
68	Crystal Engineering of Self-Assembled Porous Protein Materials in Living Cells. <i>ACS Nano</i> , 2017 , 11, 2410-2419	18.7	46
67	X-ray structures of endothelin ET receptor bound to clinical antagonist bosentan and its analog. <i>Nature Structural and Molecular Biology</i> , 2017 , 24, 758-764	17.6	45
66	Protein microcrystallography using synchrotron radiation. <i>IUCrJ</i> , 2017 , 4, 529-539	4.7	42
65	Structural basis for the facilitative diffusion mechanism by SemiSWEET transporter. <i>Nature Communications</i> , 2015 , 6, 6112	17.4	42
64	Molecular basis of dihydrouridine formation on tRNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 19593-8	11.5	42
63	Crystal Structures of Human Orexin 2 Receptor Bound to the Subtype-Selective Antagonist EMPA. <i>Structure</i> , 2018 , 26, 7-19.e5	5.2	41
62	Structural insights into the subtype-selective antagonist binding to the M muscarinic receptor. <i>Nature Chemical Biology</i> , 2018 , 14, 1150-1158	11.7	39
61	Crystal structure of heliorhodopsin. <i>Nature</i> , 2019 , 574, 132-136	50.4	35
60	X-ray Crystallographic Structure of Thermophilic Rhodopsin: IMPLICATIONS FOR HIGH THERMAL STABILITY AND OPTOGENETIC FUNCTION. <i>Journal of Biological Chemistry</i> , 2016 , 291, 12223-32	5.4	33
59	Crystal structure of the endogenous agonist-bound prostanoid receptor EP3. <i>Nature Chemical Biology</i> , 2019 , 15, 8-10	11.7	33
58	Structure of the triose-phosphate/phosphate translocator reveals the basis of substrate specificity. <i>Nature Plants</i> , 2017 , 3, 825-832	11.5	31
57	Crystal structures of human ET receptor provide mechanistic insight into receptor activation and partial activation. <i>Nature Communications</i> , 2018 , 9, 4711	17.4	29
56	Development of a dose-limiting data collection strategy for serial synchrotron rotation crystallography. <i>Journal of Synchrotron Radiation</i> , 2017 , 24, 29-41	2.4	28
55	Structural basis for ion selectivity revealed by high-resolution crystal structure of Mg ²⁺ channel MgtE. <i>Nature Communications</i> , 2014 , 5, 5374	17.4	28
54	Structure of the miniature type V-F CRISPR-Cas effector enzyme. <i>Molecular Cell</i> , 2021 , 81, 558-570.e3	17.6	28

53	Crystal structure of plant vacuolar iron transporter VIT1. <i>Nature Plants</i> , 2019 , 5, 308-315	11.5	27
52	Structural basis of reverse nucleotide polymerization. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 20970-5	11.5	23
51	Experimental phase determination with selenomethionine or mercury-derivatization in serial femtosecond crystallography. <i>IUCrJ</i> , 2017 , 4, 639-647	4.7	22
50	An unprecedented dioxygen species revealed by serial femtosecond rotation crystallography in copper nitrite reductase. <i>IUCrJ</i> , 2018 , 5, 22-31	4.7	22
49	Crystal structure of Drosophila Piwi. <i>Nature Communications</i> , 2020 , 11, 858	17.4	22
48	Remote access and automation of SPring-8 MX beamlines 2016 ,		20
47	Structural basis for promotion of duodenal iron absorption by enteric ferric reductase with ascorbate. <i>Communications Biology</i> , 2018 , 1, 120	6.7	18
46	Catalytically important damage-free structures of a copper nitrite reductase obtained by femtosecond X-ray laser and room-temperature neutron crystallography. <i>IUCrJ</i> , 2019 , 6, 761-772	4.7	18
45	Cryo-EM structures of calcium homeostasis modulator channels in diverse oligomeric assemblies. <i>Science Advances</i> , 2020 , 6, eaba8105	14.3	17
44	Efficient synthesis of β -galactosyl oligosaccharides using a mutant <i>Bacteroides thetaiotaomicron</i> retaining β -galactosidase (BtGH97b). <i>FEBS Journal</i> , 2017 , 284, 766-783	5.7	16
43	Structural basis for ligand capture and release by the endocytic receptor ApoER2. <i>EMBO Reports</i> , 2017 , 18, 982-999	6.5	16
42	B/N-Doped -Arylenevinylene Chromophores: Synthesis, Properties, and Microcrystal Electron Crystallographic Study. <i>Journal of the American Chemical Society</i> , 2020 , 142, 18990-18996	16.4	16
41	Structural insights into the mechanism of rhodopsin phosphodiesterase. <i>Nature Communications</i> , 2020 , 11, 5605	17.4	15
40	Asymmetric Trimeric Ring Structure of the Nucleocapsid Protein of Tosopovirus. <i>Journal of Virology</i> , 2017 , 91,	6.6	15
39	The loop structure of Actinomycete glycoside hydrolase family 5 mannanases governs substrate recognition. <i>FEBS Journal</i> , 2015 , 282, 4001-14	5.7	15
38	Crystal structures of the TRIC trimeric intracellular cation channel orthologues. <i>Cell Research</i> , 2016 , 26, 1288-1301	24.7	15
37	Cryo-EM single-particle structure refinement and map calculation using Servalcat. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021 , 77, 1282-1291	5.5	15
36	Time-resolved serial femtosecond crystallography reveals early structural changes in channelrhodopsin. <i>ELife</i> , 2021 , 10,	8.9	13

35	Alternating Heterochiral Supramolecular Copolymerization. <i>Journal of the American Chemical Society</i> , 2021 , 143, 5121-5126	16.4	12
34	Structural advantage of sugar beet β -glucosidase to stabilize the Michaelis complex with long-chain substrate. <i>Journal of Biological Chemistry</i> , 2015 , 290, 1796-803	5.4	10
33	An unprecedented insight into the catalytic mechanism of copper nitrite reductase from atomic-resolution and damage-free structures. <i>Science Advances</i> , 2021 , 7,	14.3	10
32	Supramolecular protein cages constructed from a crystalline protein matrix. <i>Chemical Communications</i> , 2018 , 54, 1988-1991	5.8	9
31	Consensus mutagenesis approach improves the thermal stability of system x transporter, xCT, and enables cryo-EM analyses. <i>Protein Science</i> , 2020 , 29, 2398-2407	6.3	9
30	Cryo-EM structure of the human MT-G signaling complex. <i>Nature Structural and Molecular Biology</i> , 2021 , 28, 694-701	17.6	9
29	Isoprenoid-chained lipid EROCO: a new matrix for membrane protein crystallization and a crystal delivery medium in serial femtosecond crystallography. <i>Scientific Reports</i> , 2020 , 10, 19305	4.9	8
28	Spiro-Conjugated Carbon/Heteroatom-Bridged p-Phenylenevinyls: Synthesis, Properties, and Microcrystal Electron Crystallographic Analysis of Racemic Solid Solutions. <i>Bulletin of the Chemical Society of Japan</i> , 2020 , 93, 776-782	5.1	8
27	Design of an In-Cell Protein Crystal for the Environmentally Responsive Construction of a Supramolecular Filament. <i>Angewandte Chemie - International Edition</i> , 2021 , 60, 12341-12345	16.4	8
26	XFEL Crystal Structures of Peroxidase Compound II. <i>Angewandte Chemie - International Edition</i> , 2021 , 60, 14578-14585	16.4	8
25	New model-fitting and model-completion programs for automated iterative nucleic acid refinement. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013 , 69, 1171-9		7
24	Structural basis for channel conduction in the pump-like channel rhodopsin ChRmine.. <i>Cell</i> , 2022 ,	56.2	7
23	In-Cell Engineering of Protein Crystals with Nanoporous Structures for Promoting Cascade Reactions. <i>ACS Applied Nano Materials</i> , 2021 , 4, 1672-1681	5.6	7
22	Cryo-EM reveals mechanistic insights into lipid-facilitated polyamine export by human ATP13A2. <i>Molecular Cell</i> , 2021 , 81, 4799-4809.e5	17.6	5
21	B2N2-Doped Dibenzo[a,m]Rubicene: Modular Synthesis, Properties, and Coordination-Induced Color Tunability. <i>Chemistry of Materials</i> , 2021 , 33, 5337-5344	9.6	5
20	EMDA: A Python package for Electron Microscopy Data Analysis.. <i>Journal of Structural Biology</i> , 2021 , 214, 107826	3.4	4
19	Structural basis for unique color tuning mechanism in heliorhodopsin. <i>Biochemical and Biophysical Research Communications</i> , 2020 , 533, 262-267	3.4	4
18	Structure of in cell protein crystals containing organometallic complexes. <i>Physical Chemistry Chemical Physics</i> , 2018 , 20, 2986-2989	3.6	4

17	Cryo-EM structure of the β -adrenergic receptor reveals the molecular basis of subtype selectivity. <i>Molecular Cell</i> , 2021 , 81, 3205-3215.e5	17.6	4
16	Structural basis for channel conduction in the pump-like channel rhodopsin ChRmine		4
15	Crystallization and preliminary X-ray crystallographic analysis of a bacterial Asn-transamidosome. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014 , 70, 790-3	1.1	3
14	Cryo-EM single particle structure refinement and map calculation using Servalcat		3
13	Crystal structure of the <i>Agrobacterium tumefaciens</i> type VI effector-immunity complex. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2018 , 74, 810-816	1.1	2
12	Structural insights into the mechanism of rhodopsin phosphodiesterase		2
11	Short-lived intermediate in NO generation by P450 NO reductase captured by time-resolved IR spectroscopy and XFEL crystallography. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	2
10	KAMO: Automated Data Processing System for Microcrystals. <i>Nihon Kessho Gakkaishi</i> , 2017 , 59, 207-208		1
9	X-ray structures of human ETB receptor provide mechanistic insight into receptor activation and partial activation		1
8	Cryo-EM structures capturing the entire transport cycle of the P4-ATPase flippase		1
7	Cryo-EM structures of calcium homeostasis modulator channels in diverse oligomeric assemblies		1
6	Bipartite binding and partial inhibition links DEPTOR and mTOR in a mutually antagonistic embrace. <i>ELife</i> , 2021 , 10,	8.9	1
5	Cryo-EM structures of thylakoid-located voltage-dependent chloride channel VCCN1.. <i>Nature Communications</i> , 2022 , 13, 2505	17.4	0
4	Design of an In-Cell Protein Crystal for the Environmentally Responsive Construction of a Supramolecular Filament. <i>Angewandte Chemie</i> , 2021 , 133, 12449-12453	3.6	
3	XFEL Crystal Structures of Peroxidase Compound II. <i>Angewandte Chemie</i> , 2021 , 133, 14699-14706	3.6	
2	Development of X-ray Data Processing System for Protein Microcrystals. <i>Nihon Kessho Gakkaishi</i> , 2018 , 60, 104-112	0	
1	Structure Refinement and Map Calculation for Single Particle Analysis Using Servalcat. <i>Nihon Kessho Gakkaishi</i> , 2022 , 64, 118-124	0	