

Takanori Nakane

List of Publications by Year in descending order

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69
papers

12,321
citations

94381

37
h-index

102432

66
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87
all docs

87
docs citations

87
times ranked

16505
citing authors

#	ARTICLE	IF	CITATIONS
1	Conformational alterations in unidirectional ion transport of a light-driven chloride pump revealed using X-ray free electron lasers. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	11
2	Crystal structure of CmABCB1 multi-drug exporter in lipidic mesophase revealed by LCP-SFX. IUCrJ, 2022, 9, 134-145.	1.0	2
3	High Resolution Structure Determination by Cryo-Electron Microscopy Single Particle Analysis. Nihon Kessho Gakkaishi, 2022, 64, 125-131.	0.0	0
4	Exploiting prior knowledge about biological macromolecules in cryo-EM structure determination. IUCrJ, 2021, 8, 60-75.	1.0	14
5	Time-resolved serial femtosecond crystallography reveals early structural changes in channelrhodopsin. ELife, 2021, 10, .	2.8	41
6	Capturing structural changes of the S ₁ to S ₂ transition of photosystem II using time-resolved serial femtosecond crystallography. IUCrJ, 2021, 8, 431-443.	1.0	24
7	Multi-body Refinement of Cryo-EM Images in RELION. Methods in Molecular Biology, 2021, 2215, 145-160.	0.4	39
8	Heavy Atom Detergent/Lipid Combined X-ray Crystallography for Elucidating the Structure-Function Relationships of Membrane Proteins. Membranes, 2021, 11, 823.	1.4	5
9	Pink beam crystallography demonstrated in SFX. IUCrJ, 2021, 8, 853-854.	1.0	1
10	New tools for automated cryo-EM single-particle analysis in RELION-4.0. Biochemical Journal, 2021, 478, 4169-4185.	1.7	396
11	Single-particle cryo-EM at atomic resolution. Nature, 2020, 587, 152-156.	13.7	572
12	Cryo-EM structures of holo condensin reveal a subunit flip-flop mechanism. Nature Structural and Molecular Biology, 2020, 27, 743-751.	3.6	90
13	Mitigating local over-fitting during single particle reconstruction with SIDESPLITTER. Journal of Structural Biology, 2020, 211, 107545.	1.3	77
14	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
15	Structures and distributions of SARS-CoV-2 spike proteins on intact virions. Nature, 2020, 588, 498-502.	13.7	918
16	A tool for visualizing protein motions in time-resolved crystallography. Structural Dynamics, 2020, 7, 024701.	0.9	20
17	Structure of the dopamine D2 receptor in complex with the antipsychotic drug spiperone. Nature Communications, 2020, 11, 6442.	5.8	47
18	Estimation of high-order aberrations and anisotropic magnification from cryo-EM data sets in RELION-3.1. IUCrJ, 2020, 7, 253-267.	1.0	574

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19	Comparing serial X-ray crystallography and microcrystal electron diffraction (MicroED) as methods for routine structure determination from small macromolecular crystals. <i>IUCr</i> , 2020, 7, 306-323.	1.0	32
20	CryoTEM with a Cold Field Emission Gun That Moves Structural Biology into a New Stage. <i>Microscopy and Microanalysis</i> , 2019, 25, 998-999.	0.2	45
21	Improvement of Production and Isolation of Human Neuraminidase-1 <i>in Cellulo</i> Crystals. <i>ACS Applied Bio Materials</i> , 2019, 2, 4941-4952.	2.3	5
22	Cryo-EM structure of the human L-type amino acid transporter 1 in complex with glycoprotein CD98hc. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 510-517.	3.6	110
23	Crystal structure of plant vacuolar iron transporter VIT1. <i>Nature Plants</i> , 2019, 5, 308-315.	4.7	51
24	Ligand binding to human prostaglandin E receptor EP4 at the lipid-bilayer interface. <i>Nature Chemical Biology</i> , 2019, 15, 18-26.	3.9	85
25	High-viscosity sample-injection device for serial femtosecond crystallography at atmospheric pressure. <i>Journal of Applied Crystallography</i> , 2019, 52, 1280-1288.	1.9	43
26	A Bayesian approach to beam-induced motion correction in cryo-EM single-particle analysis. <i>IUCr</i> , 2019, 6, 5-17.	1.0	696
27	Toward G protein-coupled receptor structure-based drug design using X-ray lasers. <i>IUCr</i> , 2019, 6, 1106-1119.	1.0	53
28	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
29	Serial femtosecond crystallography at the SACLA: breakthrough to dynamic structural biology. <i>Biophysical Reviews</i> , 2018, 10, 209-218.	1.5	22
30	Cryo-EM structures of the human volume-regulated anion channel LRRC8. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 797-804.	3.6	104
31	Structural basis for light control of cell development revealed by crystal structures of a myxobacterial phytochrome. <i>IUCr</i> , 2018, 5, 619-634.	1.0	33
32	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
33	Characterisation of molecular motions in cryo-EM single-particle data by multi-body refinement in RELION. <i>ELife</i> , 2018, 7, .	2.8	434
34	New tools for automated high-resolution cryo-EM structure determination in RELION-3. <i>ELife</i> , 2018, 7, .	2.8	3,965
35	Microcrystal-carrier matrices for serial crystallography. <i>Journal of Biological Macromolecules</i> , 2018, 18, 15-22.	0.2	0
36	Recent Developments of Single Particle Analysis with Cryo-electron Microscopy. <i>Nihon Kessho Gakkaishi</i> , 2018, 60, 230-232.	0.0	0

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37	Light-induced structural changes and the site of O=O bond formation in PSII caught by XFEL. <i>Nature</i> , 2017, 543, 131-135.	13.7	515
38	Hydroxyethyl cellulose matrix applied to serial crystallography. <i>Scientific Reports</i> , 2017, 7, 703.	1.6	74
39	Crystal Structure of the Minimal Cas9 from <i>Campylobacter jejuni</i> Reveals the Molecular Diversity in the CRISPR-Cas9 Systems. <i>Molecular Cell</i> , 2017, 65, 1109-1121.e3.	4.5	145
40	Structural insights into the competitive inhibition of the ATP-gated P2X receptor channel. <i>Nature Communications</i> , 2017, 8, 876.	5.8	75
41	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.	3.3	64
42	Serial femtosecond crystallography structure of cytochrome c oxidase at room temperature. <i>Scientific Reports</i> , 2017, 7, 4518.	1.6	34
43	Coincidence timing of femtosecond optical pulses in an X-ray free electron laser. <i>Journal of Applied Physics</i> , 2017, 122, 203105.	1.1	14
44	Structural basis for xenobiotic extrusion by eukaryotic MATE transporter. <i>Nature Communications</i> , 2017, 8, 1633.	5.8	69
45	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.	5.8	74
46	Atomic resolution structure of serine protease proteinase K at ambient temperature. <i>Scientific Reports</i> , 2017, 7, 45604.	1.6	25
47	Nanosecond pump-probe device for time-resolved serial femtosecond crystallography developed at SACLA. <i>Journal of Synchrotron Radiation</i> , 2017, 24, 1086-1091.	1.0	28
48	X-ray Free Electron Laser Determination of Crystal Structures of Dark and Light States of a Reversibly Photoswitching Fluorescent Protein at Room Temperature. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1918.	1.8	14
49	Experimental phase determination with selenomethionine or mercury-derivatization in serial femtosecond crystallography. <i>IUCr</i> , 2017, 4, 639-647.	1.0	24
50	Serial Femtosecond Crystallography at SACLA: Current Situation and Future Prospects. <i>Nihon Kessho Gakkaishi</i> , 2017, 59, 12-17.	0.0	1
51	Crystal structures of the TRIC trimeric intracellular cation channel orthologues. <i>Cell Research</i> , 2016, 26, 1288-1301.	5.7	21
52	A three-dimensional movie of structural changes in bacteriorhodopsin. <i>Science</i> , 2016, 354, 1552-1557.	6.0	350
53	Oil-free hyaluronic acid matrix for serial femtosecond crystallography. <i>Scientific Reports</i> , 2016, 6, 24484.	1.6	46
54	Crystal Structure of Cpf1 in Complex with Guide RNA and Target DNA. <i>Cell</i> , 2016, 165, 949-962.	13.5	552

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55	Data processing pipeline for serial femtosecond crystallography at SACLA. <i>Journal of Applied Crystallography</i> , 2016, 49, 1035-1041.	1.9	76
56	The room temperature crystal structure of a bacterial phytochrome determined by serial femtosecond crystallography. <i>Scientific Reports</i> , 2016, 6, 35279.	1.6	39
57	Crystal structure of the plant receptor-like kinase TDR in complex with the TDIF peptide. <i>Nature Communications</i> , 2016, 7, 12383.	5.8	64
58	Haem-dependent dimerization of PGRMC1/Sigma-2 receptor facilitates cancer proliferation and chemoresistance. <i>Nature Communications</i> , 2016, 7, 11030.	5.8	153
59	Structural and Functional Analysis of DDX41: a bispecific immune receptor for DNA and cyclic dinucleotide. <i>Scientific Reports</i> , 2016, 6, 34756.	1.6	43
60	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.	3.3	43
61	Redox-coupled structural changes in nitrite reductase revealed by serial femtosecond and microfocus crystallography. <i>Journal of Biochemistry</i> , 2016, 159, 527-538.	0.9	26
62	Structure and Engineering of <i>Francisella novicida</i> Cas9. <i>Cell</i> , 2016, 164, 950-961.	13.5	296
63	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.	3.3	88
64	Recent developments in <i>CrystFEL</i> . <i>Journal of Applied Crystallography</i> , 2016, 49, 680-689.	1.9	222
65	Native sulfur/chlorine SAD phasing for serial femtosecond crystallography. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 2519-2525.	2.5	51
66	RCSB PDB <i>Mobile</i> : iOS and Android mobile apps to provide data access and visualization to the RCSB Protein Data Bank. <i>Bioinformatics</i> , 2015, 31, 126-127.	1.8	12
67	iview: an interactive WebGL visualizer for protein-ligand complex. <i>BMC Bioinformatics</i> , 2014, 15, 56.	1.2	54
68	JSmol and the Next-Generation Web-Based Representation of 3D Molecular Structure as Applied to <i>Proteopedia</i> . <i>Israel Journal of Chemistry</i> , 2013, 53, 207-216.	1.0	210
69	Evaluation of the <i>Pichia pastoris</i> expression system for the production of GPCRs for structural analysis. <i>Microbial Cell Factories</i> , 2011, 10, 24.	1.9	35