

# Keitaro Yamashita

## List of Publications by Year in Descending Order

**Source:** <https://exaly.com/author-pdf/5001630/keitaro-yamashita-publications-by-year.pdf>

**Version:** 2024-04-24

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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	Structural basis for channel conduction in the pump-like channelrhodopsin ChRmine.. <i>Cell</i> , <b>2022</b> ,	56.2	7
87	Cryo-EM structures of thylakoid-located voltage-dependent chloride channel VCCN1.. <i>Nature Communications</i> , <b>2022</b> , 13, 2505	17.4	0
86	Structure Refinement and Map Calculation for Single Particle Analysis Using Servalcat. <i>Nihon Kessho Gakkaishi</i> , <b>2022</b> , 64, 118-124	0	
85	Cryo-EM reveals mechanistic insights into lipid-facilitated polyamine export by human ATP13A2. <i>Molecular Cell</i> , <b>2021</b> , 81, 4799-4809.e5	17.6	5
84	EMDA: A Python package for Electron Microscopy Data Analysis.. <i>Journal of Structural Biology</i> , <b>2021</b> , 214, 107826	3.4	4
83	Time-resolved serial femtosecond crystallography reveals early structural changes in channelrhodopsin. <i>ELife</i> , <b>2021</b> , 10,	8.9	13
82	Alternating Heterochiral Supramolecular Copolymerization. <i>Journal of the American Chemical Society</i> , <b>2021</b> , 143, 5121-5126	16.4	12
81	Design of an In-Cell Protein Crystal for the Environmentally Responsive Construction of a Supramolecular Filament. <i>Angewandte Chemie - International Edition</i> , <b>2021</b> , 60, 12341-12345	16.4	8
80	Design of an In-Cell Protein Crystal for the Environmentally Responsive Construction of a Supramolecular Filament. <i>Angewandte Chemie</i> , <b>2021</b> , 133, 12449-12453	3.6	
79	XFEL Crystal Structures of Peroxidase Compound II. <i>Angewandte Chemie - International Edition</i> , <b>2021</b> , 60, 14578-14585	16.4	8
78	XFEL Crystal Structures of Peroxidase Compound II. <i>Angewandte Chemie</i> , <b>2021</b> , 133, 14699-14706	3.6	
77	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> , <b>2021</b> , 118,	11.5	2
76	B2N2-Doped Dibenzo[a,m]Rubicene: Modular Synthesis, Properties, and Coordination-Induced Color Tunability. <i>Chemistry of Materials</i> , <b>2021</b> , 33, 5337-5344	9.6	5
75	Structure of the miniature type V-F CRISPR-Cas effector enzyme. <i>Molecular Cell</i> , <b>2021</b> , 81, 558-570.e3	17.6	28
74	An unprecedented insight into the catalytic mechanism of copper nitrite reductase from atomic-resolution and damage-free structures. <i>Science Advances</i> , <b>2021</b> , 7,	14.3	10
73	In-Cell Engineering of Protein Crystals with Nanoporous Structures for Promoting Cascade Reactions. <i>ACS Applied Nano Materials</i> , <b>2021</b> , 4, 1672-1681	5.6	7
72	Cryo-EM structure of the $\beta$ -adrenergic receptor reveals the molecular basis of subtype selectivity. <i>Molecular Cell</i> , <b>2021</b> , 81, 3205-3215.e5	17.6	4

71	Cryo-EM structure of the human MT-G signaling complex. <i>Nature Structural and Molecular Biology</i> , <b>2021</b> , 28, 694-701	17.6	9
70	Bipartite binding and partial inhibition links DEPTOR and mTOR in a mutually antagonistic embrace. <i>ELife</i> , <b>2021</b> , 10,	8.9	1
69	Cryo-EM single-particle structure refinement and map calculation using Servalcat. <i>Acta Crystallographica Section D: Structural Biology</i> , <b>2021</b> , 77, 1282-1291	5.5	15
68	Isoprenoid-chained lipid EROCO: a new matrix for membrane protein crystallization and a crystal delivery medium in serial femtosecond crystallography. <i>Scientific Reports</i> , <b>2020</b> , 10, 19305	4.9	8
67	Structural insights into the mechanism of rhodopsin phosphodiesterase. <i>Nature Communications</i> , <b>2020</b> , 11, 5605	17.4	15
66	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> , <b>2020</b> , 93, 776-782	5.1	8
65	Crystal structure of <i>Drosophila</i> Piwi. <i>Nature Communications</i> , <b>2020</b> , 11, 858	17.4	22
64	Structural basis for unique color tuning mechanism in heliorhodopsin. <i>Biochemical and Biophysical Research Communications</i> , <b>2020</b> , 533, 262-267	3.4	4
63	B/N-Doped -Arylenevinylene Chromophores: Synthesis, Properties, and Microcrystal Electron Crystallographic Study. <i>Journal of the American Chemical Society</i> , <b>2020</b> , 142, 18990-18996	16.4	16
62	Consensus mutagenesis approach improves the thermal stability of system x transporter, xCT, and enables cryo-EM analyses. <i>Protein Science</i> , <b>2020</b> , 29, 2398-2407	6.3	9
61	Cryo-EM structures of calcium homeostasis modulator channels in diverse oligomeric assemblies. <i>Science Advances</i> , <b>2020</b> , 6, eaba8105	14.3	17
60	Crystal structure of plant vacuolar iron transporter VIT1. <i>Nature Plants</i> , <b>2019</b> , 5, 308-315	11.5	27
59	Cryo-EM structures capture the transport cycle of the P4-ATPase flippase. <i>Science</i> , <b>2019</b> , 365, 1149-1155	33.3	88
58	Catalytically important damage-free structures of a copper nitrite reductase obtained by femtosecond X-ray laser and room-temperature neutron crystallography. <i>IUCrJ</i> , <b>2019</b> , 6, 761-772	4.7	18
57	An oxyl/oxo mechanism for oxygen-oxygen coupling in PSII revealed by an x-ray free-electron laser. <i>Science</i> , <b>2019</b> , 366, 334-338	33.3	143
56	ZOO: an automatic data-collection system for high-throughput structure analysis in protein microcrystallography. <i>Acta Crystallographica Section D: Structural Biology</i> , <b>2019</b> , 75, 138-150	5.5	77
55	Crystal structure of heliorhodopsin. <i>Nature</i> , <b>2019</b> , 574, 132-136	50.4	35
54	Ligand binding to human prostaglandin E receptor EP at the lipid-bilayer interface. <i>Nature Chemical Biology</i> , <b>2019</b> , 15, 18-26	11.7	58

53	Crystal structure of the endogenous agonist-bound prostanoid receptor EP3. <i>Nature Chemical Biology</i> , <b>2019</b> , 15, 8-10	11.7	33
52	Supramolecular protein cages constructed from a crystalline protein matrix. <i>Chemical Communications</i> , <b>2018</b> , 54, 1988-1991	5.8	9
51	Na-mimicking ligands stabilize the inactive state of leukotriene B receptor BLT1. <i>Nature Chemical Biology</i> , <b>2018</b> , 14, 262-269	11.7	60
50	Structural basis for promotion of duodenal iron absorption by enteric ferric reductase with ascorbate. <i>Communications Biology</i> , <b>2018</b> , 1, 120	6.7	18
49	An unprecedented dioxygen species revealed by serial femtosecond rotation crystallography in copper nitrite reductase. <i>IUCrJ</i> , <b>2018</b> , 5, 22-31	4.7	22
48	Crystal structure of the <i>Agrobacterium tumefaciens</i> type VI effector-immunity complex. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , <b>2018</b> , 74, 810-816	1.1	2
47	KAMO: towards automated data processing for microcrystals. <i>Acta Crystallographica Section D: Structural Biology</i> , <b>2018</b> , 74, 441-449	5.5	110
46	Crystal Structures of Human Orexin 2 Receptor Bound to the Subtype-Selective Antagonist EMPA. <i>Structure</i> , <b>2018</b> , 26, 7-19.e5	5.2	41
45	Structure of in cell protein crystals containing organometallic complexes. <i>Physical Chemistry Chemical Physics</i> , <b>2018</b> , 20, 2986-2989	3.6	4
44	Crystal structures of human ET receptor provide mechanistic insight into receptor activation and partial activation. <i>Nature Communications</i> , <b>2018</b> , 9, 4711	17.4	29
43	Structural insights into the subtype-selective antagonist binding to the M muscarinic receptor. <i>Nature Chemical Biology</i> , <b>2018</b> , 14, 1150-1158	11.7	39
42	Crystal structure of the red light-activated channelrhodopsin Chrimson. <i>Nature Communications</i> , <b>2018</b> , 9, 3949	17.4	58
41	Development of X-ray Data Processing System for Protein Microcrystals. <i>Nihon Kessho Gakkaishi</i> , <b>2018</b> , 60, 104-112	0	
40	Structural mechanisms of selectivity and gating in anion channelrhodopsins. <i>Nature</i> , <b>2018</b> , 561, 349-354	50.4	48
39	Crystal structure of the natural anion-conducting channelrhodopsin GtACR1. <i>Nature</i> , <b>2018</b> , 561, 343-348	50.4	55
38	Crystal Engineering of Self-Assembled Porous Protein Materials in Living Cells. <i>ACS Nano</i> , <b>2017</b> , 11, 2410-2419	18.4	46
37	Efficient synthesis of $\beta$ -galactosyl oligosaccharides using a mutant <i>Bacteroides thetaiotaomicron</i> retaining $\beta$ -galactosidase (BtGH97b). <i>FEBS Journal</i> , <b>2017</b> , 284, 766-783	5.7	16
36	Light-induced structural changes and the site of O=O bond formation in PSII caught by XFEL. <i>Nature</i> , <b>2017</b> , 543, 131-135	50.4	400

35	Structural basis for ligand capture and release by the endocytic receptor ApoER2. <i>EMBO Reports</i> , <b>2017</b> , 18, 982-999	6.5	16
34	Development of a dose-limiting data collection strategy for serial synchrotron rotation crystallography. <i>Journal of Synchrotron Radiation</i> , <b>2017</b> , 24, 29-41	2.4	28
33	Structure of the triose-phosphate/phosphate translocator reveals the basis of substrate specificity. <i>Nature Plants</i> , <b>2017</b> , 3, 825-832	11.5	31
32	Protein microcrystallography using synchrotron radiation. <i>IUCrJ</i> , <b>2017</b> , 4, 529-539	4.7	42
31	A nanosecond time-resolved XFEL analysis of structural changes associated with CO release from cytochrome c oxidase. <i>Science Advances</i> , <b>2017</b> , 3, e1603042	14.3	52
30	Asymmetric Trimeric Ring Structure of the Nucleocapsid Protein of Tospovirus. <i>Journal of Virology</i> , <b>2017</b> , 91,	6.6	15
29	Structural insights into ligand recognition by the lysophosphatidic acid receptor LPA. <i>Nature</i> , <b>2017</b> , 548, 356-360	50.4	66
28	X-ray structures of endothelin ET receptor bound to clinical antagonist bosentan and its analog. <i>Nature Structural and Molecular Biology</i> , <b>2017</b> , 24, 758-764	17.6	45
27	Structural basis for xenobiotic extrusion by eukaryotic MATE transporter. <i>Nature Communications</i> , <b>2017</b> , 8, 1633	17.4	47
26	Capturing an initial intermediate during the P450nor enzymatic reaction using time-resolved XFEL crystallography and caged-substrate. <i>Nature Communications</i> , <b>2017</b> , 8, 1585	17.4	52
25	KAMO: Automated Data Processing System for Microcrystals. <i>Nihon Kessho Gakkaishi</i> , <b>2017</b> , 59, 207-208	0	1
24	Experimental phase determination with selenomethionine or mercury-derivatization in serial femtosecond crystallography. <i>IUCrJ</i> , <b>2017</b> , 4, 639-647	4.7	22
23	Recent developments in. <i>Journal of Applied Crystallography</i> , <b>2016</b> , 49, 680-689	3.8	166
22	Remote access and automation of SPring-8 MX beamlines <b>2016</b> ,		20
21	Crystal structures of the TRIC trimeric intracellular cation channel orthologues. <i>Cell Research</i> , <b>2016</b> , 26, 1288-1301	24.7	15
20	X-ray Crystallographic Structure of Thermophilic Rhodopsin: IMPLICATIONS FOR HIGH THERMAL STABILITY AND OPTOGENETIC FUNCTION. <i>Journal of Biological Chemistry</i> , <b>2016</b> , 291, 12223-32	5.4	33
19	Structural advantage of sugar beet $\beta$ -glucosidase to stabilize the Michaelis complex with long-chain substrate. <i>Journal of Biological Chemistry</i> , <b>2015</b> , 290, 1796-803	5.4	10
18	Structural basis for Na(+) transport mechanism by a light-driven Na(+) pump. <i>Nature</i> , <b>2015</b> , 521, 48-53	50.4	167

17	Native structure of photosystem II at 1.95Å resolution viewed by femtosecond X-ray pulses. <i>Nature</i> , <b>2015</b> , 517, 99-103	50.4	887
16	An isomorphous replacement method for efficient de novo phasing for serial femtosecond crystallography. <i>Scientific Reports</i> , <b>2015</b> , 5, 14017	4.9	49
15	The loop structure of Actinomycete glycoside hydrolase family 5 mannanases governs substrate recognition. <i>FEBS Journal</i> , <b>2015</b> , 282, 4001-14	5.7	15
14	Structural basis for the facilitative diffusion mechanism by SemiSWEET transporter. <i>Nature Communications</i> , <b>2015</b> , 6, 6112	17.4	42
13	Structural basis for ion selectivity revealed by high-resolution crystal structure of Mg <sup>2+</sup> channel MgtE. <i>Nature Communications</i> , <b>2014</b> , 5, 5374	17.4	28
12	Crystallization and preliminary X-ray crystallographic analysis of a bacterial Asn-transamidosome. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , <b>2014</b> , 70, 790-3	1.1	3
11	New model-fitting and model-completion programs for automated iterative nucleic acid refinement. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2013</b> , 69, 1171-9		7
10	Molecular basis for the recognition of long-chain substrates by plant β-glucosidases. <i>Journal of Biological Chemistry</i> , <b>2013</b> , 288, 19296-303	5.4	57
9	Structural basis of reverse nucleotide polymerization. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2013</b> , 110, 20970-5	11.5	23
8	Molecular basis of dihydrouridine formation on tRNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2011</b> , 108, 19593-8	11.5	42
7	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> , <b>2011</b> , 108, 17314-9	11.5	125
6	X-ray structures of human ETB receptor provide mechanistic insight into receptor activation and partial activation		1
5	Cryo-EM structures capturing the entire transport cycle of the P4-ATPase flippase		1
4	Cryo-EM structures of calcium homeostasis modulator channels in diverse oligomeric assemblies		1
3	Structural insights into the mechanism of rhodopsin phosphodiesterase		2
2	Cryo-EM single particle structure refinement and map calculation using Servalcat		3
1	Structural basis for channel conduction in the pump-like channel rhodopsin ChRmine		4