

# Tomohiro Nishizawa

## List of Publications by Year in descending order

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Version: 2024-02-01

37  
papers

2,685  
citations

257450

24  
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345221

36  
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43  
all docs

43  
docs citations

43  
times ranked

3824  
citing authors

#	ARTICLE	IF	CITATIONS
1	Cryo-EM of the ATP11C flippase reconstituted in Nanodiscs shows a distended phospholipid bilayer inner membrane around transmembrane helix 2. <i>Journal of Biological Chemistry</i> , 2022, 298, 101498.	3.4	7
2	Structure of the type V-C CRISPR-Cas effector enzyme. <i>Molecular Cell</i> , 2022, 82, 1865-1877.e4.	9.7	12
3	Cryo-EM structures of thylakoid-located voltage-dependent chloride channel VCCN1. <i>Nature Communications</i> , 2022, 13, 2505.	12.8	5
4	Structural insights into the HBV receptor and bile acid transporter NTCP. <i>Nature</i> , 2022, 606, 1027-1031.	27.8	44
5	Structure of the Dicer-2/R2D2 heterodimer bound to a small RNA duplex. <i>Nature</i> , 2022, 607, 393-398.	27.8	20
6	Structure of the miniature type V-F CRISPR-Cas effector enzyme. <i>Molecular Cell</i> , 2021, 81, 558-570.e3.	9.7	95
7	Cryo-EM structures of Toll-like receptors in complex with UNC93B1. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 173-180.	8.2	45
8	Mitochondrial sorting and assembly machinery operates by $\beta$ -barrel switching. <i>Nature</i> , 2021, 590, 163-169.	27.8	60
9	Time-resolved serial femtosecond crystallography reveals early structural changes in channelrhodopsin. <i>ELife</i> , 2021, 10, .	6.0	41
10	Cryo-EM structure of the $\beta$ 3-adrenergic receptor reveals the molecular basis of subtype selectivity. <i>Molecular Cell</i> , 2021, 81, 3205-3215.e5.	9.7	21
11	Cryo-EM structure of the human MT1/Gi signaling complex. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 694-701.	8.2	31
12	Structural basis of gating modulation of Kv4 channel complexes. <i>Nature</i> , 2021, 599, 158-164.	27.8	35
13	Gastric proton pump with two occluded K <sup>+</sup> engineered with sodium pump-mimetic mutations. <i>Nature Communications</i> , 2021, 12, 5709.	12.8	8
14	Structural basis of the regulation of the normal and oncogenic methylation of nucleosomal histone H3 Lys36 by NSD2. <i>Nature Communications</i> , 2021, 12, 6605.	12.8	23
15	Cryo-EM reveals mechanistic insights into lipid-facilitated polyamine export by human ATP13A2. <i>Molecular Cell</i> , 2021, 81, 4799-4809.e5.	9.7	22
16	Consensus mutagenesis approach improves the thermal stability of system x <sub>c</sub> <sup>+</sup> transporter, xCT, and enables cryo-EM analyses. <i>Protein Science</i> , 2020, 29, 2398-2407.	7.6	19
17	Transport Cycle of Plasma Membrane Flippase ATP11C by Cryo-EM. <i>Cell Reports</i> , 2020, 32, 108208.	6.4	50
18	Cryo-EM structures of calcium homeostasis modulator channels in diverse oligomeric assemblies. <i>Science Advances</i> , 2020, 6, eaba8105.	10.3	32

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19	Cryo-EM structures of SERCA2b reveal the mechanism of regulation by the luminal extension tail. <i>Science Advances</i> , 2020, 6, eabb0147.	10.3	22
20	Cryo-EM structure of the volume-regulated anion channel LRRC8D isoform identifies features important for substrate permeation. <i>Communications Biology</i> , 2020, 3, 240.	4.4	35
21	The structure of lipid nanodisc-reconstituted TRPV3 reveals the gating mechanism. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 645-652.	8.2	51
22	Cryo-EM structure of the human PAC1 receptor coupled to an engineered heterotrimeric G protein. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 274-280.	8.2	39
23	Structural insights into tetraspanin CD9 function. <i>Nature Communications</i> , 2020, 11, 1606.	12.8	114
24	Cryo-EM structures capture the transport cycle of the P4-ATPase flippase. <i>Science</i> , 2019, 365, 1149-1155.	12.6	143
25	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
26	Crystal structure of plant vacuolar iron transporter VIT1. <i>Nature Plants</i> , 2019, 5, 308-315.	9.3	51
27	Crystallization of the human tetraspanin protein CD9. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2019, 75, 254-259.	0.8	14
28	Crystal structures of human ETB receptor provide mechanistic insight into receptor activation and partial activation. <i>Nature Communications</i> , 2018, 9, 4711.	12.8	60
29	Crystal structure of the red light-activated channelrhodopsin Chrimson. <i>Nature Communications</i> , 2018, 9, 3949.	12.8	112
30	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
31	Structural insights into ligand recognition by the lysophosphatidic acid receptor LPA6. <i>Nature</i> , 2017, 548, 356-360.	27.8	101
32	X-ray structures of endothelin ETB receptor bound to clinical antagonist bosentan and its analog. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 758-764.	8.2	79
33	A three-dimensional movie of structural changes in bacteriorhodopsin. <i>Science</i> , 2016, 354, 1552-1557.	12.6	350
34	Activation mechanism of endothelin ETB receptor by endothelin-1. <i>Nature</i> , 2016, 537, 363-368.	27.8	148
35	Structural Basis for the Counter-Transport Mechanism of a H <sup>+</sup> /Ca <sup>2+</sup> Exchanger. <i>Science</i> , 2013, 341, 168-172.	12.6	73
36	Crystal structure of the channelrhodopsin light-gated cation channel. <i>Nature</i> , 2012, 482, 369-374.	27.8	503

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37	Cryo-EM Structure of the $\beta_2$ Adrenergic Receptor Reveals the Molecular Basis of Subtype Selectivity. SSRN Electronic Journal, 0, , .	0.4	0