

# Yusuke Yamada

## List of Publications by Year in descending order

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47  
papers

715  
citations

567281

15  
h-index

552781

26  
g-index

51  
all docs

51  
docs citations

51  
times ranked

1008  
citing authors

#	ARTICLE	IF	CITATIONS
1	Serial crystallography with multi-stage merging of thousands of images. Acta Crystallographica Section F, Structural Biology Communications, 2022, 78, 281-288.	0.8	4
2	A fully automated crystallization apparatus for small protein quantities. Acta Crystallographica Section F, Structural Biology Communications, 2021, 77, 29-36.	0.8	11
3	Fully Automated Unattended Data Collection and Remote Interactive Data Collection at the Photon Factory Macromolecular Crystallography Beamlines. Nihon Kessho Gakkaishi, 2021, 63, 208-211.	0.0	0
4	Macromolecular Crystallography Using Long Wavelength X-ray. Nihon Kessho Gakkaishi, 2020, 62, 56-61.	0.0	0
5	RFID tag system for sample tracking at structural biology beamlines. AIP Conference Proceedings, 2019, , .	0.4	0
6	Long-wavelength native-SAD phasing: opportunities and challenges. IUCr, 2019, 6, 373-386.	2.2	22
7	Crystallographic analysis of murine p24 <sup>32</sup> Golgi dynamics domain. Proteins: Structure, Function and Bioinformatics, 2017, 85, 764-770.	2.6	10
8	The first crystal structure of a family 129 glycoside hydrolase from a probiotic bacterium reveals critical residues and metal cofactors. Journal of Biological Chemistry, 2017, 292, 12126-12138.	3.4	20
9	Construction and commissioning of direct beam transport line for PF-AR. Journal of Physics: Conference Series, 2017, 874, 012024.	0.4	0
10	Development of Database System for Structural Biology Beamlines in the Photon Factory. Nihon Kessho Gakkaishi, 2017, 59, 281-282.	0.0	0
11	Protein crystallography beamline BL2S1 at the Aichi synchrotron. Journal of Synchrotron Radiation, 2017, 24, 338-343.	2.4	32
12	Developments of Sample Exchange Robot at Protein Crystallography Beamline and Sample Preparation Cooperative Robot. The Proceedings of JSME Annual Conference on Robotics and Mechatronics (Robomec), 2017, 2017, 2A2-H10.	0.0	0
13	Crystal structure of an IclR homologue from <i>Microbacterium</i> sp. strain HM58-2. Acta Crystallographica Section F, Structural Biology Communications, 2017, 73, 16-23.	0.8	2
14	In-situ data collection at the photon factory macromolecular crystallography beamlines. AIP Conference Proceedings, 2016, , .	0.4	1
15	Development of sample exchange robot PAM-HC for beamline BL-1A at the photon factory. AIP Conference Proceedings, 2016, , .	0.4	2
16	On the influence of crystal size and wavelength on native SAD phasing. Acta Crystallographica Section D: Structural Biology, 2016, 72, 728-741.	2.3	32
17	Expanded potential of seleno-carbohydrates as a molecular tool for X-ray structural determination of a carbohydrate-protein complex with single/multi-wavelength anomalous dispersion phasing. Bioorganic and Medicinal Chemistry, 2014, 22, 2090-2101.	3.0	29
18	X-Ray Crystallographic Structure of RNase Po1 That Exhibits Anti-tumor Activity. Biological and Pharmaceutical Bulletin, 2014, 37, 968-978.	1.4	6

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19	Structural basis of preferential binding of fucose-containing saccharide by the <i>Caenorhabditis elegans</i> galectin LEC-6. <i>Glycobiology</i> , 2013, 23, 797-805.	2.5	11
20	New methodologies at PF AR-NW12A: the implementation of high-pressure macromolecular crystallography. <i>Journal of Synchrotron Radiation</i> , 2013, 20, 838-842.	2.4	4
21	Improvement of an automated protein crystal exchange system PAM for high-throughput data collection. <i>Journal of Synchrotron Radiation</i> , 2013, 20, 890-893.	2.4	10
22	Improvements toward highly accurate diffraction experiments at the macromolecular micro-crystallography beamline BL-17A. <i>Journal of Synchrotron Radiation</i> , 2013, 20, 938-942.	2.4	1
23	UV LED lighting for automated crystal centring. <i>Journal of Synchrotron Radiation</i> , 2011, 18, 11-15.	2.4	14
24	Fully Automated Data Collection Using PAM and the Development of PAM-SPACE Reversible Cassettes. , 2010, , .		2
25	AR-NE3A, a New Macromolecular Crystallography Beamline for Pharmaceutical Applications at the Photon Factory. , 2010, , .		5
26	Crystallization of small proteins assisted by green fluorescent protein. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 1059-1066.	2.5	31
27	High-throughput operation of sample-exchange robots with double tongs at the Photon Factory beamlines. <i>Journal of Synchrotron Radiation</i> , 2008, 15, 300-303.	2.4	28
28	X-ray beam stabilization at BL-17A, the protein microcrystallography beamline of the Photon Factory. <i>Journal of Synchrotron Radiation</i> , 2008, 15, 292-295.	2.4	13
29	Implementation of remote monitoring and diffraction evaluation systems at the Photon Factory macromolecular crystallography beamlines. <i>Journal of Synchrotron Radiation</i> , 2008, 15, 296-299.	2.4	12
30	Development of an X-ray HARP- $\mu$ FEA detector system for high-throughput protein crystallography. <i>Journal of Synchrotron Radiation</i> , 2008, 15, 281-284.	2.4	16
31	1S6-4 Structure determination of a native protein crystal by S-SAD phasing with synchrotron radiation(1S6 Cutting edge of protein crystallography with synchrotron radiation,The 46th Annual) Tj ETQq1 1 0.784314 rgB0 /Overlo		
32	2P-031 Structure determination of a native protein crystal by S-SAD phasing with synchrotron radiation(The 46th Annual Meeting of the Biophysical Society of Japan). <i>Seibutsu Butsuri</i> , 2008, 48, S79.	0.1	0
33	Automated Sample Exchange Robots for the Structural Biology Beam Lines at the Photon Factory. <i>AIP Conference Proceedings</i> , 2007, , .	0.4	2
34	Design and Construction of a High-speed Network Connecting All the Protein Crystallography Beamlines at the Photon Factory. <i>AIP Conference Proceedings</i> , 2007, , .	0.4	0
35	BL-17A, A New Protein Micro-Crystallography Beam Line of the Photon Factory. <i>AIP Conference Proceedings</i> , 2007, , .	0.4	7
36	Development of Control Applications for High-Throughput Protein Crystallography Experiments. <i>AIP Conference Proceedings</i> , 2007, , .	0.4	1

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37	Design of Disulfide-linked Thioredoxin Dimers and Multimers Through Analysis of Crystal Contacts. <i>Journal of Molecular Biology</i> , 2007, 372, 1278-1292.	4.2	19
38	Molecular Basis for Autoregulatory Interaction Between GAE Domain and Hinge Region of GGA1. <i>Traffic</i> , 2007, 8, 904-913.	2.7	11
39	Automation in Structural Biology Beamlines of the Photon Factory. <i>Nihon Kessho Gakkaishi</i> , 2007, 49, 359-363.	0.0	0
40	Development of an automated large-scale protein-crystallization and monitoring system for high-throughput protein-structure analyses. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 1058-1065.	2.5	62
41	Structures of the Carbohydrate Recognition Domain of Ca <sup>2+</sup> -independent Cargo Receptors Emp46p and Emp47p. <i>Journal of Biological Chemistry</i> , 2006, 281, 10410-10419.	3.4	29
42	Structural consequences of hen egg-white lysozyme orthorhombic crystal growth in a high magnetic field: validation of X-ray diffraction intensity, conformational energy searching and quantitative analysis of Bfactors and mosaicity. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 207-217.	2.5	32
43	Structure determination of GGA-GAE and $\hat{I}^31$ -ear in complex with peptides: crystallization of low-affinity complexes in membrane traffic. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 731-736.	2.5	6
44	The 2.0 Å... crystal structure of catalase-peroxidase from <i>Haloarcula marismortui</i> . <i>Nature Structural Biology</i> , 2002, 9, 691-695.	9.7	142
45	Crystallization and preliminary X-ray analysis of catalase-peroxidase from the halophilic archaeon <i>Haloarcula marismortui</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 1157-1158.	2.5	10
46	Improvement in diffraction maxima in orthorhombic HEWL crystal grown under high magnetic field. <i>Journal of Crystal Growth</i> , 2001, 232, 229-236.	1.5	18
47	Enhancement in the perfection of orthorhombic lysozyme crystals grown in a high magnetic field (10 <sup>4</sup> T). <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 1079-1083.	2.5	45