

# Atsushi Nakagawa

## List of Publications by Year in descending order

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43  
papers

1,739  
citations

430442

18  
h-index

276539

41  
g-index

44  
all docs

44  
docs citations

44  
times ranked

2743  
citing authors

#	ARTICLE	IF	CITATIONS
1	Host Innate Immune Receptors and Beyond: Making Sense of Microbial Infections. <i>Cell Host and Microbe</i> , 2008, 3, 352-363.	5.1	439
2	Crystal structure of the macrophage migration inhibitory factor from rat liver. <i>Nature Structural Biology</i> , 1996, 3, 259-266.	9.7	173
3	Crystal structure of nitric oxide reductase from denitrifying fungus <i>Fusarium oxysporum</i> . <i>Nature Structural Biology</i> , 1997, 4, 827-832.	9.7	172
4	Immunogenicity of Whole-Parasite Vaccines against <i>Plasmodium falciparum</i> Involves Malarial Hemozoin and Host TLR9. <i>Cell Host and Microbe</i> , 2010, 7, 50-61.	5.1	135
5	A new protein complex promoting the assembly of Rad51 filaments. <i>Nature Communications</i> , 2013, 4, 1676.	5.8	91
6	The cytoplasmic coiled-coil mediates cooperative gating temperature sensitivity in the voltage-gated H <sup>+</sup> channel Hv1. <i>Nature Communications</i> , 2012, 3, 816.	5.8	90
7	<i>Escherichia coli</i> positive regulator OmpR has a large loop structure at the putative RNA polymerase interaction site. <i>Nature Structural and Molecular Biology</i> , 1997, 4, 28-31.	3.6	87
8	Structures of the wild-type MexAB-OprM tripartite pump reveal its complex formation and drug efflux mechanism. <i>Nature Communications</i> , 2019, 10, 1520.	5.8	77
9	Structural basis for the assembly of the Ragulator-Rag GTPase complex. <i>Nature Communications</i> , 2017, 8, 1625.	5.8	55
10	Lipocalin 2 Bolsters Innate and Adaptive Immune Responses to Blood-Stage Malaria Infection by Reinforcing Host Iron Metabolism. <i>Cell Host and Microbe</i> , 2012, 12, 705-716.	5.1	50
11	Phage tail fibre assembly proteins employ a modular structure to drive the correct folding of diverse fibres. <i>Nature Microbiology</i> , 2019, 4, 1645-1653.	5.9	45
12	Matching the crystallographic structure of ribosomal protein S7 to a three-dimensional model of the 16S ribosomal RNA. <i>Rna</i> , 1998, 4, 542-550.	1.6	29
13	Orexin-A is composed of a highly conserved C-terminal and a specific, hydrophilic N-terminal region, revealing the structural basis of specific recognition by the orexin-1 receptor. <i>Journal of Peptide Science</i> , 2006, 12, 443-454.	0.8	27
14	The tertiary structure of the human Xkr8-Basigin complex that scrambles phospholipids at plasma membranes. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 825-834.	3.6	26
15	Crystallization of Rat Liver Macrophage Migration Inhibitory Factor for MAD Analysis. <i>Journal of Structural Biology</i> , 1995, 115, 331-334.	1.3	22
16	The host-binding domain of the P2 phage tail spike reveals a trimeric iron-binding structure. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 837-841.	0.7	21
17	Crystal structure of the C-terminal domain of Mu phage central spike and functions of bound calcium ion. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013, 1834, 284-291.	1.1	21
18	Remarkably Intense Emission from Ruthenium(II) Complexes with Multiple Borane Centers. <i>Inorganic Chemistry</i> , 2015, 54, 10287-10295.	1.9	20

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19	Crystallization and preliminary X-ray diffraction analysis of recombinant hepatitis E virus-like particle. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 318-322.	0.7	18
20	Crystallization and Preliminary X-Ray Analysis of Humand-Dopachrome Tautomerase. <i>Journal of Structural Biology</i> , 1997, 120, 105-108.	1.3	16
21	Crystallization and preliminary X-ray analysis of hyperthermophilic L-threonine dehydrogenase from the archaeon <i>Pyrococcus horikoshii</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 432-434.	0.7	11
22	Emission Tuning of Heteroleptic Arylborane-Ruthenium(II) Complexes by Ancillary Ligands: Observation of Strickler-Berg-Type Relation. <i>Inorganic Chemistry</i> , 2018, 57, 9055-9066.	1.9	11
23	Crystallization and preliminary X-ray diffraction analysis of a chitin-binding domain of hyperthermophilic chitinase from <i>Pyrococcus furiosus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 476-478.	0.7	10
24	Structural basis of Gip1 for cytosolic sequestration of G protein in wide-range chemotaxis. <i>Nature Communications</i> , 2018, 9, 4635.	5.8	10
25	Dual Emissions from Ruthenium(II) Complexes Having 4-Arylethynyl-1,10-phenanthroline at Low Temperature. <i>Inorganic Chemistry</i> , 2015, 54, 3245-3252.	1.9	9
26	Evaluation of transition-state mimics in a superior BACE1 cleavage sequence as peptide-mimetic BACE1 inhibitors. <i>Bioorganic and Medicinal Chemistry</i> , 2015, 23, 5626-5640.	1.4	9
27	The hydrophobic nature of a novel membrane interface regulates the enzyme activity of a voltage-sensing phosphatase. <i>ELife</i> , 2018, 7, .	2.8	9
28	Bright and Long-Lived Emission from a Starburst-Type Arylborane-Appended Polypyridyl Ruthenium(II) Complex. <i>European Journal of Inorganic Chemistry</i> , 2017, 2017, 3794-3798.	1.0	8
29	Thermoelectric Generation Using Water Lenses. <i>Journal of Electronic Materials</i> , 2013, 42, 1960-1965.	1.0	6
30	Plant-specific DUF1110 protein from <i>Oryza sativa</i> : expression, purification and crystallization. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016, 72, 480-484.	0.4	6
31	Interaction between S4 and the phosphatase domain mediates electrochemical coupling in voltage-sensing phosphatase (VSP). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	6
32	Crystallization and Preliminary X-Ray Crystallographic Study of a 23S rRNA Binding Domain of the Ribosomal Protein L2 from <i>Bacillus stearothermophilus</i> . <i>Journal of Structural Biology</i> , 1998, 124, 99-101.	1.3	5
33	Hierarchical structure assembly model of rice dwarf virus particle formation. <i>Biophysical Reviews</i> , 2018, 10, 659-665.	1.5	5
34	Preliminary crystallographic analysis of the antibiotic discharge outer membrane lipoprotein OprM of <i>Pseudomonas aeruginosa</i> with an exceptionally long unit cell and complex lattice structure. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 131-133.	0.7	3
35	Crystallization and preliminary X-ray analysis of rat SHPS-1. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 189-191.	0.7	3
36	All-atom molecular dynamics study of hepatitis B virus containing pregenome RNA in solution. <i>Journal of Chemical Physics</i> , 2021, 155, 145101.	1.2	3

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37	Crystallization and Preliminary X-Ray Studies of Two Serine Proteinase Inhibitors, BGIA and BGIT, from the Seeds of Bitter Gourd. <i>Journal of Structural Biology</i> , 1997, 120, 204-206.	1.3	2
38	Refolding, crystallization and preliminary X-ray crystallographic study of the whole extracellular regions of nectins. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 344-348.	0.7	2
39	A novel multimode sensor showing cation-dependent fluorescence colour. <i>Physical Chemistry Chemical Physics</i> , 2017, 19, 28943-28949.	1.3	2
40	SPring-8 BL44XU, a synchrotron radiation beamline for biological macromolecular assemblies, operated by the Institute for Protein Research, Osaka University. <i>Biophysical Reviews</i> , 2019, 11, 521-523.	1.5	2
41	Residue Assignment in Crystallographic Protein Electron Density Maps With 3D Convolutional Networks. <i>IEEE Access</i> , 2022, 10, 28760-28772.	2.6	2
42	High-Resolution Crystals of the HU Mutant K38N from <i>Bacillus stearothermophilus</i> . <i>Journal of Structural Biology</i> , 1999, 125, 86-89.	1.3	1
43	Noncrystallographic symmetry-constrained map obtained by direct density optimization. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 147-154.	1.1	0