

Michihiro Sugahara

List of Publications by Year in descending order

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54
papers

2,513
citations

236912

25
h-index

197805

49
g-index

58
all docs

58
docs citations

58
times ranked

2924
citing authors

#	ARTICLE	IF	CITATIONS
1	Light-induced structural changes and the site of O=O bond formation in PSII caught by XFEL. <i>Nature</i> , 2017, 543, 131-135.	27.8	515
2	A three-dimensional movie of structural changes in bacteriorhodopsin. <i>Science</i> , 2016, 354, 1552-1557.	12.6	350
3	Grease matrix as a versatile carrier of proteins for serial crystallography. <i>Nature Methods</i> , 2015, 12, 61-63.	19.0	193
4	Redox-coupled proton transfer mechanism in nitrite reductase revealed by femtosecond crystallography. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 2928-2933.	7.1	88
5	Diverse application platform for hard X-ray diffraction in SACLA (DAPHNIS): application to serial protein crystallography using an X-ray free-electron laser. <i>Journal of Synchrotron Radiation</i> , 2015, 22, 532-537.	2.4	80
6	Hydroxyethyl cellulose matrix applied to serial crystallography. <i>Scientific Reports</i> , 2017, 7, 703.	3.3	74
7	Capturing an initial intermediate during the P450 _{nor} enzymatic reaction using time-resolved XFEL crystallography and caged-substrate. <i>Nature Communications</i> , 2017, 8, 1585.	12.8	74
8	XFEL structures of the influenza M2 proton channel: Room temperature water networks and insights into proton conduction. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 13357-13362.	7.1	64
9	Controlled Expansion of a Molecular Cavity in a Steroid Host Compound. <i>Journal of the American Chemical Society</i> , 2001, 123, 4386-4392.	13.7	54
10	A Novel Induced-fit Reaction Mechanism of Asymmetric Hot Dog Thioesterase Paal. <i>Journal of Molecular Biology</i> , 2005, 352, 212-228.	4.2	54
11	An isomorphous replacement method for efficient de novo phasing for serial femtosecond crystallography. <i>Scientific Reports</i> , 2015, 5, 14017.	3.3	54
12	Native sulfur/chlorine SAD phasing for serial femtosecond crystallography. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 2519-2525.	2.5	51
13	Proteinase K-Catalyzed Synthesis of Linear and Star Oligo(<i>l</i> -phenylalanine) Conjugates. <i>Biomacromolecules</i> , 2013, 14, 3635-3642.	5.4	46
14	Oil-free hyaluronic acid matrix for serial femtosecond crystallography. <i>Scientific Reports</i> , 2016, 6, 24484.	3.3	46
15	The Structural Role of Cholesterol in Biological Membranes. <i>Journal of the American Chemical Society</i> , 2001, 123, 7939-7940.	13.7	44
16	Nucleant-mediated protein crystallization with the application of microporous synthetic zeolites. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2008, 64, 686-695.	2.5	44
17	Membrane protein structure determination by SAD, SIR, or SIRAS phasing in serial femtosecond crystallography using an iododetergent. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 13039-13044.	7.1	43
18	Serial Femtosecond Crystallography and Ultrafast Absorption Spectroscopy of the Photoswitchable Fluorescent Protein IrisFP. <i>Journal of Physical Chemistry Letters</i> , 2016, 7, 882-887.	4.6	43

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19	High-viscosity sample-injection device for serial femtosecond crystallography at atmospheric pressure. <i>Journal of Applied Crystallography</i> , 2019, 52, 1280-1288.	4.5	43
20	Time-resolved serial femtosecond crystallography reveals early structural changes in channelrhodopsin. <i>ELife</i> , 2021, 10, .	6.0	41
21	Selective Sterol-Phospholipid Associations in Fluid Bilayers. <i>Journal of the American Chemical Society</i> , 2002, 124, 4253-4256.	13.7	34
22	Selective Association of Cholesterol with Long-Chain Phospholipids in Liquid-Ordered Bilayers:Â Support for the Existence of Lipid Rafts. <i>Journal of the American Chemical Society</i> , 2003, 125, 13040-13041.	13.7	34
23	Chemical crystallography by serial femtosecond X-ray diffraction. <i>Nature</i> , 2022, 601, 360-365.	27.8	33
24	Comparing serial X-ray crystallography and microcrystal electron diffraction (MicroED) as methods for routine structure determination from small macromolecular crystals. <i>IUCrJ</i> , 2020, 7, 306-323.	2.2	32
25	Derivatization of Proteinase K with Heavy Atoms Enhances Its Thermal Stability. <i>ACS Catalysis</i> , 2016, 6, 3036-3046.	11.2	28
26	Redox-coupled structural changes in nitrite reductase revealed by serial femtosecond and microfocus crystallography. <i>Journal of Biochemistry</i> , 2016, 159, 527-538.	1.7	26
27	High-throughput crystallization-to-structure pipeline at RIKEN SPring-8 Center. <i>Journal of Structural and Functional Genomics</i> , 2008, 9, 21-28.	1.2	25
28	Atomic resolution structure of serine protease proteinase K at ambient temperature. <i>Scientific Reports</i> , 2017, 7, 45604.	3.3	25
29	Capturing structural changes of the S ₁ to S ₂ transition of photosystem II using time-resolved serial femtosecond crystallography. <i>IUCrJ</i> , 2021, 8, 431-443.	2.2	24
30	Experimental phase determination with selenomethionine or mercury-derivatization in serial femtosecond crystallography. <i>IUCrJ</i> , 2017, 4, 639-647.	2.2	24
31	Serial crystallography captures dynamic control of sequential electron and proton transfer events in a flavoenzyme. <i>Nature Chemistry</i> , 2022, 14, 677-685.	13.6	24
32	Systematic Structural Study of Asymmetric Supramolecular Assembly by a Series of Bile Acid Derivatives with Different Side-Chain Lengths. <i>Crystal Growth and Design</i> , 2004, 4, 263-272.	3.0	22
33	Heavy-atom Database System: a tool for the preparation of heavy-atom derivatives of protein crystals based on amino-acid sequence and crystallization conditions. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 1302-1305.	2.5	15
34	Crystal structure of dehydroquinase synthase from <i>Thermus thermophilus</i> HB8 showing functional importance of the dimeric state. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 58, 249-252.	2.6	14
35	HATODAS II – heavy-atom database system with potentiality scoring. <i>Journal of Applied Crystallography</i> , 2009, 42, 540-544.	4.5	12
36	Effect of Heavy Atoms on the Thermal Stability of Î±-Amylase from <i>Aspergillus oryzae</i> . <i>PLoS ONE</i> , 2013, 8, e57432.	2.5	11

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37	A Technique for High-Throughput Protein Crystallization in Ionically Cross-Linked Polysaccharide Gel Beads for X-Ray Diffraction Experiments. <i>PLoS ONE</i> , 2014, 9, e95017.	2.5	11
38	Conformational alterations in unidirectional ion transport of a light-driven chloride pump revealed using X-ray free electron lasers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	11
39	Drastic Increase in the Flexibility of Open Host Frameworks of a Steroidal Host Compound upon Shortening Its Spacer. <i>European Journal of Organic Chemistry</i> , 2004, 2004, 981-994.	2.4	10
40	Structure of ATP-dependent phosphoenolpyruvate carboxykinase from <i>Thermus thermophilus</i> HB8 showing the structural basis of induced fit and thermostability. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 1500-1507.	2.5	10
41	Novel versatile cryoprotectants for heavy-atom derivatization of protein crystals. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 520-526.	2.5	10
42	Packing Space Expansion of Protein Crystallization Screening with Synthetic Zeolite as a Heteroepitaxial Nucleant. <i>Crystal Growth and Design</i> , 2011, 11, 110-120.	3.0	10
43	Viscosity-adjustable grease matrices for serial nanocrystallography. <i>Scientific Reports</i> , 2020, 10, 1371.	3.3	10
44	Inclusion Abilities of Bile Acids with Different Side Chain Length. <i>Molecular Crystals and Liquid Crystals</i> , 2001, 356, 155-162.	0.3	9
45	Subatomic structure of hyper-sweet thaumatin D21N mutant reveals the importance of flexible conformations for enhanced sweetness. <i>Biochimie</i> , 2019, 157, 57-63.	2.6	8
46	Protein-ligand complex structure from serial femtosecond crystallography using soaked thermolysin microcrystals and comparison with structures from synchrotron radiation. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 702-709.	2.3	8
47	Sample Delivery Techniques for Serial Crystallography. , 2018, , 109-184.		6
48	Autolabo: an automated system for ligand-soaking experiments with protein crystals. <i>Journal of Applied Crystallography</i> , 2010, 43, 940-944.	4.5	5
49	A fibre-based crystal mounting technique for protein cryocrystallography. <i>Journal of Applied Crystallography</i> , 2012, 45, 362-366.	4.5	5
50	Improvement of Production and Isolation of Human Neuraminidase-1 in Cellulose Crystals. <i>ACS Applied Bio Materials</i> , 2019, 2, 4941-4952.	4.6	5
51	Integrated database of information from structural genomics experiments. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 914-919.	2.5	2
52	Microcrystal preparation for serial femtosecond X-ray crystallography of bacterial copper amine oxidase. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2021, 77, 356-363.	0.8	2
53	Sugar-Based Lipid Headgroups: How Sticky Are They?. <i>Langmuir</i> , 2002, 18, 981-983.	3.5	1
54	Microcrystal-carrier matrices for serial crystallography. <i>Journal of Biological Macromolecules</i> , 2018, 18, 15-22.	0.3	0