

Osamu Nureki

List of Publications by Year in descending order

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121
papers

14,350
citations

44042

48
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22147

113
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142
all docs

142
docs citations

142
times ranked

17877
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural basis for channel conduction in the pump-like channelrhodopsin ChRmine. <i>Cell</i> , 2022, 185, 672-689.e23.	13.5	72
2	Lateral access mechanism of LPA receptor probed by molecular dynamics simulation. <i>PLoS ONE</i> , 2022, 17, e0263296.	1.1	3
3	Cell-Free Synthesis of Human Endothelin Receptors and Its Application to Ribosome Display. <i>Analytical Chemistry</i> , 2022, 94, 3831-3839.	3.2	6
4	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
5	Engineered <i>Campylobacter jejuni</i> Cas9 variant with enhanced activity and broader targeting range. <i>Communications Biology</i> , 2022, 5, 211.	2.0	19
6	Structure of the type V-C CRISPR-Cas effector enzyme. <i>Molecular Cell</i> , 2022, 82, 1865-1877.e4.	4.5	12
7	Cryo-EM structures of the β_3 adrenergic receptor bound to solabegron and isoproterenol. <i>Biochemical and Biophysical Research Communications</i> , 2022, 611, 158-164.	1.0	9
8	Recent Advances in the Structural Biology of the Volume-Regulated Anion Channel LRRC8. <i>Frontiers in Pharmacology</i> , 2022, 13, .	1.6	8
9	Cryo-EM structures of thylakoid-located voltage-dependent chloride channel VCCN1. <i>Nature Communications</i> , 2022, 13, 2505.	5.8	5
10	Automated amplification-free digital RNA detection platform for rapid and sensitive SARS-CoV-2 diagnosis. <i>Communications Biology</i> , 2022, 5, .	2.0	28
11	Structure of the Dicer-2 heterodimer bound to a small RNA duplex. <i>Nature</i> , 2022, 607, 393-398.	13.7	20
12	Structure of the miniature type V-F CRISPR-Cas effector enzyme. <i>Molecular Cell</i> , 2021, 81, 558-570.e3.	4.5	95
13	Taste transduction and channel synapses in taste buds. <i>Pflügers Archiv European Journal of Physiology</i> , 2021, 473, 3-13.	1.3	70
14	Time-resolved serial femtosecond crystallography reveals early structural changes in channelrhodopsin. <i>ELife</i> , 2021, 10, .	2.8	41
15	Cex1 is a component of the COPI intracellular trafficking machinery. <i>Biology Open</i> , 2021, 10, .	0.6	0
16	Crystal structure of schizorhodopsin reveals mechanism of inward proton pumping. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	26
17	Amplification-free RNA detection with CRISPR-Cas13. <i>Communications Biology</i> , 2021, 4, 476.	2.0	119
18	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.	4.5	21

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19	Cryo-EM structure of the human MT1 α -Gi signaling complex. Nature Structural and Molecular Biology, 2021, 28, 694-701.	3.6	31
20	Structural basis of gating modulation of Kv4 channel complexes. Nature, 2021, 599, 158-164.	13.7	35
21	Structural basis of the regulation of the normal and oncogenic methylation of nucleosomal histone H3 Lys36 by NSD2. Nature Communications, 2021, 12, 6605.	5.8	23
22	Peripheral tolerance by Treg via constraining OX40 signal in autoreactive T cells against desmoglein 3, a target antigen in pemphigus. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, e2026763118.	3.3	11
23	Cryo-EM reveals mechanistic insights into lipid-facilitated polyamine export by human ATP13A2. Molecular Cell, 2021, 81, 4799-4809.e5.	4.5	22
24	Structural basis for unique color tuning mechanism in heliorhodopsin. Biochemical and Biophysical Research Communications, 2020, 533, 262-267.	1.0	14
25	Consensus mutagenesis approach improves the thermal stability of system α -glucosyltransferase transporter, α -glucosyltransferase, and enables cryo-EM analyses. Protein Science, 2020, 29, 2398-2407.	3.1	19
26	Structure of the human secretin receptor coupled to an engineered heterotrimeric G protein. Biochemical and Biophysical Research Communications, 2020, 533, 861-866.	1.0	15
27	Transport Cycle of Plasma Membrane Flippase ATP11C by Cryo-EM. Cell Reports, 2020, 32, 108208.	2.9	50
28	Cryo-EM structures of calcium homeostasis modulator channels in diverse oligomeric assemblies. Science Advances, 2020, 6, eaba8105.	4.7	32
29	Structural insights into the mechanism of rhodopsin phosphodiesterase. Nature Communications, 2020, 11, 5605.	5.8	30
30	Cryo-EM structure of the volume-regulated anion channel LRRC8D isoform identifies features important for substrate permeation. Communications Biology, 2020, 3, 240.	2.0	35
31	The structure of lipid nanodisc-reconstituted TRPV3 reveals the gating mechanism. Nature Structural and Molecular Biology, 2020, 27, 645-652.	3.6	51
32	Cryo-EM structure of the human PAC1 receptor coupled to an engineered heterotrimeric G protein. Nature Structural and Molecular Biology, 2020, 27, 274-280.	3.6	39
33	Crystal structure of human endothelin ETB receptor in complex with sarafotoxin S6b. Biochemical and Biophysical Research Communications, 2020, 528, 383-388.	1.0	19
34	Structural insights into tetraspanin CD9 function. Nature Communications, 2020, 11, 1606.	5.8	114
35	Crystal structure of Drosophila Piwi. Nature Communications, 2020, 11, 858.	5.8	42
36	Base editors for simultaneous introduction of C-to-T and A-to-G mutations. Nature Biotechnology, 2020, 38, 865-869.	9.4	137

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37	Cryo-EM structures capture the transport cycle of the P4-ATPase flippase. <i>Science</i> , 2019, 365, 1149-1155.	6.0	143
38	Crystal structure of human endothelin ETB receptor in complex with peptide inverse agonist IRL2500. <i>Communications Biology</i> , 2019, 2, 236.	2.0	33
39	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
40	Structural basis for the promiscuous PAM recognition by <i>Corynebacterium diphtheriae</i> Cas9. <i>Nature Communications</i> , 2019, 10, 1968.	5.8	33
41	Ultrafast Dynamics of Heliorhodopsins. <i>Journal of Physical Chemistry B</i> , 2019, 123, 2507-2512.	1.2	24
42	Crystal structure of plant vacuolar iron transporter VIT1. <i>Nature Plants</i> , 2019, 5, 308-315.	4.7	51
43	Spectroscopic study of the transmembrane domain of a rhodopsin-phosphodiesterase fusion protein from a unicellular eukaryote. <i>Journal of Biological Chemistry</i> , 2019, 294, 3432-3443.	1.6	22
44	Crystal structure of heliorhodopsin. <i>Nature</i> , 2019, 574, 132-136.	13.7	71
45	Cap-specific terminal N ⁶ -methylation of RNA by an RNA polymerase II-associated methyltransferase. <i>Science</i> , 2019, 363, .	6.0	262
46	Crystallization of the human tetraspanin protein CD9. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2019, 75, 254-259.	0.4	14
47	Structural basis for oligomerization of the prokaryotic peptide transporter PepT _{So2} . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2019, 75, 348-358.	0.4	10
48	Real-time observation of flexible domain movements in CRISPR-Cas9. <i>EMBO Journal</i> , 2018, 37, .	3.5	39
49	Crystal structures of human ETB receptor provide mechanistic insight into receptor activation and partial activation. <i>Nature Communications</i> , 2018, 9, 4711.	5.8	60
50	Crystal structure of the red light-activated channelrhodopsin Chrimson. <i>Nature Communications</i> , 2018, 9, 3949.	5.8	112
51	Vibrational and Molecular Properties of Mg ²⁺ Binding and Ion Selectivity in the Magnesium Channel MgtE. <i>Journal of Physical Chemistry B</i> , 2018, 122, 9681-9696.	1.2	5
52	An Atomistic Model of a Precursor State of Light-Induced Channel Opening of Channelrhodopsin. <i>Biophysical Journal</i> , 2018, 115, 1281-1291.	0.2	15
53	Structural insights into cGAMP degradation by Ecto-nucleotide pyrophosphatase phosphodiesterase 1. <i>Nature Communications</i> , 2018, 9, 4424.	5.8	108
54	Resonance Raman Investigation of the Chromophore Structure of Heliorhodopsins. <i>Journal of Physical Chemistry Letters</i> , 2018, 9, 6431-6436.	2.1	33

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55	DUSP10 constrains innate IL-33-mediated cytokine production in ST2hi memory-type pathogenic Th2 cells. <i>Nature Communications</i> , 2018, 9, 4231.	5.8	35
56	Engineered CRISPR-Cas9 nuclease with expanded targeting space. <i>Science</i> , 2018, 361, 1259-1262.	6.0	783
57	Free Energy Landscape for the Entire Transport Cycle of Triose-Phosphate/Phosphate Translocator. <i>Structure</i> , 2018, 26, 1284-1296.e4.	1.6	17
58	Functional roles of Mg ²⁺ binding sites in ion-dependent gating of a Mg ²⁺ channel, MgtE, revealed by solution NMR. <i>ELife</i> , 2018, 7, .	2.8	10
59	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
60	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
61	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
62	Structure of the triose-phosphate/phosphate translocator reveals the basis of substrate specificity. <i>Nature Plants</i> , 2017, 3, 825-832.	4.7	51
63	Structural insights into ligand recognition by the lysophosphatidic acid receptor LPA6. <i>Nature</i> , 2017, 548, 356-360.	13.7	101
64	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.	3.6	79
65	Structural Basis for the Canonical and Non-canonical PAM Recognition by CRISPR-Cpf1. <i>Molecular Cell</i> , 2017, 67, 633-645.e3.	4.5	206
66	Capturing an initial intermediate during the P450 _{nor} enzymatic reaction using time-resolved XFEL crystallography and caged-substrate. <i>Nature Communications</i> , 2017, 8, 1585.	5.8	74
67	Real-space and real-time dynamics of CRISPR-Cas9 visualized by high-speed atomic force microscopy. <i>Nature Communications</i> , 2017, 8, 1430.	5.8	184
68	Engineered Cpf1 variants with altered PAM specificities. <i>Nature Biotechnology</i> , 2017, 35, 789-792.	9.4	351
69	A three-dimensional movie of structural changes in bacteriorhodopsin. <i>Science</i> , 2016, 354, 1552-1557.	6.0	350
70	Structural and functional insights into IZUMO1 recognition by JUNO in mammalian fertilization. <i>Nature Communications</i> , 2016, 7, 12198.	5.8	58
71	Crystal Structure of Cpf1 in Complex with Guide RNA and Target DNA. <i>Cell</i> , 2016, 165, 949-962.	13.5	552
72	Activation mechanism of endothelin ETB receptor by endothelin-1. <i>Nature</i> , 2016, 537, 363-368.	13.7	148

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73	Crystal Structure of Silkworm PIWI-Clade Argonaute Siwi Bound to piRNA. <i>Cell</i> , 2016, 167, 484-497.e9.	13.5	116
74	<scp>ENPP</scp>1 processes protein <scp>ADP</scp>â€ribosylation <i>in vitro</i>. <i>FEBS Journal</i> , 2016, 283, 3371-3388.	2.2	63
75	Data processing pipeline for serial femtosecond crystallography at SACLA. <i>Journal of Applied Crystallography</i> , 2016, 49, 1035-1041.	1.9	76
76	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
77	Structural basis for amino acid export by DMT superfamily transporter YddG. <i>Nature</i> , 2016, 534, 417-420.	13.7	60
78	Mechanisms for Two-Step Proton Transfer Reactions in the Outward-Facing Form of MATE Transporter. <i>Biophysical Journal</i> , 2016, 110, 1346-1354.	0.2	16
79	Structure and Engineering of <i>Francisella novicida</i> Cas9. <i>Cell</i> , 2016, 164, 950-961.	13.5	296
80	t<scp>RNA</scp>â€dependent alanylation of diacylglycerol and phosphatidylglycerol in <scp><i>C</i></scp><i>orynebacterium glutamicum</i>. <i>Molecular Microbiology</i> , 2015, 98, 681-693.	1.2	13
81	Atomistic design of microbial opsin-based blue-shifted optogenetics tools. <i>Nature Communications</i> , 2015, 6, 7177.	5.8	78
82	Chimeras of Channelrhodopsin-1 and -2 from <i>Chlamydomonas reinhardtii</i> Exhibit Distinctive Light-induced Structural Changes from Channelrhodopsin-2. <i>Journal of Biological Chemistry</i> , 2015, 290, 11623-11634.	1.6	31
83	Structural basis for Na ⁺ transport mechanism by a light-driven Na ⁺ pump. <i>Nature</i> , 2015, 521, 48-53.	13.7	224
84	Outward- and inward-facing structures of a putative bacterial transition-metal transporter with homology to ferroportin. <i>Nature Communications</i> , 2015, 6, 8545.	5.8	103
85	Crystal Structure of <i>Staphylococcus aureus</i> Cas9. <i>Cell</i> , 2015, 162, 1113-1126.	13.5	357
86	Genome-scale transcriptional activation by an engineered CRISPR-Cas9 complex. <i>Nature</i> , 2015, 517, 583-588.	13.7	2,272
87	Structural basis for ion selectivity revealed by high-resolution crystal structure of Mg ²⁺ channel MgtE. <i>Nature Communications</i> , 2014, 5, 5374.	5.8	41
88	Structural Basis for Dynamic Mechanism of Proton-Coupled Symport by the Peptide Transporter POT. <i>Seibutsu Butsuri</i> , 2014, 54, 085-090.	0.0	1
89	Crystal structure of <i>Saccharomyces cerevisiae</i> mitochondrial GatFAB reveals a novel subunit assembly in tRNA-dependent amidotransferases. <i>Nucleic Acids Research</i> , 2014, 42, 6052-6063.	6.5	12
90	Crystal Structure of Cas9 in Complex with Guide RNA and Target DNA. <i>Cell</i> , 2014, 156, 935-949.	13.5	1,690

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91	Recurrent somatic mutations underlie corticotropin-independent Cushing's syndrome. <i>Science</i> , 2014, 344, 917-920.	6.0	177
92	Somatic RHOA mutation in angioimmunoblastic T cell lymphoma. <i>Nature Genetics</i> , 2014, 46, 171-175.	9.4	542
93	Water-Containing Hydrogen-Bonding Network in the Active Center of Channelrhodopsin. <i>Journal of the American Chemical Society</i> , 2014, 136, 3475-3482.	6.6	59
94	Structural Basis for Potent Inhibition of SIRT2 Deacetylase by a Macrocyclic Peptide Inducing Dynamic Structural Change. <i>Structure</i> , 2014, 22, 345-352.	1.6	79
95	Is zucchini a phosphodiesterase or a ribonuclease?. <i>Biomedical Journal</i> , 2014, 37, 369.	1.4	3
96	Structural Basis for the Counter-Transport Mechanism of a H ⁺ /Ca ²⁺ Exchanger. <i>Science</i> , 2013, 341, 168-172.	6.0	73
97	Crystal structure of channelrhodopsin, a light-gated cation channel - all cations lead through the monomer. <i>Biophysics (Nagoya-shi, Japan)</i> , 2013, 9, 57-61.	0.4	7
98	Crystal structure of Cex1p reveals the mechanism of tRNA trafficking between nucleus and cytoplasm. <i>Nucleic Acids Research</i> , 2013, 41, 3901-3914.	6.5	13
99	Recent structural studies on Dom34/aPelota and Hbs1/aEF1 \pm : important factors for solving general problems of ribosomal stall in translation. <i>Biophysics (Nagoya-shi, Japan)</i> , 2013, 9, 131-140.	0.4	5
100	Structural basis for dynamic mechanism of proton-coupled symport by the peptide transporter POT. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 11343-11348.	3.3	197
101	The Catalytic Domain of Topological Knot tRNA Methyltransferase (TrmH) Discriminates between Substrate tRNA and Nonsubstrate tRNA via an Induced-fit Process. <i>Journal of Biological Chemistry</i> , 2013, 288, 25562-25574.	1.6	32
102	Somatic G17V Rhoa Mutation Specifies Angioimmunoblastic T-Cell Lymphoma. <i>Blood</i> , 2013, 122, 815-815.	0.6	2
103	Crystal Structure of Channelrhodopsin, a Light-Gated Cation Channel. <i>Seibutsu Butsuri</i> , 2013, 53, 246-249.	0.0	0
104	Crystal structure of Enpp1, an extracellular glycoprotein involved in bone mineralization and insulin signaling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 16876-16881.	3.3	114
105	Crystal structure of the channelrhodopsin light-gated cation channel. <i>Nature</i> , 2012, 482, 369-374.	13.7	503
106	Spatial distribution of cytoplasmic domains of the Mg ²⁺ -transporter MgtE, in a solution lacking Mg ²⁺ , revealed by paramagnetic relaxation enhancement. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2012, 1824, 1129-1135.	1.1	5
107	Expression, purification, crystallization and preliminary X-ray crystallographic analysis of Enpp1. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 778-782.	0.7	16
108	Structural Basis for mRNA Surveillance by Archaeal Pelota and GTP-bound EF1 \pm Complex. <i>Seibutsu Butsuri</i> , 2012, 52, 182-185.	0.0	0

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109	The mechanism of protein export enhancement by the SecDF membrane component. <i>Biophysics</i> (Nagoya-shi, Japan), 2011, 7, 129-133.	0.4	7
110	Mg ²⁺ -dependent gating of bacterial MgtE channel underlies Mg ²⁺ homeostasis. <i>EMBO Journal</i> , 2009, 28, 3602-3612.	3.5	94
111	Crystallization and preliminary X-ray diffraction analysis of the full-length Mg ²⁺ transporter MgtE. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 682-684.	0.7	9
112	Crystal structure of the MgtE Mg ²⁺ transporter. <i>Nature</i> , 2007, 448, 1072-1075.	13.7	166
113	An enzyme with a deep trefoil knot for the active-site architecture. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 1129-1137.	2.5	122
114	Structural basis for recognition of the tra mRNA precursor by the Sex-lethal protein. <i>Nature</i> , 1999, 398, 579-585.	13.7	349
115	The identity determinants required for the discrimination between tRNA ^{Glu} and tRNA ^{Asp} by glutamyl-tRNA synthetase from <i>Escherichia coli</i> . <i>FEBS Journal</i> , 1999, 261, 354-360.	0.2	18
116	Structural Basis for the Molecular Evolution of Glutamyl-tRNA Synthetase.. <i>Seibutsu Butsuri</i> , 1997, 37, 321-325.	0.0	0
117	Aminoacyl-tRNA Synthetase : Structural Basis for the Substrate Recognition and the Molecular Evolution. <i>Nihon Kessho Gakkaishi</i> , 1996, 38, 60-67.	0.0	0
118	A three-dimensional structure model of the complex of glutamyl-tRNA synthetase and its cognate tRNA. <i>FEBS Letters</i> , 1995, 377, 77-81.	1.3	11
119	Recognition of the Anticodon Loop of tRNA ^{Ile} ₁ by Isoleucyl-tRNA Synthetase from <i>Escherichia coli</i> . <i>Nucleosides & Nucleotides</i> , 1994, 13, 1231-1237.	0.5	13
120	Glutamyl-tRNA synthetase from <i>Thermus thermophilus</i> HB8. Molecular cloning of the <i>gltX</i> gene and crystallization of the overproduced protein. <i>FEBS Journal</i> , 1992, 204, 465-472.	0.2	22
121	Cryo-EM Structure of the β_2 Adrenergic Receptor Reveals the Molecular Basis of Subtype Selectivity. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0