Shuya Fukai

List of Publications by Year in descending order

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Version: 2024-02-01

		71102	74163
93	5,965	41	75
papers	citations	h-index	g-index
95	95	95	9529
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Crystal Structure of the Complex of Human Epidermal Growth Factor and Receptor Extracellular Domains. Cell, 2002, 110, 775-787.	28.9	1,013
2	Enzyme Structure with Two Catalytic Sites for Double-Sieve Selection of Substrate. Science, 1998, 280, 578-582.	12.6	347
3	Structural basis for specific cleavage of Lysâ€‰63-linked polyubiquitin chains. Nature, 2008, 455, 358-362.	27.8	300
4	Structural Basis for Double-Sieve Discrimination of L-Valine from L-Isoleucine and L-Threonine by the Complex of tRNAVal and Valyl-tRNA Synthetase. Cell, 2000, 103, 793-803.	28.9	268
5	Crystal Structure of the Homologous-Pairing Domain from the Human Rad52 Recombinase in the Undecameric Form. Molecular Cell, 2002, 10, 359-371.	9.7	210
6	Conformational transition of Sec machinery inferred from bacterial SecYE structures. Nature, 2008, 455, 988-991.	27.8	206
7	Structure and function of a membrane component SecDF that enhances protein export. Nature, 2011, 474, 235-238.	27.8	202
8	Structural basis for specific recognition of Lys 63-linked polyubiquitin chains by tandem UIMs of RAP80. EMBO Journal, 2009, 28, 2461-2468.	7.8	180
9	Crystal structure of the MgtE Mg2+ transporter. Nature, 2007, 448, 1072-1075.	27.8	166
10	Snapshots of tRNA sulphuration via an adenylated intermediate. Nature, 2006, 442, 419-424.	27.8	123
11	Structural basis for specific recognition of Lys 63-linked polyubiquitin chains by NZF domains of TAB2 and TAB3. EMBO Journal, 2009, 28, 3903-3909.	7.8	118
12	Deep Knot Structure for Construction of Active Site and Cofactor Binding Site of tRNA Modification Enzyme. Structure, 2004, 12, 593-602.	3.3	107
13	Structures of CYLD USP with Met1- or Lys63-linked diubiquitin reveal mechanisms for dual specificity. Nature Structural and Molecular Biology, 2015, 22, 222-229.	8.2	105
14	Structural basis of the interaction between RalA and Sec5, a subunit of the sec6/8 complex. EMBO Journal, 2003, 22, 3267-3278.	7.8	103
15	Specific recognition of linear ubiquitin chains by the Npl4 zinc finger (NZF) domain of the HOIL-1L subunit of the linear ubiquitin chain assembly complex. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 20520-20525.	7.1	97
16	Structural basis for template-independent RNA polymerization. Nature, 2004, 430, 700-704.	27.8	96
17	Structural basis for the Rho- and phosphoinositide-dependent localization of the exocyst subunit Sec3. Nature Structural and Molecular Biology, 2010, 17, 180-186.	8.2	87
18	Structural Basis of RNA-Dependent Recruitment of Glutamine to the Genetic Code. Science, 2006, 312, 1950-1954.	12.6	80

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19	Mutational Separation of Two Pathways for Editing by a Class I tRNA Synthetase. Molecular Cell, 2002, 9, 353-362.	9.7	71
20	A short peptide insertion crucial for angiostatic activity of human tryptophanyl-tRNA synthetase. Nature Structural and Molecular Biology, 2004, 11, 149-156.	8.2	69
21	Crystal structure of the NEMO ubiquitinâ€binding domain in complex with Lys 63â€linked diâ€ubiquitin. FEBS Letters, 2009, 583, 3317-3322.	2.8	69
22	Complete crystallographic analysis of the dynamics of CCA sequence addition. Nature, 2006, 443, 956-960.	27.8	68
23	Structural basis for anticodon recognition by methionyl-tRNA synthetase. Nature Structural and Molecular Biology, 2005, 12, 931-932.	8.2	67
24	Tuberous Sclerosis Tumor Suppressor Complex-like Complexes Act as GTPase-activating Proteins for Ral GTPases. Journal of Biological Chemistry, 2009, 284, 21580-21588.	3.4	65
25	Molecular Basis of Lys-63-linked Polyubiquitination Inhibition by the Interaction between Human Deubiquitinating Enzyme OTUB1 and Ubiquitin-conjugating Enzyme UBC13. Journal of Biological Chemistry, 2012, 287, 25860-25868.	3.4	61
26	Structural basis for specific cleavage of Lys6-linked polyubiquitin chains by USP30. Nature Structural and Molecular Biology, 2017, 24, 911-919.	8.2	61
27	Crystal Structure of Archaeosine tRNA-guanine Transglycosylase. Journal of Molecular Biology, 2002, 318, 665-677.	4.2	59
28	Mechanism of molecular interactions for tRNAVal recognition by valyl-tRNA synthetase. Rna, 2003, 9, 100-111.	3.5	59
29	Roles of Conserved Amino Acid Sequence Motifs in the SpoU (TrmH) RNA Methyltransferase Family. Journal of Biological Chemistry, 2005, 280, 10368-10377.	3.4	59
30	Biochemical Characterization of the Rho GTPase-regulated Actin Assembly by Diaphanous-related Formins, mDia1 and Daam1, in Platelets. Journal of Biological Chemistry, 2008, 283, 8746-8755.	3.4	55
31	Crystal structures of leucyl/phenylalanyl-tRNA-protein transferase and its complex with an aminoacyl-tRNA analog. EMBO Journal, 2006, 25, 5942-5950.	7.8	54
32	Mechanisms of splicing-dependent trans-synaptic adhesion by PTPÎ´â€“IL1RAPL1/IL-1RAcP for synaptic differentiation. Nature Communications, 2015, 6, 6926.	12.8	54
33	Structural basis of epilepsy-related ligandâ€“receptor complex LGI1â€“ADAM22. Nature Communications, 2018, 9, 1546.	12.8	54
34	Structural insight into the membrane insertion of tailâ€anchored proteins by Get3. Genes To Cells, 2010, 15, 29-41.	1.2	51
35	Crystal Structures of the CP1 Domain from Thermus thermophilus Isoleucyl-tRNA Synthetase and Its Complex with l-Valine. Journal of Biological Chemistry, 2004, 279, 8396-8402.	3.4	50
36	Crystal structure of the Sec4p{middle dot}Sec2p complex in the nucleotide exchanging intermediate state. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 8305-8310.	7.1	50

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37	Structural basis for CRMP2-induced axonal microtubule formation. Scientific Reports, 2017, 7, 10681.	3.3	50
38	LGI1â€“ADAM22â€“MAGUK configures transsynaptic nanoalignment for synaptic transmission and epilepsy prevention. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	49
39	Structural basis for lysidine formation by ATP pyrophosphatase accompanied by a lysine-specific loop and a tRNA-recognition domain. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 7487-7492.	7.1	47
40	Mechanism for the definition of elongation and termination by the class II CCA-adding enzyme. EMBO Journal, 2009, 28, 3353-3365.	7.8	46
41	Structure of Slitrk2â€“PTPÎ´ complex reveals mechanisms for splicing-dependent trans-synaptic adhesion. Scientific Reports, 2015, 5, 9686.	3.3	46
42	Structural Basis for Sulfur Relay to RNA Mediated by Heterohexameric TusBCD Complex. Structure, 2006, 14, 357-366.	3.3	44
43	Regulation of Platelet Dense Granule Secretion by the Ral GTPase-Exocyst Pathway. Journal of Biological Chemistry, 2008, 283, 166-174.	3.4	42
44	Crystal structure of human DAAM1 formin homology 2 domain. Genes To Cells, 2007, 12, 1255-1265.	1.2	41
45	Distinct Roles for the N- and C-terminal Regions of M-Sec in Plasma Membrane Deformation during Tunneling Nanotube Formation. Scientific Reports, 2016, 6, 33548.	3.3	41
46	A <scp>SNARE</scp> geranylgeranyltransferase essential for the organization of the Golgi apparatus. EMBO Journal, 2020, 39, e104120.	7.8	41
47	Molecular bases for HOIPINs-mediated inhibition of LUBAC and innate immune responses. Communications Biology, 2020, 3, 163.	4.4	38
48	Structure of TCR and antigen complexes at an immunodominant CTL epitope in HIV-1 infection. Scientific Reports, 2013, 3, 3097.	3.3	35
49	Structural insights into ubiquitin phosphorylation by PINK1. Scientific Reports, 2018, 8, 10382.	3.3	35
50	Functional Categorization of the Conserved Basic Amino Acid Residues in TrmH (tRNA (Gm18)) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 22	3.4	33
51	Structural basis of trans-synaptic interactions between PTPÎ´ and SALMs for inducing synapse formation. Nature Communications, 2018, 9, 269.	12.8	33
52	Crystal Structure of Human AUH Protein, a Single-Stranded RNA Binding Homolog of Enoyl-CoA Hydratase. Structure, 2001, 9, 1253-1263.	3.3	31
53	Asymmetric Coiled-Coil Structure with Guanine Nucleotide Exchange Activity. Structure, 2007, 15, 245-252.	3.3	29
54	Structural insights into modulation and selectivity of transsynaptic neurexinâ€“LRRTM interaction. Nature Communications, 2018, 9, 3964.	12.8	29

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55	Structural insights into ubiquitin recognition and Ufd1 interaction of Npl4. Nature Communications, 2019, 10, 5708.	12.8	28
56	Insights into the mechanisms of epilepsy from structural biology of LGI1â€“ADAM22. Cellular and Molecular Life Sciences, 2020, 77, 267-274.	5.4	26
57	Purification, crystallization and preliminary X-ray diffraction of SecDF, a translocon-associated membrane protein, fromThermus thermophilus. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 376-380.	0.7	22
58	Get1 Stabilizes an Open Dimer Conformation of Get3 ATPase by Binding Two Distinct Interfaces. Journal of Molecular Biology, 2012, 422, 366-375.	4.2	22
59	Structural insights into two distinct binding modules for Lys63-linked polyubiquitin chains in RNF168. Nature Communications, 2018, 9, 170.	12.8	21
60	Structural basis of the interaction between Topoisomerase IIIÎ² and the TDRD3 auxiliary factor. Scientific Reports, 2017, 7, 42123.	3.3	20
61	Subquinocin, a small molecule inhibitor of CYLD and USP-family deubiquitinating enzymes, promotes NF-ÎºB signaling. Biochemical and Biophysical Research Communications, 2020, 524, 1-7.	2.1	20
62	Crystallization and preliminary X-ray analysis of the tRNA thiolation enzyme MnmA fromEscherichia colicomplexed with tRNAGlu. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 368-371.	0.7	19
63	Canonical versus non-canonical transsynaptic signaling of neuroligin 3 tunes development of sociality in mice. Nature Communications, 2021, 12, 1848.	12.8	19
64	Structural basis of ubiquitin recognition by the winged-helix domain of Cockayne syndrome group B protein. Nucleic Acids Research, 2019, 47, 3784-3794.	14.5	17
65	A Human DUB Protein Array for Clarification of Linkage Specificity of Polyubiquitin Chain and Application to Evaluation of Its Inhibitors. Biomedicines, 2020, 8, 152.	3.2	17
66	Roles of type IIa receptor protein tyrosine phosphatases as synaptic organizers. FEBS Journal, 2021, 288, 6913-6926.	4.7	15
67	Crystal structure of Sec10, a subunit of the exocyst complex. Scientific Reports, 2017, 7, 40909.	3.3	14
68	Switching and emergence of CTL epitopes in HIV-1 infection. Retrovirology, 2014, 11, 38.	2.0	13
69	Structural insights into selective interaction between type IIa receptor protein tyrosine phosphatases and Liprin-Î±. Nature Communications, 2020, 11, 649.	12.8	12
70	Structural Basis for Ubiquitin Recognition by Ubiquitin-Binding Zinc Finger of FAAP20. PLoS ONE, 2015, 10, e0120887.	2.5	11
71	14-3-3 proteins stabilize LGI1-ADAM22 levels to regulate seizure thresholds in mice. Cell Reports, 2021, 37, 110107.	6.4	10
72	Crystallization and preliminary X-ray diffraction analysis of the full-length Mg²⁺transporter MgtE. Acta Crystallographica Section F: Structural Biology Communications, 2007, 63, 682-684.	0.7	9

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73	Crystallization and preliminary X-ray diffraction analysis of GCIP/HHM transcriptional regulator. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 21-24.	0.7	9
74	Crystallization and preliminary X-ray diffraction analysis of the cytosolic domain of the Mg²⁺transporter MgtE. Acta Crystallographica Section F: Structural Biology Communications, 2007, 63, 678-681.	0.7	8
75	Neurexins play a crucial role in cerebellar granule cell survival by organizing autocrine machinery for neurotrophins. Cell Reports, 2022, 39, 110624.	6.4	8
76	Structural basis of guanine nucleotide exchange for Rab11 by SH3BP5. Life Science Alliance, 2019, 2, e201900297.	2.8	7
77	Crystal structure of the central and the C-terminal RNase domains of colicin D implicated its translocation pathway through inner membrane of target cell. Journal of Biochemistry, 2018, 164, 329-339.	1.7	6
78	Structural insights into leucine-rich repeat-containing synaptic cleft molecules. Current Opinion in Structural Biology, 2019, 54, 68-77.	5.7	6
79	Structural basis for specific recognition of K6-linked polyubiquitin chains by the TAB2 NZF domain. Biophysical Journal, 2021, 120, 3355-3362.	0.5	6
80	Crystallization and crystallographic analysis of yeast Sec2p, a guanine nucleotide-exchange factor for the yeast Rab GTPase Sec4p. Acta Crystallographica Section F: Structural Biology Communications, 2007, 63, 616-619.	0.7	2
81	Core Structures of Ubiquitin Dictate Its Dynamics and Function. Journal of Molecular Biology, 2014, 426, 1367-1369.	4.2	2
82	Features of Aminoacyl-tRNA Synthesis Unique to Archaea. , 0, , 198-208.		1
83	Functional Structures of Class-I Aminoacyl-tRNA Synthetases. , 1999, , 149-158.		0
84	1P358 Structural analysis of the Mammalian Exocyst Complex(13. Membrane transport,Poster) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 30	0.1	0
85	1P014 Snapshots of tRNA sulfuration via an adenylated intermediate(1. Protein structure and dynamics) Tj ETQq1 1 0.784314 rgBT /Ov	0.1	0
86	2P151 Crystallization and preliminary X-ray analysis of the bacterial membrane transporters(34.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 2 2006, 46, S333.	0.1	0
87	2P168 Structural Basis of RNA-Dependent Recruitment of Glutamine to the Genetic Code(35. RNA) Tj ETQq1 1 0.784314 rgBT /Overlock	0.1	0
88	S06A2 Structural insights into the chemical modification in non-coding RNAs(Structural Biology of) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.1	0
89	1P-033 Crystal structures of the cytosolic domain of the Mg^<2+> transporter MgtE(The 46th) Tj ETQq1 1 0.784314 rgBT /Overloc	0.1	0
90	Application of MultiBac System to Large Complexes. Springer Protocols, 2016, , 47-65.	0.3	0

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91	Structural Basis for Specific Recognition and Cleavage of Polyubiquitin Chains. Nihon Kessho Gakkaishi, 2010, 52, 20-24.	0.0	0
92	Structural basis for the membrane targeting of the exocyst complex. Acta Crystallographica Section A: Foundations and Advances, 2010, 66, s27-s27.	0.3	0
93	Ubiquitin recognition by UBZ and UMI domains for DNA damage response. Acta Crystallographica Section A: Foundations and Advances, 2014, 70, C1642-C1642.	0.1	0