Mikako Shirouzu

List of Publications by Year
in descending order

76 papers	3,336 citations	186209 28 h-index	168321 53 g-index
84 all docs	84 docs citations	84 times ranked	5377 citing authors

#	Article	IF	Citations
1	A small-molecule AdipoR agonist for type 2 diabetes and short life in obesity. Nature, 2013, 503, 493-499.	13.7	565
2	Crystal structures of the human adiponectin receptors. Nature, 2015, 520, 312-316.	13.7	176
3	Structure of the complete elongation complex of RNA polymerase II with basal factors. Science, 2017, 357, 921-924.	6.0	162
4	Structural basis of the nucleosome transition during RNA polymerase II passage. Science, 2018, 362, 595-598.	6.0	157
5	Structural insight into nucleosome transcription by RNA polymerase II with elongation factors. Science, 2019, 363, 744-747.	6.0	126
6	TNIK inhibition abrogates colorectal cancer stemness. Nature Communications, 2016, 7, 12586.	5.8	117
7	Rotation mechanism of Enterococcus hirae V1-ATPase based on asymmetric crystal structures. Nature, 2013, 493, 703-707.	13.7	114
8	Structural insights into tetraspanin CD9 function. Nature Communications, 2020, 11, 1606.	5.8	114
9	Cryo-EM structures of the human volume-regulated anion channel LRRC8. Nature Structural and Molecular Biology, 2018, 25, 797-804.	3.6	104
10	Structural basis for mutual relief of the Rac guanine nucleotide exchange factor DOCK2 and its partner ELMO1 from their autoinhibited forms. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 3305-3310.	3.3	95
11	ISRIB Blunts the Integrated Stress Response by Allosterically Antagonising the Inhibitory Effect of Phosphorylated eIF2 on eIF2B. Molecular Cell, 2021, 81, 88-103.e6.	4.5	93
12	Structural basis for eIF2B inhibition in integrated stress response. Science, 2019, 364, 495-499.	6.0	91
13	A Pyrrolo-Pyrimidine Derivative Targets Human Primary AML Stem Cells in Vivo. Science Translational Medicine, 2013, 5, 181ra52.	5.8	75
14	Allosteric regulation of Î³-secretase activity by a phenylimidazole-type Î³-secretase modulator. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 10544-10549.	3.3	72
15	Molecular pathogenesis of Spondylocheirodysplastic Ehlersâ€Danlos syndrome caused by mutant ZIP13 proteins. EMBO Molecular Medicine, 2014, 6, 1028-1042.	3.3	56
16	Lysosome-associated membrane proteins-1 and -2 (LAMP-1 and LAMP-2) assemble via distinct modes. Biochemical and Biophysical Research Communications, 2016, 479, 489-495.	1.0	55
17	Gilteritinib overcomes lorlatinib resistance in ALK-rearranged cancer. Nature Communications, 2021, 12, 1261.	5.8	52
18	Basic Properties of Rotary Dynamics of the Molecular Motor Enterococcus hirae V1-ATPase. Journal of Biological Chemistry, 2013, 288, 32700-32707.	1.6	51

#	Article	IF	Citations
19	Crystal structure of the central axis DF complex of the prokaryotic V-ATPase. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 19955-19960.	3.3	47
20	Crystal structure of nanoKAZ: The mutated 19ÂkDa component of Oplophorus luciferase catalyzing the bioluminescent reaction with coelenterazine. Biochemical and Biophysical Research Communications, 2016, 470, 88-93.	1.0	44
21	Structural insights into the HBV receptor and bile acid transporter NTCP. Nature, 2022, 606, 1027-1031.	13.7	44
22	HCV IRES Captures an Actively Translating 80S Ribosome. Molecular Cell, 2019, 74, 1205-1214.e8.	4.5	42
23	Crystal structures of the ATP-binding and ADP-release dwells of the V1 rotary motor. Nature Communications, 2016, 7, 13235.	5.8	40
24	CDK1 dependent phosphorylation of hTERT contributes to cancer progression. Nature Communications, 2020, 11, 1557.	5.8	38
25	Structural Basis for the Specific Recognition of the Major Antigenic Peptide from the Japanese Cedar Pollen Allergen Cry j 1 by HLA-DP5. Journal of Molecular Biology, 2014, 426, 3016-3027.	2.0	37
26	Protein stabilization utilizing a redefined codon. Scientific Reports, 2015, 5, 9762.	1.6	35
27	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
28	Structural Mechanism for Light-driven Transport by a New Type of Chloride Ion Pump, Nonlabens marinus Rhodopsin-3. Journal of Biological Chemistry, 2016, 291, 17488-17495.	1.6	34
29	A reproducible and scalable procedure for preparing bacterial extracts for cell-free protein synthesis. Journal of Biochemistry, 2017, 162, 357-369.	0.9	34
30	Cryo-EM structure of the photosynthetic RC-LH1-PufX supercomplex at 2.8-Ã... resolution. Science Advances, 2021, 7, .	4.7	29
31	Translation of â€˜rareâ€™ Codons in a Cell-free Protein Synthesis System from Escherichia coli. Journal of Structural and Functional Genomics, 2006, 7, 31-36.	1.2	28
32	RBFOX and SUP-12 sandwich a G base to cooperatively regulate tissue-specific splicing. Nature Structural and Molecular Biology, 2014, 21, 778-786.	3.6	27
33	Cell-Free Expression of Protein Complexes for Structural Biology. Methods in Molecular Biology, 2014, 1091, 151-159.	0.4	25
34	A redox switch shapes the Lon protease exit pore to facultatively regulate proteolysis. Nature Chemical Biology, 2015, 11, 46-51.	3.9	25
35	Crystal structure of human acetylcholinesterase in complex with tacrine: Implications for drug discovery. International Journal of Biological Macromolecules, 2022, 210, 172-181.	3.6	23
36	Reduced efficacy of a Src kinase inhibitor in crowded protein solution. Nature Communications, 2021, 12, 4099.	5.8	22

#	Article	IF	Citations
37	Structural basis for the assembly and quinone transport mechanisms of the dimeric photosynthetic RCâ€“LH1 supercomplex. Nature Communications, 2022, 13, 1977.	5.8	22
38	Crystal structural characterization reveals novel oligomeric interactions of human voltageâ€dependent anion channel 1. Protein Science, 2017, 26, 1749-1758.	3.1	20
39	Cell-free synthesis of functional antibody fragments to provide a structural basis for antibodyâ€“antigen interaction. PLoS ONE, 2018, 13, e0193158.	1.1	20
40	Structural Basis for the Dual Substrate Specificity of DOCK7 Guanine Nucleotide Exchange Factor. Structure, 2019, 27, 741-748.e3.	1.6	19
41	Amyloid conformation-dependent disaggregation in a reconstituted yeast prion system. Nature Chemical Biology, 2022, 18, 321-331.	3.9	18
42	The zincâ€binding region (ZBR) fragment of Emi2 can inhibit APC/C by targeting its association with the coactivator Cdc20 and UBE2Câ€mediated ubiquitylation. FEBS Open Bio, 2014, 4, 689-703.	1.0	17
43	Cryo-EM structure of the human ELMO1-DOCK5-Rac1 complex. Science Advances, 2021, 7, .	4.7	17
44	Structural Basis for the Inhibition of Cyclin Gâ€Associated Kinase by Gefitinib. ChemistryOpen, 2018, 7, 713-719.	0.9	15
45	Human adiponectin receptor AdipoR1 assumes closed and open structures. Communications Biology, 2020, 3, 446.	2.0	15
46	Chemical reversal of abnormalities in cells carrying mitochondrial DNA mutations. Nature Chemical Biology, 2021, 17, 335-343.	3.9	15
47	Expression, purification, crystallization, and preliminary X-ray crystallographic studies of the human adiponectin receptors, AdipoR1 and AdipoR2. Journal of Structural and Functional Genomics, 2015, 16, 11-23.	1.2	14
48	Thioether Macrocyclic Peptides Selected against TET1 Compact Catalytic Domain Inhibit TET1 Catalytic Activity. ChemBioChem, 2018, 19, 979-985.	1.3	14
49	Structural basis for inhibitory effects of Smad7 on TGF-Î² family signaling. Journal of Structural Biology, 2020, 212, 107661.	1.3	14
50	Kastor and Polluks polypeptides encoded by a single gene locus cooperatively regulate VDAC and spermatogenesis. Nature Communications, 2022, 13, 1071.	5.8	14
51	Charge-state-distribution analysis of Bach2 intrinsically disordered heme binding region. Journal of Biochemistry, 2016, 160, 291-298.	0.9	13
52	Metastable asymmetrical structure of a shaftless V ₁ motor. Science Advances, 2019, 5, eaau8149.	4.7	13
53	Serum anti-DIDO1, anti-CPSF2, and anti-FOXJ2 antibodies as predictive risk markers for acute ischemic stroke. BMC Medicine, 2021, 19, 131.	2.3	13
54	Structural insights into the small GTPase specificity of the DOCK guanine nucleotide exchange factors. Current Opinion in Structural Biology, 2021, 71, 249-258.	2.6	13

#	Article	IF	Citations
55	Piperidine-4-carboxamide as a new scaffold for designing secretory glutaminyl cyclase inhibitors. International Journal of Biological Macromolecules, 2021, 170, 415-423.	3.6	13
56	Characterization of crystal water molecules in a high-affinity inhibitor and hematopoietic prostaglandin D synthase complex by interaction energy studies. Bioorganic and Medicinal Chemistry, 2018, 26, 4726-4734.	1.4	12
57	POLArIS, a versatile probe for molecular orientation, revealed actin filaments associated with microtubule asters in early embryos. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	12
58	CAMSAP2 organizes a Î³-tubulin-independent microtubule nucleation centre through phase separation. ELife, 0, 11, .	2.8	12
59	Structural basis of cucumisin protease activity regulation by its propeptide. Journal of Biochemistry, 2017, 161, 45-53.	0.9	11
60	Structural basis for heme detoxification by an ATP-binding cassetteâ€“type efflux pump in gram-positive pathogenic bacteria. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	10
61	Activity cliff for 7-substituted pyrrolo-pyrimidine inhibitors of HCK explained in terms of predicted basicity of the amine nitrogen. Bioorganic and Medicinal Chemistry, 2017, 25, 4259-4264.	1.4	9
62	Chemical and structural characterization of a model Post-Termination Complex (PoTC) for the ribosome recycling reaction: Evidence for the release of the mRNA by RRF and EF-G. PLoS ONE, 2017, 12, e0177972.	1.1	9
63	Design and Synthesis of Tranylcypromine-Derived LSD1 Inhibitors with Improved hERG and Microsomal Stability Profiles. ACS Medicinal Chemistry Letters, 2022, 13, 848-854.	1.3	9
64	Serine hydroxymethyltransferase as a potential target of antibacterial agents acting synergistically with one-carbon metabolism-related inhibitors. Communications Biology, 2022, 5, .	2.0	9
65	Kinase crystal identification and ATP-competitive inhibitor screening using the fluorescent ligand SKF86002. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 392-404.	2.5	8
66	Establishment of a Monoclonal Antibody against Human NTCP That Blocks Hepatitis B Virus Infection. Journal of Virology, 2022, 96, JVI0168621.	1.5	8
67	Investigating the Roles of the C-Terminal Domain of Plasmodium falciparum GyrA. PLoS ONE, 2015, 10, e0142313.	1.1	6
68	Identification of pyrrolo[2,3- d]pyrimidines as potent HCK and FLT3-ITD dual inhibitors. Bioorganic and Medicinal Chemistry Letters, 2017, 27, 4994-4998.	1.0	6
69	Central catalytic domain of BRAP (RNF52) recognizes the types of ubiquitin chains and utilizes oligo-ubiquitin for ubiquitylation. Biochemical Journal, 2017, 474, 3207-3226.	1.7	6
70	Phosphorylated and non-phosphorylated HCK kinase domains produced by cell-free protein expression. Protein Expression and Purification, 2018, 150, 92-99.	0.6	6
71	Slow luminescence kinetics of semi-synthetic aequorin: expression, purification and structure determination of cf3-aequorin. Journal of Biochemistry, 2018, 164, 247-255.	0.9	6
72	Development of a simple new flow cytometric antibody-dependent cellular cytotoxicity (ADCC) assay with excellent sensitivity. Journal of Immunological Methods, 2019, 464, 74-86.	0.6	5

#	Article	IF	Citations
73	Interhelical interactions between D92 and C218 in the cytoplasmic domain regulate proton uptake upon N-decay in the proton transport of Acetabularia rhodopsin II. Journal of Photochemistry and Photobiology B: Biology, 2018, 183, 35-45.	1.7	4
74	The NFâ€ºB regulator IºBÎ² exhibits different molecular interactivity and phosphorylation status from IºBÎ± in an IKK2â€catalysed reaction. FEBS Letters, 2020, 594, 1532-1549.	1.3	4
75	Mutant LV476-7AA of A-subunit of Enterococcus hirae V1-ATPase: High affinity of A3B3 complex to DF axis and low ATPase activity. SpringerPlus, 2013, 2, 689.	1.2	0
76	Structure-Function Analysis of the EFC/F-BAR Domain-Mechanism of Membrane Invagination in Endocytosis-. Nihon Kessho Gakkaishi, 2008, 50, 161-168.	0.0	0