

Takanori Nakane

List of Publications by Year in descending order

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Version: 2024-02-01

69
papers

12,321
citations

94433

37
h-index

102487

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, . | 6.0 | 3,965 |
| 2 | Structures and distributions of SARS-CoV-2 spike proteins on intact virions. <i>Nature</i> , 2020, 588, 498-502. | 27.8 | 918 |
| 3 | A Bayesian approach to beam-induced motion correction in cryo-EM single-particle analysis. <i>IUCr</i> , 2019, 6, 5-17. | 2.2 | 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. | 2.2 | 574 |
| 5 | Single-particle cryo-EM at atomic resolution. <i>Nature</i> , 2020, 587, 152-156. | 27.8 | 572 |
| 6 | Crystal Structure of Cpf1 in Complex with Guide RNA and Target DNA. <i>Cell</i> , 2016, 165, 949-962. | 28.9 | 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. | 27.8 | 515 |
| 8 | Characterisation of molecular motions in cryo-EM single-particle data by multi-body refinement in RELION. <i>ELife</i> , 2018, 7, . | 6.0 | 434 |
| 9 | New tools for automated cryo-EM single-particle analysis in RELION-4.0. <i>Biochemical Journal</i> , 2021, 478, 4169-4185. | 3.7 | 396 |
| 10 | A three-dimensional movie of structural changes in bacteriorhodopsin. <i>Science</i> , 2016, 354, 1552-1557. | 12.6 | 350 |
| 11 | Structure and Engineering of <i>Francisella novicida</i> Cas9. <i>Cell</i> , 2016, 164, 950-961. | 28.9 | 296 |
| 12 | Recent developments in <i>CrytFEL</i>. <i>Journal of Applied Crystallography</i> , 2016, 49, 680-689. | 4.5 | 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. | 2.3 | 210 |
| 14 | Haem-dependent dimerization of PGRMC1/Sigma-2 receptor facilitates cancer proliferation and chemoresistance. <i>Nature Communications</i> , 2016, 7, 11030. | 12.8 | 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. | 9.7 | 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. | 8.2 | 110 |
| 17 | Cryo-EM structures of the human volume-regulated anion channel LRRC8. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 797-804. | 8.2 | 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. | 8.2 | 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. | 7.1 | 88 |
| 20 | Ligand binding to human prostaglandin E receptor EP4 at the lipid-bilayer interface. <i>Nature Chemical Biology</i> , 2019, 15, 18-26. | 8.0 | 85 |
| 21 | Mitigating local over-fitting during single particle reconstruction with SIDESPLITTER. <i>Journal of Structural Biology</i> , 2020, 211, 107545. | 2.8 | 77 |
| 22 | Data processing pipeline for serial femtosecond crystallography at SACLA. <i>Journal of Applied Crystallography</i> , 2016, 49, 1035-1041. | 4.5 | 76 |
| 23 | Structural insights into the competitive inhibition of the ATP-gated P2X receptor channel. <i>Nature Communications</i> , 2017, 8, 876. | 12.8 | 75 |
| 24 | Hydroxyethyl cellulose matrix applied to serial crystallography. <i>Scientific Reports</i> , 2017, 7, 703. | 3.3 | 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. | 12.8 | 74 |
| 26 | Structural basis for xenobiotic extrusion by eukaryotic MATE transporter. <i>Nature Communications</i> , 2017, 8, 1633. | 12.8 | 69 |
| 27 | Crystal structure of the plant receptor-like kinase TDR in complex with the TDIF peptide. <i>Nature Communications</i> , 2016, 7, 12383. | 12.8 | 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. | 7.1 | 64 |
| 29 | Crystal Structures of Human Orexin 2 Receptor Bound to the Subtype-Selective Antagonist EMPA. <i>Structure</i> , 2018, 26, 7-19.e5. | 3.3 | 55 |
| 30 | iview: an interactive WebGL visualizer for protein-ligand complex. <i>BMC Bioinformatics</i> , 2014, 15, 56. | 2.6 | 54 |
| 31 | Toward G protein-coupled receptor structure-based drug design using X-ray lasers. <i>IUCr</i> , 2019, 6, 1106-1119. | 2.2 | 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. | 9.3 | 51 |
| 34 | Structure of the dopamine D2 receptor in complex with the antipsychotic drug spiperone. <i>Nature Communications</i> , 2020, 11, 6442. | 12.8 | 47 |
| 35 | Oil-free hyaluronic acid matrix for serial femtosecond crystallography. <i>Scientific Reports</i> , 2016, 6, 24484. | 3.3 | 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. | 0.4 | 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. | 3.3 | 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. | 7.1 | 43 |
| 39 | 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 |
| 40 | Time-resolved serial femtosecond crystallography reveals early structural changes in channelrhodopsin. <i>ELife</i> , 2021, 10, . | 6.0 | 41 |
| 41 | The room temperature crystal structure of a bacterial phytochrome determined by serial femtosecond crystallography. <i>Scientific Reports</i> , 2016, 6, 35279. | 3.3 | 39 |
| 42 | Multi-body Refinement of Cryo-EM Images in RELION. <i>Methods in Molecular Biology</i> , 2021, 2215, 145-160. | 0.9 | 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. | 4.0 | 35 |
| 44 | Serial femtosecond crystallography structure of cytochrome c oxidase at room temperature. <i>Scientific Reports</i> , 2017, 7, 4518. | 3.3 | 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. | 2.2 | 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. | 2.2 | 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. | 2.4 | 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. | 1.7 | 26 |
| 49 | Atomic resolution structure of serine protease proteinase K at ambient temperature. <i>Scientific Reports</i> , 2017, 7, 45604. | 3.3 | 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. | 2.2 | 24 |
| 51 | Experimental phase determination with selenomethionine or mercury-derivatization in serial femtosecond crystallography. <i>IUCrJ</i> , 2017, 4, 639-647. | 2.2 | 24 |
| 52 | Serial femtosecond crystallography at the SACLA: breakthrough to dynamic structural biology. <i>Biophysical Reviews</i> , 2018, 10, 209-218. | 3.2 | 22 |
| 53 | Crystal structures of the TRIC trimeric intracellular cation channel orthologues. <i>Cell Research</i> , 2016, 26, 1288-1301. | 12.0 | 21 |
| 54 | A tool for visualizing protein motions in time-resolved crystallography. <i>Structural Dynamics</i> , 2020, 7, 024701. | 2.3 | 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. | 3.3 | 16 |
| 56 | Coincidence timing of femtosecond optical pulses in an X-ray free electron laser. <i>Journal of Applied Physics</i> , 2017, 122, 203105. | 2.5 | 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. | 4.1 | 14 |
| 58 | Exploiting prior knowledge about biological macromolecules in cryo-EM structure determination. <i>IUCr</i> , 2021, 8, 60-75. | 2.2 | 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. | 4.1 | 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, . | 7.1 | 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. | 4.6 | 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. | 3.0 | 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. | 0.8 | 3 |
| 64 | Crystal structure of CmABCB1 multi-drug exporter in lipidic mesophase revealed by LCP-SFX. <i>IUCr</i> , 2022, 9, 134-145. | 2.2 | 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. | 2.2 | 1 |
| 67 | Microcrystal-carrier matrices for serial crystallography. <i>Journal of Biological Macromolecules</i> , 2018, 18, 15-22. | 0.3 | 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 |