Osamu Nureki

List of Articles by Year
in descending order

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319 peer-reviewed articles	23,267 peer-reviewed citations	10449 72 peer-reviewed h-index	127843 6.26 score
335 documents	27894 doc citations	10290 78 h-index	57789 citing authors

#	Article	IF	Citations
1	A mini-hairpin shaped nascent peptide blocks translation termination by a distinct mechanism. Nature Communications, 2025, 16, .	10.8	6
2	AAV-mediated base editing restores cochlear gap junction in GJB2 dominant-negative mutation-associated syndromic hearing loss model. JCI Insight, 2025, 10, .	3.7	10
3	Structure of a lasso peptide bound ETB receptor provides insights into the mechanism of GPCR inverse agonism. Nature Communications, 2025, 16, .	10.8	4
4	Structural basis for target DNA cleavage and guide RNA processing by CRISPR-Casλ2. Communications Biology, 2025, 8, .	3.1	4
5	Cryo-EM structure of a blue-shifted channelrhodopsin from Klebsormidium nitens. Nature Communications, 2025, 16, .	10.8	7
6	Structural insights into ligand recognition and G protein preferences across histamine receptors. Communications Biology, 2025, 8, .	3.1	4
7	Optimizing cryo-EM structural analysis of Gi-coupling receptors via engineered Gt and Nb35 application. Biochemical and Biophysical Research Communications, 2024, 693, 149361.	1.5	6
8	Molecular insights into atypical modes of β-arrestin interaction with seven transmembrane receptors. Science, 2024, 383, 101-108.	26.1	34
9	Structural basis for lysophosphatidylserine recognition by GPR34. Nature Communications, 2024, 15, .	10.8	19
10	Bicarbonate signalling via G protein-coupled receptor regulates ischaemia-reperfusion injury. Nature Communications, 2024, 15, .	10.8	19
11	Structure of full-length ERGIC-53 in complex with MCFD2 for cargo transport. Nature Communications, 2024, 15, .	10.8	11
12	Structure of the human Bre1 complex bound to the nucleosome. Nature Communications, 2024, 15, .	10.8	18
13	Cryo-EM advances in GPCR structure determination. Journal of Biochemistry, 2024, 176, 1-10.	1.4	32
14	Melatonin receptor structure and signaling. Journal of Pineal Research, 2024, 76, .	4.3	49
15	Cryo-EM structure of I domain-containing integrin αEβ7. Biochemical and Biophysical Research Communications, 2024, 721, 150121.	1.5	3
16	Structural basis for pegRNA-guided reverse transcription by a prime editor. Nature, 2024, 631, 224-231.	30.6	41
17	PAM-flexible Engineered FnCas9 variants for robust and ultra-precise genome editing and diagnostics. Nature Communications, 2024, 15, .	10.8	41
18	Structure and engineering of Brevibacillus laterosporus Cas9. Communications Biology, 2024, 7, .	3.1	3

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19	Structure and dynamics of the pyroglutamylated RF-amide peptide QRFP receptor GPR103. Nature Communications, 2024, 15, .	10.8	12
20	Dimeric transport mechanism of human vitamin C transporter SVCT1. Nature Communications, 2024, 15, .	10.8	20
21	Molecular mechanism of the endothelin receptor type B interactions with Gs, Gi, and Gq. Structure, 2024, 32, 1632-1639.e4.	2.4	5
22	The high-light-sensitivity mechanism and optogenetic properties of the bacteriorhodopsin-like channelrhodopsin GtCCR4. Molecular Cell, 2024, 84, 3530-3544.e6.	8.6	7
23	Systemic delivery of engineered compact AsCas12f by a positive-strand RNA virus vector enables highly efficient targeted mutagenesis in plants. Frontiers in Plant Science, 2024, 15, .	3.0	16
24	Verification of the interaction between human bitter taste receptor T2R46 and polyphenols; Computational chemistry approach. Current Research in Food Science, 2024, 9, 100914.	4.9	8
25	Structural mechanisms of potent lysophosphatidic acid receptor 1 activation by nonlipid basic agonists. Communications Biology, 2024, 7, .	3.1	7
26	Cure of Congenital Purpura Fulminans via Expression of Engineered Protein C Through Neonatal Genome Editing in Mice. Arteriosclerosis, Thrombosis, and Vascular Biology, 2024, 44, 2616-2627.	4.3	4
27	Structural insights into the agonist selectivity of the adenosine A3 receptor. Nature Communications, 2024, 15, .	10.8	11
28	Structural insights into how Cas9 targets nucleosomes. Nature Communications, 2024, 15, .	10.8	10
29	Cryo-EM structure of the transposon-associated TnpB enzyme. Nature, 2023, 616, 390-397.	30.6	105
30	Phototrophy by antenna-containing rhodopsin pumps in aquatic environments. Nature, 2023, 615, 535-540.	30.6	46
31	Genome editing in rice mediated by miniature size Cas nuclease SpCas12f. Frontiers in Genome Editing, 2023, 5, .	3.1	32
32	PAM-flexible Cas9-mediated base editing of a hemophilia B mutation in induced pluripotent stem cells. Communications Medicine, 2023, 3, .	3.1	28
33	Class B1 GPCR activation by an intracellular agonist. Nature, 2023, 618, 1085-1093.	30.6	56
34	Mechanistic and evolutionary insights into a type V-M CRISPR–Cas effector enzyme. Nature Structural and Molecular Biology, 2023, 30, 1172-1182.	5.8	34
35	Structural insights into endothelin receptor signalling. Journal of Biochemistry, 2023, 174, 317-325.	1.4	25
36	SOCS3 deletion in effector T cells confers an anti-tumorigenic role of IL-6 to the pro-tumorigenic cytokine. Cell Reports, 2023, 42, 112940.	4.4	21

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37	An AsCas12f-based compact genome-editing tool derived by deep mutational scanning and structural analysis. Cell, 2023, 186, 4920-4935.e23.	23.4	126
38	Genome editing of patient-derived iPSCs identifies a deep intronic variant causing aberrant splicing in hemophilia A. Blood Advances, 2023, 7, 7017-7027.	3.7	3
39	Time-resolved serial crystallography to track the dynamics of carbon monoxide in the active site of cytochrome c oxidase. Science Advances, 2023, 9, .	8.1	14
40	Dual allosteric modulation of voltage and calcium sensitivities of the Slo1-LRRC channel complex. Molecular Cell, 2023, 83, 4555-4569.e4.	8.6	19
41	Transport and inhibition mechanism of the human SGLT2–MAP17 glucose transporter. Nature Structural and Molecular Biology, 2023, 31, 159-169.	5.8	63
42	Structural basis for channel conduction in the pump-like channelrhodopsin ChRmine. Cell, 2022, 185, 672-689.e23.	23.4	157
43	Lateral access mechanism of LPA receptor probed by molecular dynamics simulation. PLoS ONE, 2022, 17, e0263296.	1.5	9
44	Cell-Free Synthesis of Human Endothelin Receptors and Its Application to Ribosome Display. Analytical Chemistry, 2022, 94, 3831-3839.	5.2	12
45	Conformational alterations in unidirectional ion transport of a light-driven chloride pump revealed using X-ray free electron lasers. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	5.2	23
46	Engineered Campylobacter jejuni Cas9 variant with enhanced activity and broader targeting range. Communications Biology, 2022, 5, .	3.1	44
47	Structure of the type V-C CRISPR-Cas effector enzyme. Molecular Cell, 2022, 82, 1865-1877.e4.	8.6	39
48	Cryo-EM structures of the β3 adrenergic receptor bound to solabegron and isoproterenol. Biochemical and Biophysical Research Communications, 2022, 611, 158-164.	1.5	29
49	Recent Advances in the Structural Biology of the Volume-Regulated Anion Channel LRRC8. Frontiers in Pharmacology, 2022, 13, .	2.6	16
50	Cryo-EM structures of thylakoid-located voltage-dependent chloride channel VCCN1. Nature Communications, 2022, 13, .	10.8	15
51	Automated amplification-free digital RNA detection platform for rapid and sensitive SARS-CoV-2 diagnosis. Communications Biology, 2022, 5, .	3.1	71
52	Structure of the Dicer-2–R2D2 heterodimer bound to a small RNA duplex. Nature, 2022, 607, 393-398.	30.6	63
53	Mechanistic insights into intramembrane proteolysis by E. coli site-2 protease homolog RseP. Science Advances, 2022, 8, .	8.1	26
54	Structural insights into inhibitory mechanism of human excitatory amino acid transporter EAAT2. Nature Communications, 2022, 13, .	10.8	42

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55	Structure of the active Gi-coupled human lysophosphatidic acid receptor 1 complexed with a potent agonist. Nature Communications, 2022, 13, .	10.8	39
56	Cryo-EM structures of thermostabilized prestin provide mechanistic insights underlying outer hair cell electromotility. Nature Communications, 2022, 13, .	10.8	46
57	Structural Basis for Activation Mechanism of MT₁. Seibutsu Butsuri, 2022, 62, 341-344.	0.0	0
58	Structure of the miniature type V-F CRISPR-Cas effector enzyme. Molecular Cell, 2021, 81, 558-570.e3.	8.6	192
59	Conserved binding site in the N-lobe of prokaryotic MATE transporters suggests a role for Na+ in ion-coupled drug efflux. Journal of Biological Chemistry, 2021, 296, 100262.	1.3	10
60	Cex1 is a component of the COPI intracellular trafficking machinery. Biology Open, 2021, 10, .	0.7	1
61	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, .	5.2	43
62	Amplification-free RNA detection with CRISPR–Cas13. Communications Biology, 2021, 4, .	3.1	235
63	Precise CAG repeat contraction in a Huntington's Disease mouse model is enabled by gene editing with SpCas9-NG. Communications Biology, 2021, 4, .	3.1	36
64	Cryo-EM structure of the β3-adrenergic receptor reveals the molecular basis of subtype selectivity. Molecular Cell, 2021, 81, 3205-3215.e5.	8.6	50
65	Cryo-EM structure of the human MT1–Gi signaling complex. Nature Structural and Molecular Biology, 2021, 28, 694-701.	5.8	63
66	Structural basis of gating modulation of Kv4 channel complexes. Nature, 2021, 599, 158-164.	30.6	82
67	Structural basis of the regulation of the normal and oncogenic methylation of nucleosomal histone H3 Lys36 by NSD2. Nature Communications, 2021, 12, .	10.8	42
68	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, .	5.2	31
69	Cryo-EM reveals mechanistic insights into lipid-facilitated polyamine export by human ATP13A2. Molecular Cell, 2021, 81, 4799-4809.e5.	8.6	44
70	Generation of novel <i>Il2rg</i>-knockout mice with clustered regularly interspaced short palindromic repeats (CRISPR) and Cas9. Experimental Animals, 2020, 69, 189-198.	12.5	6
71	Structural biology of the multidrug and toxic compound extrusion superfamily transporters. Biochimica Et Biophysica Acta - Biomembranes, 2020, 1862, 183154.	1.5	91
72	TMC1 and TMC2 Proteins Are Pore-Forming Subunits of Mechanosensitive Ion Channels. Neuron, 2020, 105, 310-321.e3.	8.2	164

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73	Structural basis for unique color tuning mechanism in heliorhodopsin. Biochemical and Biophysical Research Communications, 2020, 533, 262-267.	1.5	21
74	Consensus mutagenesis approach improves the thermal stability of system xc− transporter, xCT, and enables cryo-EM analyses. Protein Science, 2020, 29, 2398-2407.	3.5	34
75	Structure of the human secretin receptor coupled to an engineered heterotrimeric G protein. Biochemical and Biophysical Research Communications, 2020, 533, 861-866.	1.5	23
76	Transport Cycle of Plasma Membrane Flippase ATP11C by Cryo-EM. Cell Reports, 2020, 32, 108208.	4.4	75
77	Cryo-EM structures of calcium homeostasis modulator channels in diverse oligomeric assemblies. Science Advances, 2020, 6, .	8.1	51
78	Structural insights into the mechanism of rhodopsin phosphodiesterase. Nature Communications, 2020, 11, .	10.8	41
79	Cryo-EM structure of the volume-regulated anion channel LRRC8D isoform identifies features important for substrate permeation. Communications Biology, 2020, 3, .	3.1	57
80	The structure of lipid nanodisc-reconstituted TRPV3 reveals the gating mechanism. Nature Structural and Molecular Biology, 2020, 27, 645-652.	5.8	84
81	Cryo-EM structure of the human PAC1 receptor coupled to an engineered heterotrimeric G protein. Nature Structural and Molecular Biology, 2020, 27, 274-280.	5.8	54
82	Crystal structure of human endothelin ETB receptor in complex with sarafotoxin S6b. Biochemical and Biophysical Research Communications, 2020, 528, 383-388.	1.5	26
83	Structural insights into tetraspanin CD9 function. Nature Communications, 2020, 11, .	10.8	202
84	Taste transduction and channel synapses in taste buds. Pflugers Archiv European Journal of Physiology, 2020, 473, 3-13.	1.7	138
85	Crystal structure of Drosophila Piwi. Nature Communications, 2020, 11, .	10.8	76
86	Base editors for simultaneous introduction of C-to-T and A-to-G mutations. Nature Biotechnology, 2020, 38, 865-869.	19.7	200
87	Cryo-EM structures capture the transport cycle of the P4-ATPase flippase. Science, 2019, 365, 1149-1155.	26.1	195
88	Crystal structure of human endothelin ETB receptor in complex with peptide inverse agonist IRL2500. Communications Biology, 2019, 2, .	3.1	46
89	Cryo-EM structure of the human L-type amino acid transporter 1 in complex with glycoprotein CD98hc. Nature Structural and Molecular Biology, 2019, 26, 510-517.	5.8	171
90	Structural basis for the promiscuous PAM recognition by Corynebacterium diphtheriae Cas9. Nature Communications, 2019, 10, .	10.8	51

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91	Ultrafast Dynamics of Heliorhodopsins. Journal of Physical Chemistry B, 2019, 123, 2507-2512.	2.0	30
92	Crystal structure of plant vacuolar iron transporter VIT1. Nature Plants, 2019, 5, 308-315.	8.0	72
93	Spectroscopic study of the transmembrane domain of a rhodopsin–phosphodiesterase fusion protein from a unicellular eukaryote. Journal of Biological Chemistry, 2019, 294, 3432-3443.	1.3	29
94	Crystal structure of heliorhodopsin. Nature, 2019, 574, 132-136.	30.6	104
95	Structural Basis of H+-Dependent Conformational Change in a Bacterial MATE Transporter. Structure, 2019, 27, 293-301.e3.	2.4	27
96	Cap-specific terminal N 6 -methylation of RNA by an RNA polymerase II–associated methyltransferase. Science, 2019, 363, .	26.1	368
97	Crystallization of the human tetraspanin protein CD9. Acta Crystallographica Section F, Structural Biology Communications, 2019, 75, 254-259.	0.6	18
98	Structural basis for oligomerization of the prokaryotic peptide transporter PepT So2. Acta Crystallographica Section F, Structural Biology Communications, 2019, 75, 348-358.	0.6	12
99	Structural basis for molecular mechanisms of novel membrane transporters and channels. Proceedings for Annual Meeting of the Japanese Pharmacological Society, 2019, 92, 1-SL04.	0.0	0
100	Real-time observation of flexible domain movements in CRISPR–Cas9. EMBO Journal, 2018, 37, .	5.1	48
101	Crystal structures of human ETB receptor provide mechanistic insight into receptor activation and partial activation. Nature Communications, 2018, 9, .	10.8	79
102	Crystal structure of the red light-activated channelrhodopsin Chrimson. Nature Communications, 2018, 9, .	10.8	164
103	Vibrational and Molecular Properties of Mg2+ Binding and Ion Selectivity in the Magnesium Channel MgtE. Journal of Physical Chemistry B, 2018, 122, 9681-9696.	2.0	5
104	An Atomistic Model of a Precursor State of Light-Induced Channel Opening of Channelrhodopsin. Biophysical Journal, 2018, 115, 1281-1291.	1.5	22
105	Structural insights into cGAMP degradation by Ecto-nucleotide pyrophosphatase phosphodiesterase 1. Nature Communications, 2018, 9, .	10.8	174
106	Resonance Raman Investigation of the Chromophore Structure of Heliorhodopsins. Journal of Physical Chemistry Letters, 2018, 9, 6431-6436.	2.9	42
107	DUSP10 constrains innate IL-33-mediated cytokine production in ST2hi memory-type pathogenic Th2 cells. Nature Communications, 2018, 9, .	10.8	46
108	Free Energy Landscape for the Entire Transport Cycle of Triose-Phosphate/Phosphate Translocator. Structure, 2018, 26, 1284-1296.e4.	2.4	22

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109	Cryo-EM structures of the human volume-regulated anion channel LRRC8. Nature Structural and Molecular Biology, 2018, 25, 797-804.	5.8	131
110	Genome editing in plants by engineered CRISPR–Cas9 recognizing NG PAM. Nature Plants, 2018, 5, 14-17.	8.0	192
111	Crystal structure of the Agrobacterium tumefaciens type VI effector–immunity complex. Acta Crystallographica Section F, Structural Biology Communications, 2018, 74, 810-816.	0.6	5
112	Light-induced structural changes and the site of O=O bond formation in PSII caught by XFEL. Nature, 2017, 543, 131-135.	30.6	618
113	Cyclic GMP–AMP as an Endogenous Second Messenger in Innate Immune Signaling by Cytosolic DNA. Annual Review of Biochemistry, 2017, 86, 541-566.	14.0	246
114	Applications of the CRISPR-Cas9 system in kidney research. Kidney International, 2017, 92, 324-335.	4.2	21
115	Structures and mechanisms of CRISPR RNA-guided effector nucleases. Current Opinion in Structural Biology, 2017, 43, 68-78.	4.6	94
116	Structural Basis for the Altered PAM Recognition by Engineered CRISPR-Cpf1. Molecular Cell, 2017, 67, 139-147.e2.	8.6	113
117	Structural insights into the nucleotide base specificity of P2X receptors. Scientific Reports, 2017, 7, .	2.7	51
118	Crystal Structure of the Minimal Cas9 from Campylobacter jejuni Reveals the Molecular Diversity in the CRISPR-Cas9 Systems. Molecular Cell, 2017, 65, 1109-1121.e3.	8.6	187
119	Structure of the triose-phosphate/phosphate translocator reveals the basis of substrate specificity. Nature Plants, 2017, 3, 825-832.	8.0	72
120	Structural insights into the competitive inhibition of the ATP-gated P2X receptor channel. Nature Communications, 2017, 8, .	10.8	99
121	ATP-dependent modulation of MgtE in Mg2+ homeostasis. Nature Communications, 2017, 8, .	10.8	82
122	Structural insights into ligand recognition by the lysophosphatidic acid receptor LPA6. Nature, 2017, 548, 356-360.	30.6	123
123	X-ray structures of endothelin ETB receptor bound to clinical antagonist bosentan and its analog. Nature Structural and Molecular Biology, 2017, 24, 758-764.	5.8	98
124	Structural Basis for the Canonical and Non-canonical PAM Recognition by CRISPR-Cpf1. Molecular Cell, 2017, 67, 633-645.e3.	8.6	320
125	Structural basis for xenobiotic extrusion by eukaryotic MATE transporter. Nature Communications, 2017, 8, .	10.8	99
126	Capturing an initial intermediate during the P450nor enzymatic reaction using time-resolved XFEL crystallography and caged-substrate. Nature Communications, 2017, 8, .	10.8	106

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127	Real-space and real-time dynamics of CRISPR-Cas9 visualized by high-speed atomic force microscopy. Nature Communications, 2017, 8, .	10.8	230
128	Engineered Cpf1 variants with altered PAM specificities. Nature Biotechnology, 2017, 35, 789-792.	19.7	447
129	Structure Based Engineering of Blue-shifted Optogenetics Tools. Seibutsu Butsuri, 2017, 57, 196-199.	0.0	0
130	SecY-SecA fusion protein retains the ability to mediate protein transport. PLoS ONE, 2017, 12, e0183434.	1.5	12
131	Crystal structures of the TRIC trimeric intracellular cation channel orthologues. Cell Research, 2016, 26, 1288-1301.	10.1	27
132	LCP crystallization and X-ray diffraction analysis of VcmN, a MATE transporter fromVibrio cholerae. Acta Crystallographica Section F, Structural Biology Communications, 2016, 72, 552-557.	0.6	5
133	A three-dimensional movie of structural changes in bacteriorhodopsin. Science, 2016, 354, 1552-1557.	26.1	423
134	Structural and functional insights into IZUMO1 recognition by JUNO in mammalian fertilization. Nature Communications, 2016, 7, .	10.8	88
135	Structural basis for specific inhibition of Autotaxin by a DNA aptamer. Nature Structural and Molecular Biology, 2016, 23, 395-401.	5.8	69
136	Crystal Structure of Cpf1 in Complex with Guide RNA and Target DNA. Cell, 2016, 165, 949-962.	23.4	784
137	Activation mechanism of endothelin ETB receptor by endothelin-1. Nature, 2016, 537, 363-368.	30.6	173
138	Role of Asn112 in a Light-Driven Sodium Ion-Pumping Rhodopsin. Biochemistry, 2016, 55, 5790-5797.	1.5	30
139	Crystal Structure of Silkworm PIWI-Clade Argonaute Siwi Bound to piRNA. Cell, 2016, 167, 484-497.e9.	23.4	160
140	ENPP1 processes protein ADP-ribosylation in vitro. FEBS Journal, 2016, 283, 3371-3388.	3.3	75
141	Data processing pipeline for serial femtosecond crystallography at SACLA. Journal of Applied Crystallography, 2016, 49, 1035-1041.	1.7	97
142	Crystal structure of the plant receptor-like kinase TDR in complex with the TDIF peptide. Nature Communications, 2016, 7, .	10.8	81
143	Structural and Functional Analysis of DDX41: a bispecific immune receptor for DNA and cyclic dinucleotide. Scientific Reports, 2016, 6, .	2.7	51
144	Structural basis for amino acid export by DMT superfamily transporter YddG. Nature, 2016, 534, 417-420.	30.6	85

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145	Mechanisms for Two-Step Proton Transfer Reactions in the Outward-Facing Form of MATE Transporter. Biophysical Journal, 2016, 110, 1346-1354.	1.5	18
146	Structural Insights into Divalent Cation Modulations of ATP-Gated P2X Receptor Channels. Cell Reports, 2016, 14, 932-944.	4.4	76
147	Mutant of a Light-Driven Sodium Ion Pump Can Transport Cesium Ions. Journal of Physical Chemistry Letters, 2016, 7, 51-55.	2.9	46
148	Structural Basis for the Altered PAM Specificities of Engineered CRISPR-Cas9. Molecular Cell, 2016, 61, 886-894.	8.6	151
149	Structure and Engineering of Francisella novicida Cas9. Cell, 2016, 164, 950-961.	23.4	360
150	tRNA-dependent alanylation of diacylglycerol and phosphatidylglycerol inCorynebacterium glutamicum. Molecular Microbiology, 2015, 98, 681-693.	1.8	18
151	Molecular Dynamics of Channelrhodopsin at the Early Stages of Channel Opening. PLoS ONE, 2015, 10, e0131094.	1.5	38
152	Atomistic design of microbial opsin-based blue-shifted optogenetics tools. Nature Communications, 2015, 6, .	10.8	95
153	Structural basis for the facilitative diffusion mechanism by SemiSWEET transporter. Nature Communications, 2015, 6, .	10.8	92
154	Structural Basis for the Catalytic Mechanism of DncV, Bacterial Homolog of Cyclic GMP-AMP Synthase. Structure, 2015, 23, 843-850.	2.4	34
155	Chimeras of Channelrhodopsin-1 and -2 from Chlamydomonas reinhardtii Exhibit Distinctive Light-induced Structural Changes from Channelrhodopsin-2. Journal of Biological Chemistry, 2015, 290, 11623-11634.	1.3	33
156	Structural basis for Na+ transport mechanism by a light-driven Na+ pump. Nature, 2015, 521, 48-53.	30.6	242
157	Hydrophilic microenvironment required for the channel-independent insertase function of YidC protein. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 5063-5068.	5.2	41
158	Structural basis for dynamic mechanism of nitrate/nitrite antiport by NarK. Nature Communications, 2015, 6, .	10.8	78
159	Outward- and inward-facing structures of a putative bacterial transition-metal transporter with homology to ferroportin. Nature Communications, 2015, 6, .	10.8	117
160	Crystal Structure of Staphylococcus aureus Cas9. Cell, 2015, 162, 1113-1126.	23.4	446
161	Structural basis for ion selectivity revealed by high-resolution crystal structure of Mg2+ channel MgtE. Nature Communications, 2014, 5, .	10.8	52
162	Structural Basis for Dynamic Mechanism of Proton-Coupled Symport by the Peptide Transporter POT. Seibutsu Butsuri, 2014, 54, 085-090.	0.0	1

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163	Crystal structure of Saccharomyces cerevisiae mitochondrial GatFAB reveals a novel subunit assembly in tRNA-dependent amidotransferases. Nucleic Acids Research, 2014, 42, 6052-6063.	10.7	15
164	The non-canonical hydroxylase structure of YfcM reveals a metal ion-coordination motif required for EF-P hydroxylation. Nucleic Acids Research, 2014, 42, 12295-12305.	10.7	17
165	Expression, purification, crystallization and preliminary X-ray crystallographic analysis of Enpp6. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 794-799.	0.6	6
166	Crystallization and preliminary X-ray crystallographic analysis of YfcM: an important factor for EF-P hydroxylation. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 1236-1239.	0.6	4
167	Crystal Structure of Cas9 in Complex with Guide RNA and Target DNA. Cell, 2014, 156, 935-949.	23.4	2,146
168	Structural basis of Sec-independent membrane protein insertion by YidC. Nature, 2014, 509, 516-520.	30.6	250
169	Somatic RHOA mutation in angioimmunoblastic T cell lymphoma. Nature Genetics, 2014, 46, 171-175.	14.1	634
170	Structure ofSaccharomyces cerevisiaemitochondrial Qri7 in complex with AMP. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 1009-1014.	0.6	9
171	Water-Containing Hydrogen-Bonding Network in the Active Center of Channelrhodopsin. Journal of the American Chemical Society, 2014, 136, 3475-3482.	11.7	65
172	Exciton Circular Dichroism in Channelrhodopsin. Journal of Physical Chemistry B, 2014, 118, 11873-11885.	2.0	14
173	Structural Basis for Potent Inhibition of SIRT2 Deacetylase by a Macrocyclic Peptide Inducing Dynamic Structural Change. Structure, 2014, 22, 345-352.	2.4	93
174	Crystal structure of Escherichia coli YidC, a membrane protein chaperone and insertase. Scientific Reports, 2014, 4, .	2.7	138
175	Genome-scale transcriptional activation by an engineered CRISPR-Cas9 complex. Nature, 2014, 517, 583-588.	30.6	2,813
176	Is zucchini a phosphodiesterase or a ribonuclease?. Biomedical Journal, 2014, 37, 369.	2.8	4
177	Crystallization of Membrane Proteins in Lipidic Cubic Phase. Nihon Kessho Gakkaishi, 2014, 56, 230-235.	0.0	0
178	Screening and X-ray Crystal Structure-based Optimization of Autotaxin (ENPP2) Inhibitors, Using a Newly Developed Fluorescence Probe. ACS Chemical Biology, 2013, 8, 1713-1721.	2.5	57
179	Structural and spectral characterizations of C1C2 channelrhodopsin and its mutants by molecular simulations. Chemical Physics Letters, 2013, 556, 266-271.	2.0	19
180	Structural basis for the drug extrusion mechanism by a MATE multidrug transporter. Nature, 2013, 496, 247-251.	30.6	254

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181	Crystal structure of channelrhodopsin, a light-gated cation channel - all cations lead through the monomer -. Biophysics (Nagoya-shi, Japan), 2013, 9, 57-61.	1.1	10
182	Crystal structure of Cex1p reveals the mechanism of tRNA trafficking between nucleus and cytoplasm. Nucleic Acids Research, 2013, 41, 3901-3914.	10.7	14
183	Recent structural studies on Dom34/aPelota and Hbs1/aEF1α: important factors for solving general problems of ribosomal stall in translation. Biophysics (Nagoya-shi, Japan), 2013, 9, 131-140.	1.1	6
184	Toll-Like Receptor-2 Mediates Adaptive Cardiac Hypertrophy in Response to Pressure Overload Through Interleukin-1β Upregulation via Nuclear Factor κB Activation. Journal of the American Heart Association, 2013, 2, .	3.1	95
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