

Osamu Nureki

List of Publications by Year in descending order

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121
papers

14,350
citations

44042

48
h-index

22147

113
g-index

142
all docs

142
docs citations

142
times ranked

17877
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-scale transcriptional activation by an engineered CRISPR-Cas9 complex. <i>Nature</i> , 2015, 517, 583-588.	13.7	2,272
2	Crystal Structure of Cas9 in Complex with Guide RNA and Target DNA. <i>Cell</i> , 2014, 156, 935-949.	13.5	1,690
3	Engineered CRISPR-Cas9 nuclease with expanded targeting space. <i>Science</i> , 2018, 361, 1259-1262.	6.0	783
4	Crystal Structure of Cpf1 in Complex with Guide RNA and Target DNA. <i>Cell</i> , 2016, 165, 949-962.	13.5	552
5	Somatic RHOA mutation in angioimmunoblastic T cell lymphoma. <i>Nature Genetics</i> , 2014, 46, 171-175.	9.4	542
6	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
7	Crystal structure of the channelrhodopsin light-gated cation channel. <i>Nature</i> , 2012, 482, 369-374.	13.7	503
8	Crystal Structure of <i>Staphylococcus aureus</i> Cas9. <i>Cell</i> , 2015, 162, 1113-1126.	13.5	357
9	Engineered Cpf1 variants with altered PAM specificities. <i>Nature Biotechnology</i> , 2017, 35, 789-792.	9.4	351
10	A three-dimensional movie of structural changes in bacteriorhodopsin. <i>Science</i> , 2016, 354, 1552-1557.	6.0	350
11	Structural basis for recognition of the <i>tra</i> mRNA precursor by the Sex-lethal protein. <i>Nature</i> , 1999, 398, 579-585.	13.7	349
12	Structure and Engineering of <i>Francisella novicida</i> Cas9. <i>Cell</i> , 2016, 164, 950-961.	13.5	296
13	Cap-specific terminal N^6 -methylation of RNA by an RNA polymerase II-associated methyltransferase. <i>Science</i> , 2019, 363, .	6.0	262
14	Structural basis for Na^+ transport mechanism by a light-driven Na^+ pump. <i>Nature</i> , 2015, 521, 48-53.	13.7	224
15	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
16	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
17	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
18	Recurrent somatic mutations underlie corticotropin-independent Cushing's syndrome. <i>Science</i> , 2014, 344, 917-920.	6.0	177

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19	Crystal structure of the MgtE Mg ²⁺ transporter. <i>Nature</i> , 2007, 448, 1072-1075.	13.7	166
20	Activation mechanism of endothelin ETB receptor by endothelin-1. <i>Nature</i> , 2016, 537, 363-368.	13.7	148
21	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
22	Cryo-EM structures capture the transport cycle of the P4-ATPase flippase. <i>Science</i> , 2019, 365, 1149-1155.	6.0	143
23	Base editors for simultaneous introduction of C-to-T and A-to-G mutations. <i>Nature Biotechnology</i> , 2020, 38, 865-869.	9.4	137
24	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
25	Amplification-free RNA detection with CRISPR-Cas13. <i>Communications Biology</i> , 2021, 4, 476.	2.0	119
26	Crystal Structure of Silkworm PIWI-Clade Argonaute Siwi Bound to piRNA. <i>Cell</i> , 2016, 167, 484-497.e9.	13.5	116
27	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
28	Structural insights into tetraspanin CD9 function. <i>Nature Communications</i> , 2020, 11, 1606.	5.8	114
29	Crystal structure of the red light-activated channelrhodopsin Chrimson. <i>Nature Communications</i> , 2018, 9, 3949.	5.8	112
30	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
31	Structural insights into cGAMP degradation by Ecto-nucleotide pyrophosphatase phosphodiesterase 1. <i>Nature Communications</i> , 2018, 9, 4424.	5.8	108
32	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
33	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
34	Structural insights into ligand recognition by the lysophosphatidic acid receptor LPA6. <i>Nature</i> , 2017, 548, 356-360.	13.7	101
35	Structure of the miniature type V-F CRISPR-Cas effector enzyme. <i>Molecular Cell</i> , 2021, 81, 558-570.e3.	4.5	95
36	Mg ²⁺ -dependent gating of bacterial MgtE channel underlies Mg ²⁺ homeostasis. <i>EMBO Journal</i> , 2009, 28, 3602-3612.	3.5	94

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37	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
38	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
39	Atomistic design of microbial opsin-based blue-shifted optogenetics tools. <i>Nature Communications</i> , 2015, 6, 7177.	5.8	78
40	Data processing pipeline for serial femtosecond crystallography at SACLA. <i>Journal of Applied Crystallography</i> , 2016, 49, 1035-1041.	1.9	76
41	Capturing an initial intermediate during the P450nor enzymatic reaction using time-resolved XFEL crystallography and caged-substrate. <i>Nature Communications</i> , 2017, 8, 1585.	5.8	74
42	Structural Basis for the Counter-Transport Mechanism of a H ⁺ /Ca ²⁺ Exchanger. <i>Science</i> , 2013, 341, 168-172.	6.0	73
43	Structural basis for channel conduction in the pump-like channelrhodopsin ChRmine. <i>Cell</i> , 2022, 185, 672-689.e23.	13.5	72
44	Crystal structure of heliorhodopsin. <i>Nature</i> , 2019, 574, 132-136.	13.7	71
45	Taste transduction and channel synapses in taste buds. <i>Pflügers Archiv European Journal of Physiology</i> , 2021, 473, 3-13.	1.3	70
46	ENPP1 processes protein ADP-ribosylation <i>in vitro</i> . <i>FEBS Journal</i> , 2016, 283, 3371-3388.	2.2	63
47	Structural basis for amino acid export by DMT superfamily transporter YddG. <i>Nature</i> , 2016, 534, 417-420.	13.7	60
48	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
49	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
50	Structural and functional insights into IZUMO1 recognition by JUNO in mammalian fertilization. <i>Nature Communications</i> , 2016, 7, 12198.	5.8	58
51	Structure of the triose-phosphate/phosphate translocator reveals the basis of substrate specificity. <i>Nature Plants</i> , 2017, 3, 825-832.	4.7	51
52	Crystal structure of plant vacuolar iron transporter VIT1. <i>Nature Plants</i> , 2019, 5, 308-315.	4.7	51
53	The structure of lipid nanodisc-reconstituted TRPV3 reveals the gating mechanism. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 645-652.	3.6	51
54	Transport Cycle of Plasma Membrane Flippase ATP11C by Cryo-EM. <i>Cell Reports</i> , 2020, 32, 108208.	2.9	50

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55	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
56	Crystal structure of <i>Drosophila</i> Piwi. <i>Nature Communications</i> , 2020, 11, 858.	5.8	42
57	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
58	Time-resolved serial femtosecond crystallography reveals early structural changes in channelrhodopsin. <i>ELife</i> , 2021, 10, .	2.8	41
59	Real-time observation of flexible domain movements in CRISPR-Cas9. <i>EMBO Journal</i> , 2018, 37, .	3.5	39
60	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.	3.6	39
61	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
62	Cryo-EM structure of the volume-regulated anion channel LRRC8D isoform identifies features important for substrate permeation. <i>Communications Biology</i> , 2020, 3, 240.	2.0	35
63	Structural basis of gating modulation of Kv4 channel complexes. <i>Nature</i> , 2021, 599, 158-164.	13.7	35
64	Resonance Raman Investigation of the Chromophore Structure of Heliorhodopsins. <i>Journal of Physical Chemistry Letters</i> , 2018, 9, 6431-6436.	2.1	33
65	Crystal structure of human endothelin ETB receptor in complex with peptide inverse agonist IRL2500. <i>Communications Biology</i> , 2019, 2, 236.	2.0	33
66	Structural basis for the promiscuous PAM recognition by <i>Corynebacterium diphtheriae</i> Cas9. <i>Nature Communications</i> , 2019, 10, 1968.	5.8	33
67	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
68	Cryo-EM structures of calcium homeostasis modulator channels in diverse oligomeric assemblies. <i>Science Advances</i> , 2020, 6, eaba8105.	4.7	32
69	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
70	Cryo-EM structure of the human MT1-Gi signaling complex. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 694-701.	3.6	31
71	Structural insights into the mechanism of rhodopsin phosphodiesterase. <i>Nature Communications</i> , 2020, 11, 5605.	5.8	30
72	Automated amplification-free digital RNA detection platform for rapid and sensitive SARS-CoV-2 diagnosis. <i>Communications Biology</i> , 2022, 5, .	2.0	28

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73	Crystal structure of schizorhodopsin reveals mechanism of inward proton pumping. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	26
74	Ultrafast Dynamics of Heliorhodopsins. Journal of Physical Chemistry B, 2019, 123, 2507-2512.	1.2	24
75	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
76	Glutamyl-tRNA synthetase from Thermus thermophilus HB8. Molecular cloning of the gltX gene and crystallization of the overproduced protein. FEBS Journal, 1992, 204, 465-472.	0.2	22
77	Spectroscopic study of the transmembrane domain of a rhodopsin-phosphodiesterase fusion protein from a unicellular eukaryote. Journal of Biological Chemistry, 2019, 294, 3432-3443.	1.6	22
78	Cryo-EM reveals mechanistic insights into lipid-facilitated polyamine export by human ATP13A2. Molecular Cell, 2021, 81, 4799-4809.e5.	4.5	22
79	Cryo-EM structure of the β 2-adrenergic receptor reveals the molecular basis of subtype selectivity. Molecular Cell, 2021, 81, 3205-3215.e5.	4.5	21
80	Structure of the Dicer-2-R2D2 heterodimer bound to a small RNA duplex. Nature, 2022, 607, 393-398.	13.7	20
81	Consensus mutagenesis approach improves the thermal stability of system x _c ⁺ transporter, xCT, and enables cryo-EM analyses. Protein Science, 2020, 29, 2398-2407.	3.1	19
82	Crystal structure of human endothelin ETB receptor in complex with sarafotoxin S6b. Biochemical and Biophysical Research Communications, 2020, 528, 383-388.	1.0	19
83	Engineered Campylobacter jejuni Cas9 variant with enhanced activity and broader targeting range. Communications Biology, 2022, 5, 211.	2.0	19
84	The identity determinants required for the discrimination between tRNA ^{Glu} and tRNA ^{Asp} by glutamyl-tRNA synthetase from Escherichia coli. FEBS Journal, 1999, 261, 354-360.	0.2	18
85	Free Energy Landscape for the Entire Transport Cycle of Triose-Phosphate/Phosphate Translocator. Structure, 2018, 26, 1284-1296.e4.	1.6	17
86	Expression, purification, crystallization and preliminary X-ray crystallographic analysis of Enpp1. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 778-782.	0.7	16
87	Mechanisms for Two-Step Proton Transfer Reactions in the Outward-Facing Form of MATE Transporter. Biophysical Journal, 2016, 110, 1346-1354.	0.2	16
88	An Atomistic Model of a Precursor State of Light-Induced Channel Opening of Channelrhodopsin. Biophysical Journal, 2018, 115, 1281-1291.	0.2	15
89	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
90	Structural basis for unique color tuning mechanism in heliorhodopsin. Biochemical and Biophysical Research Communications, 2020, 533, 262-267.	1.0	14

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91	Crystallization of the human tetraspanin protein CD9. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2019, 75, 254-259.	0.4	14
92	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
93	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
94	tRNA-dependent alanylation of diacylglycerol and phosphatidylglycerol in <i>Corynebacterium glutamicum</i> . <i>Molecular Microbiology</i> , 2015, 98, 681-693.	1.2	13
95	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
96	Structure of the type V-C CRISPR-Cas effector enzyme. <i>Molecular Cell</i> , 2022, 82, 1865-1877.e4.	4.5	12
97	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
98	Peripheral tolerance by Treg via constraining OX40 signal in autoreactive T cells against desmoglein 3, a target antigen in pemphigus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, e2026763118.	3.3	11
99	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
100	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
101	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
102	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
103	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
104	Recent Advances in the Structural Biology of the Volume-Regulated Anion Channel LRRC8. <i>Frontiers in Pharmacology</i> , 2022, 13, .	1.6	8
105	The mechanism of protein export enhancement by the SecDF membrane component. <i>Biophysics (Nagoya-shi, Japan)</i> , 2011, 7, 129-133.	0.4	7
106	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
107	Cell-Free Synthesis of Human Endothelin Receptors and Its Application to Ribosome Display. <i>Analytical Chemistry</i> , 2022, 94, 3831-3839.	3.2	6
108	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

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109	Recent structural studies on Dom34/aPelota and Hbs1/aEF1±: important factors for solving general problems of ribosomal stall in translation. Biophysics (Nagoya-shi, Japan), 2013, 9, 131-140.	0.4	5
110	Vibrational and Molecular Properties of Mg ²⁺ Binding and Ion Selectivity in the Magnesium Channel MgtE. Journal of Physical Chemistry B, 2018, 122, 9681-9696.	1.2	5
111	Cryo-EM structures of thylakoid-located voltage-dependent chloride channel VCCN1. Nature Communications, 2022, 13, 2505.	5.8	5
112	Is zucchini a phosphodiesterase or a ribonuclease?. Biomedical Journal, 2014, 37, 369.	1.4	3
113	Lateral access mechanism of LPA receptor probed by molecular dynamics simulation. PLoS ONE, 2022, 17, e0263296.	1.1	3
114	Somatic G17V Rhoa Mutation Specifies Angioimmunoblastic T-Cell Lymphoma. Blood, 2013, 122, 815-815.	0.6	2
115	Structural Basis for Dynamic Mechanism of Proton-Coupled Symport by the Peptide Transporter POT. Seibutsu Butsuri, 2014, 54, 085-090.	0.0	1
116	Cex1 is a component of the COPI intracellular trafficking machinery. Biology Open, 2021, 10, .	0.6	0
117	Structural Basis for mRNA Surveillance by Archaeal Pelota and GTP-bound EF1± Complex. Seibutsu Butsuri, 2012, 52, 182-185.	0.0	0
118	Crystal Structure of Channelrhodopsin, a Light-Gated Cation Channel. Seibutsu Butsuri, 2013, 53, 246-249.	0.0	0
119	Aminoacyl-tRNA Synthetase : Structural Basis for the Substrate Recognition and the Molecular Evolution. Nihon Kessho Gakkaishi, 1996, 38, 60-67.	0.0	0
120	Structural Basis for the Molecular Evolution of Glutamyl-tRNA Synthetase.. Seibutsu Butsuri, 1997, 37, 321-325.	0.0	0
121	Cryo-EM Structure of the Î²3 Adrenergic Receptor Reveals the Molecular Basis of Subtype Selectivity. SSRN Electronic Journal, 0, , .	0.4	0