

Takanori Nakane

List of Publications by Year in descending order

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Version: 2024-02-01

69
papers

12,321
citations

94381

37
h-index

102432

66
g-index

87
all docs

87
docs citations

87
times ranked

16505
citing authors

#	ARTICLE	IF	CITATIONS
1	New tools for automated high-resolution cryo-EM structure determination in RELION-3. <i>ELife</i> , 2018, 7, .	2.8	3,965
2	Structures and distributions of SARS-CoV-2 spike proteins on intact virions. <i>Nature</i> , 2020, 588, 498-502.	13.7	918
3	A Bayesian approach to beam-induced motion correction in cryo-EM single-particle analysis. <i>IUCr</i> , 2019, 6, 5-17.	1.0	696
4	Estimation of high-order aberrations and anisotropic magnification from cryo-EM data sets in <i>RELION</i>-3.1. <i>IUCr</i> , 2020, 7, 253-267.	1.0	574
5	Single-particle cryo-EM at atomic resolution. <i>Nature</i> , 2020, 587, 152-156.	13.7	572
6	Crystal Structure of Cpf1 in Complex with Guide RNA and Target DNA. <i>Cell</i> , 2016, 165, 949-962.	13.5	552
7	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
8	Characterisation of molecular motions in cryo-EM single-particle data by multi-body refinement in RELION. <i>ELife</i> , 2018, 7, .	2.8	434
9	New tools for automated cryo-EM single-particle analysis in RELION-4.0. <i>Biochemical Journal</i> , 2021, 478, 4169-4185.	1.7	396
10	A three-dimensional movie of structural changes in bacteriorhodopsin. <i>Science</i> , 2016, 354, 1552-1557.	6.0	350
11	Structure and Engineering of <i>Francisella novicida</i> Cas9. <i>Cell</i> , 2016, 164, 950-961.	13.5	296
12	Recent developments in <i>CrytFEL</i>. <i>Journal of Applied Crystallography</i> , 2016, 49, 680-689.	1.9	222
13	JSmol and the Nextâ€­Generation Webâ€­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
14	Haem-dependent dimerization of PGRMC1/Sigma-2 receptor facilitates cancer proliferation and chemoresistance. <i>Nature Communications</i> , 2016, 7, 11030.	5.8	153
15	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
16	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
17	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
18	Cryo-EM structures of holo condensin reveal a subunit flip-flop mechanism. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 743-751.	3.6	90

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19	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
20	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
21	Mitigating local over-fitting during single particle reconstruction with SIDESPLITTER. <i>Journal of Structural Biology</i> , 2020, 211, 107545.	1.3	77
22	Data processing pipeline for serial femtosecond crystallography at SACLA. <i>Journal of Applied Crystallography</i> , 2016, 49, 1035-1041.	1.9	76
23	Structural insights into the competitive inhibition of the ATP-gated P2X receptor channel. <i>Nature Communications</i> , 2017, 8, 876.	5.8	75
24	Hydroxyethyl cellulose matrix applied to serial crystallography. <i>Scientific Reports</i> , 2017, 7, 703.	1.6	74
25	Capturing an initial intermediate during the P450nor enzymatic reaction using time-resolved XFEL crystallography and caged-substrate. <i>Nature Communications</i> , 2017, 8, 1585.	5.8	74
26	Structural basis for xenobiotic extrusion by eukaryotic MATE transporter. <i>Nature Communications</i> , 2017, 8, 1633.	5.8	69
27	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
28	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
29	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
30	iview: an interactive WebGL visualizer for protein-ligand complex. <i>BMC Bioinformatics</i> , 2014, 15, 56.	1.2	54
31	Toward G protein-coupled receptor structure-based drug design using X-ray lasers. <i>IUCr</i> , 2019, 6, 1106-1119.	1.0	53
32	Native sulfur/chlorine SAD phasing for serial femtosecond crystallography. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 2519-2525.	2.5	51
33	Crystal structure of plant vacuolar iron transporter VIT1. <i>Nature Plants</i> , 2019, 5, 308-315.	4.7	51
34	Structure of the dopamine D2 receptor in complex with the antipsychotic drug spiperone. <i>Nature Communications</i> , 2020, 11, 6442.	5.8	47
35	Oil-free hyaluronic acid matrix for serial femtosecond crystallography. <i>Scientific Reports</i> , 2016, 6, 24484.	1.6	46
36	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

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37	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
38	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
39	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
40	Time-resolved serial femtosecond crystallography reveals early structural changes in channelrhodopsin. <i>ELife</i> , 2021, 10, .	2.8	41
41	The room temperature crystal structure of a bacterial phytochrome determined by serial femtosecond crystallography. <i>Scientific Reports</i> , 2016, 6, 35279.	1.6	39
42	Multi-body Refinement of Cryo-EM Images in RELION. <i>Methods in Molecular Biology</i> , 2021, 2215, 145-160.	0.4	39
43	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
44	Serial femtosecond crystallography structure of cytochrome c oxidase at room temperature. <i>Scientific Reports</i> , 2017, 7, 4518.	1.6	34
45	Structural basis for light control of cell development revealed by crystal structures of a myxobacterial phytochrome. <i>IUCrJ</i> , 2018, 5, 619-634.	1.0	33
46	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.	1.0	32
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	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
49	Atomic resolution structure of serine protease proteinase K at ambient temperature. <i>Scientific Reports</i> , 2017, 7, 45604.	1.6	25
50	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.	1.0	24
51	Experimental phase determination with selenomethionine or mercury-derivatization in serial femtosecond crystallography. <i>IUCrJ</i> , 2017, 4, 639-647.	1.0	24
52	Serial femtosecond crystallography at the SACLA: breakthrough to dynamic structural biology. <i>Biophysical Reviews</i> , 2018, 10, 209-218.	1.5	22
53	Crystal structures of the TRIC trimeric intracellular cation channel orthologues. <i>Cell Research</i> , 2016, 26, 1288-1301.	5.7	21
54	A tool for visualizing protein motions in time-resolved crystallography. <i>Structural Dynamics</i> , 2020, 7, 024701.	0.9	20

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55	Isoprenoid-chained lipid EROCO17+4: a new matrix for membrane protein crystallization and a crystal delivery medium in serial femtosecond crystallography. <i>Scientific Reports</i> , 2020, 10, 19305.	1.6	16
56	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
57	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
58	Exploiting prior knowledge about biological macromolecules in cryo-EM structure determination. <i>IUCr</i> , 2021, 8, 60-75.	1.0	14
59	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
60	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, .	3.3	11
61	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
62	Heavy Atom Detergent/Lipid Combined X-ray Crystallography for Elucidating the Structure-Function Relationships of Membrane Proteins. <i>Membranes</i> , 2021, 11, 823.	1.4	5
63	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.	0.4	3
64	Crystal structure of CmABCB1 multi-drug exporter in lipidic mesophase revealed by LCP-SFX. <i>IUCr</i> , 2022, 9, 134-145.	1.0	2
65	Serial Femtosecond Crystallography at SACLA: Current Situation and Future Prospects. <i>Nihon Kessho Gakkaishi</i> , 2017, 59, 12-17.	0.0	1
66	Pink beam crystallography demonstrated in SFX. <i>IUCr</i> , 2021, 8, 853-854.	1.0	1
67	Microcrystal-carrier matrices for serial crystallography. <i>Journal of Biological Macromolecules</i> , 2018, 18, 15-22.	0.2	0
68	Recent Developments of Single Particle Analysis with Cryo-electron Microscopy. <i>Nihon Kessho Gakkaishi</i> , 2018, 60, 230-232.	0.0	0
69	High Resolution Structure Determination by Cryo-Electron Microscopy Single Particle Analysis. <i>Nihon Kessho Gakkaishi</i> , 2022, 64, 125-131.	0.0	0