

Tomohiro Nishizawa

List of Publications by Year in descending order

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Version: 2024-02-01

37
papers

2,685
citations

257450

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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	Crystal structure of the channelrhodopsin light-gated cation channel. <i>Nature</i> , 2012, 482, 369-374.	27.8	503
2	A three-dimensional movie of structural changes in bacteriorhodopsin. <i>Science</i> , 2016, 354, 1552-1557.	12.6	350
3	Activation mechanism of endothelin ETB receptor by endothelin-1. <i>Nature</i> , 2016, 537, 363-368.	27.8	148
4	Cryo-EM structures capture the transport cycle of the P4-ATPase flippase. <i>Science</i> , 2019, 365, 1149-1155.	12.6	143
5	Structural insights into tetraspanin CD9 function. <i>Nature Communications</i> , 2020, 11, 1606.	12.8	114
6	Crystal structure of the red light-activated channelrhodopsin Chrimson. <i>Nature Communications</i> , 2018, 9, 3949.	12.8	112
7	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
8	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
9	Structural insights into ligand recognition by the lysophosphatidic acid receptor LPA6. <i>Nature</i> , 2017, 548, 356-360.	27.8	101
10	Structure of the miniature type V-F CRISPR-Cas effector enzyme. <i>Molecular Cell</i> , 2021, 81, 558-570.e3.	9.7	95
11	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
12	Structural Basis for the Counter-Transport Mechanism of a H ⁺ /Ca ²⁺ Exchanger. <i>Science</i> , 2013, 341, 168-172.	12.6	73
13	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
14	Mitochondrial sorting and assembly machinery operates by β -barrel switching. <i>Nature</i> , 2021, 590, 163-169.	27.8	60
15	Crystal structure of plant vacuolar iron transporter VIT1. <i>Nature Plants</i> , 2019, 5, 308-315.	9.3	51
16	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
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 Toll-like receptors in complex with UNC93B1. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 173-180.	8.2	45

#	ARTICLE	IF	CITATIONS
19	Structural insights into the HBV receptor and bile acid transporter NTCP. <i>Nature</i> , 2022, 606, 1027-1031.	27.8	44
20	Time-resolved serial femtosecond crystallography reveals early structural changes in channelrhodopsin. <i>ELife</i> , 2021, 10, .	6.0	41
21	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
22	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
23	Structural basis of gating modulation of Kv4 channel complexes. <i>Nature</i> , 2021, 599, 158-164.	27.8	35
24	Cryo-EM structures of calcium homeostasis modulator channels in diverse oligomeric assemblies. <i>Science Advances</i> , 2020, 6, eaba8105.	10.3	32
25	Cryo-EM structure of the human MT1 α -Gi signaling complex. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 694-701.	8.2	31
26	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
27	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
28	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
29	Cryo-EM structure of the β 3-adrenergic receptor reveals the molecular basis of subtype selectivity. <i>Molecular Cell</i> , 2021, 81, 3205-3215.e5.	9.7	21
30	Structure of the Dicer-2 α -R2D2 heterodimer bound to a small RNA duplex. <i>Nature</i> , 2022, 607, 393-398.	27.8	20
31	Consensus mutagenesis approach improves the thermal stability of system x _c ⁺ transporter, xCT, and enables cryo-EM analyses. <i>Protein Science</i> , 2020, 29, 2398-2407.	7.6	19
32	Crystallization of the human tetraspanin protein CD9. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2019, 75, 254-259.	0.8	14
33	Structure of the type V-C CRISPR-Cas effector enzyme. <i>Molecular Cell</i> , 2022, 82, 1865-1877.e4.	9.7	12
34	Gastric proton pump with two occluded K ⁺ engineered with sodium pump-mimetic mutations. <i>Nature Communications</i> , 2021, 12, 5709.	12.8	8
35	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
36	Cryo-EM structures of thylakoid-located voltage-dependent chloride channel VCCN1. <i>Nature Communications</i> , 2022, 13, 2505.	12.8	5

#	ARTICLE	IF	CITATIONS
37	Cryo-EM Structure of the β_2 Adrenergic Receptor Reveals the Molecular Basis of Subtype Selectivity. SSRN Electronic Journal, 0, , .	0.4	0