

Shuya Fukai

List of Publications by Year in descending order

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93
papers

5,965
citations

71102

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74163

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95
docs citations

95
times ranked

9529
citing authors

#	ARTICLE	IF	CITATIONS
1	Neurexins play a crucial role in cerebellar granule cell survival by organizing autocrine machinery for neurotrophins. <i>Cell Reports</i> , 2022, 39, 110624.	6.4	8
2	Roles of type IIa receptor protein tyrosine phosphatases as synaptic organizers. <i>FEBS Journal</i> , 2021, 288, 6913-6926.	4.7	15
3	Canonical versus non-canonical transsynaptic signaling of neuroligin 3 tunes development of sociality in mice. <i>Nature Communications</i> , 2021, 12, 1848.	12.8	19
4	Structural basis for specific recognition of K6-linked polyubiquitin chains by the TAB2 NZF domain. <i>Biophysical Journal</i> , 2021, 120, 3355-3362.	0.5	6
5	LGI1-ADAM22-MAGUK configures transsynaptic nanoalignment for synaptic transmission and epilepsy prevention. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	49
6	14-3-3 proteins stabilize LGI1-ADAM22 levels to regulate seizure thresholds in mice. <i>Cell Reports</i> , 2021, 37, 110107.	6.4	10
7	Insights into the mechanisms of epilepsy from structural biology of LGI1-ADAM22. <i>Cellular and Molecular Life Sciences</i> , 2020, 77, 267-274.	5.4	26
8	Subquinocin, a small molecule inhibitor of CYLD and USP-family deubiquitinating enzymes, promotes NF- κ B signaling. <i>Biochemical and Biophysical Research Communications</i> , 2020, 524, 1-7.	2.1	20
9	A <i>scn</i> SNARE geranylgeranyltransferase essential for the organization of the Golgi apparatus. <i>EMBO Journal</i> , 2020, 39, e104120.	7.8	41
10	A Human DUB Protein Array for Clarification of Linkage Specificity of Polyubiquitin Chain and Application to Evaluation of Its Inhibitors. <i>Biomedicines</i> , 2020, 8, 152.	3.2	17
11	Molecular bases for HOIPINs-mediated inhibition of LUBAC and innate immune responses. <i>Communications Biology</i> , 2020, 3, 163.	4.4	38
12	Structural insights into selective interaction between type IIa receptor protein tyrosine phosphatases and Liprin-1. <i>Nature Communications</i> , 2020, 11, 649.	12.8	12
13	Structural insights into leucine-rich repeat-containing synaptic cleft molecules. <i>Current Opinion in Structural Biology</i> , 2019, 54, 68-77.	5.7	6
14	Structural basis of ubiquitin recognition by the winged-helix domain of Cockayne syndrome group B protein. <i>Nucleic Acids Research</i> , 2019, 47, 3784-3794.	14.5	17
15	Structural insights into ubiquitin recognition and Ufd1 interaction of Npl4. <i>Nature Communications</i> , 2019, 10, 5708.	12.8	28
16	Structural basis of guanine nucleotide exchange for Rab11 by SH3BP5. <i>Life Science Alliance</i> , 2019, 2, e201900297.	2.8	7
17	Structural basis of epilepsy-related ligand-receptor complex LGI1-ADAM22. <i>Nature Communications</i> , 2018, 9, 1546.	12.8	54
18	Structural basis of trans-synaptic interactions between PTP σ and SALMs for inducing synapse formation. <i>Nature Communications</i> , 2018, 9, 269.	12.8	33

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19	Structural insights into two distinct binding modules for Lys63-linked polyubiquitin chains in RNF168. <i>Nature Communications</i> , 2018, 9, 170.	12.8	21
20	Structural insights into modulation and selectivity of transsynaptic neuroligin-1/LRRTM interaction. <i>Nature Communications</i> , 2018, 9, 3964.	12.8	29
21	Structural insights into ubiquitin phosphorylation by PINK1. <i>Scientific Reports</i> , 2018, 8, 10382.	3.3	35
22	Crystal structure of the central and the C-terminal RNase domains of colicin D implicated its translocation pathway through inner membrane of target cell. <i>Journal of Biochemistry</i> , 2018, 164, 329-339.	1.7	6
23	Structural basis of the interaction between Topoisomerase III β and the TDRD3 auxiliary factor. <i>Scientific Reports</i> , 2017, 7, 42123.	3.3	20
24	Structural basis for specific cleavage of Lys6-linked polyubiquitin chains by USP30. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 911-919.	8.2	61
25	Structural basis for CRMP2-induced axonal microtubule formation. <i>Scientific Reports</i> , 2017, 7, 10681.	3.3	50
26	Crystal structure of Sec10, a subunit of the exocyst complex. <i>Scientific Reports</i> , 2017, 7, 40909.	3.3	14
27	Distinct Roles for the N- and C-terminal Regions of M-Sec in Plasma Membrane Deformation during Tunneling Nanotube Formation. <i>Scientific Reports</i> , 2016, 6, 33548.	3.3	41
28	Application of MultiBac System to Large Complexes. <i>Springer Protocols</i> , 2016, , 47-65.	0.3	0
29	Structure of Slitrk2-PTP β complex reveals mechanisms for splicing-dependent trans-synaptic adhesion. <i>Scientific Reports</i> , 2015, 5, 9686.	3.3	46
30	Structural Basis for Ubiquitin Recognition by Ubiquitin-Binding Zinc Finger of FAAP20. <i>PLoS ONE</i> , 2015, 10, e0120887.	2.5	11
31	Structures of CYLD USP with Met1- or Lys63-linked diubiquitin reveal mechanisms for dual specificity. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 222-229.	8.2	105
32	Mechanisms of splicing-dependent trans-synaptic adhesion by PTP β -IL1RAPL1/IL-1RAcP for synaptic differentiation. <i>Nature Communications</i> , 2015, 6, 6926.	12.8	54
33	Switching and emergence of CTL epitopes in HIV-1 infection. <i>Retrovirology</i> , 2014, 11, 38.	2.0	13
34	Core Structures of Ubiquitin Dictate Its Dynamics and Function. <i>Journal of Molecular Biology</i> , 2014, 426, 1367-1369.	4.2	2
35	Ubiquitin recognition by UBZ and UMI domains for DNA damage response. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2014, 70, C1642-C1642.	0.1	0
36	Structure of TCR and antigen complexes at an immunodominant CTL epitope in HIV-1 infection. <i>Scientific Reports</i> , 2013, 3, 3097.	3.3	35

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37	Molecular Basis of Lys-63-linked Polyubiquitination Inhibition by the Interaction between Human Deubiquitinating Enzyme OTUB1 and Ubiquitin-conjugating Enzyme UBC13. <i>Journal of Biological Chemistry</i> , 2012, 287, 25860-25868.	3.4	61
38	Get1 Stabilizes an Open Dimer Conformation of Get3 ATPase by Binding Two Distinct Interfaces. <i>Journal of Molecular Biology</i> , 2012, 422, 366-375.	4.2	22
39	Structure and function of a membrane component SecDF that enhances protein export. <i>Nature</i> , 2011, 474, 235-238.	27.8	202
40	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. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 20520-20525.	7.1	97
41	Structural insight into the membrane insertion of tail-anchored proteins by Get3. <i>Genes To Cells</i> , 2010, 15, 29-41.	1.2	51
42	Structural basis for the Rho- and phosphoinositide-dependent localization of the exocyst subunit Sec3. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 180-186.	8.2	87
43	Structural Basis for Specific Recognition and Cleavage of Polyubiquitin Chains. <i>Nihon Kessho Gakkaishi</i> , 2010, 52, 20-24.	0.0	0
44	Structural basis for the membrane targeting of the exocyst complex. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2010, 66, s27-s27.	0.3	0
45	Tuberous Sclerosis Tumor Suppressor Complex-like Complexes Act as GTPase-activating Proteins for Ral GTPases. <i>Journal of Biological Chemistry</i> , 2009, 284, 21580-21588.	3.4	65
46	Crystal structure of the NEMO ubiquitin-binding domain in complex with Lys 63-linked di-ubiquitin. <i>FEBS Letters</i> , 2009, 583, 3317-3322.	2.8	69
47	Crystallization and preliminary X-ray diffraction analysis of GCIP/HHM transcriptional regulator. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 21-24.	0.7	9
48	Structural basis for specific recognition of Lys 63-linked polyubiquitin chains by tandem UIMs of RAP80. <i>EMBO Journal</i> , 2009, 28, 2461-2468.	7.8	180
49	Mechanism for the definition of elongation and termination by the class II CCA-adding enzyme. <i>EMBO Journal</i> , 2009, 28, 3353-3365.	7.8	46
50	Structural basis for specific recognition of Lys 63-linked polyubiquitin chains by NZF domains of TAB2 and TAB3. <i>EMBO Journal</i> , 2009, 28, 3903-3909.	7.8	118
51	Structural basis for specific cleavage of Lys-63-linked polyubiquitin chains. <i>Nature</i> , 2008, 455, 358-362.	27.8	300
52	Conformational transition of Sec machinery inferred from bacterial SecYE structures. <i>Nature</i> , 2008, 455, 988-991.	27.8	206
53	Regulation of Platelet Dense Granule Secretion by the Ral GTPase-Exocyst Pathway. <i>Journal of Biological Chemistry</i> , 2008, 283, 166-174.	3.4	42
54	Biochemical Characterization of the Rho GTPase-regulated Actin Assembly by Diaphanous-related Formins, mDia1 and Daam1, in Platelets. <i>Journal of Biological Chemistry</i> , 2008, 283, 8746-8755.	3.4	55

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55	1P033 Crystal structures of the cytosolic domain of the Mg ²⁺ transporter MgtE(The 46th Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 38)	0.1	0
56	S06A2 Structural insights into the chemical modification in non-coding RNAs(Structural Biology of Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 38)	0.1	0
57	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
58	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
59	Crystallization and preliminary X-ray diffraction analysis of the full-length Mg ²⁺ transporter MgtE. Acta Crystallographica Section F: Structural Biology Communications, 2007, 63, 682-684.	0.7	9
60	Crystallization and preliminary X-ray diffraction analysis of the cytosolic domain of the Mg ²⁺ transporter MgtE. Acta Crystallographica Section F: Structural Biology Communications, 2007, 63, 678-681.	0.7	8
61	Crystal structure of the MgtE Mg ²⁺ transporter. Nature, 2007, 448, 1072-1075.	27.8	166
62	Crystal structure of human DAAM1 formin homology 2 domain. Genes To Cells, 2007, 12, 1255-1265.	1.2	41
63	Asymmetric Coiled-Coil Structure with Guanine Nucleotide Exchange Activity. Structure, 2007, 15, 245-252.	3.3	29
64	1P358 Structural analysis of the Mammalian Exocyst Complex(13. Membrane transport,Poster) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 38)	0.1	0
65	1P014 Snapshots of tRNA sulfuration via an adenylated intermediate(1. Protein structure and dynamics) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 38)	0.1	0
66	2P151 Crystallization and preliminary X-ray analysis of the bacterial membrane transporters(34.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 38)	0.1	0
67	2P168 Structural Basis of RNA-Dependent Recruitment of Glutamine to the Genetic Code(35. RNA) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 38)	0.1	0
68	Crystallization and preliminary X-ray analysis of the tRNA thiolation enzyme MnmA from Escherichia coli complexed with tRNA ^{Glu} . Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 368-371.	0.7	19
69	Purification, crystallization and preliminary X-ray diffraction of SecDF, a translocon-associated membrane protein, from Thermus thermophilus. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 376-380.	0.7	22
70	Snapshots of tRNA sulphuration via an adenylated intermediate. Nature, 2006, 442, 419-424.	27.8	123
71	Complete crystallographic analysis of the dynamics of CCA sequence addition. Nature, 2006, 443, 956-960.	27.8	68
72	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

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73	Structural Basis for Sulfur Relay to RNA Mediated by Heterohexameric TusBCD Complex. <i>Structure</i> , 2006, 14, 357-366.	3.3	44
74	Functional Categorization of the Conserved Basic Amino Acid Residues in TrmH (tRNA (Gm18)) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 70	3.4	33
75	Structural Basis of RNA-Dependent Recruitment of Glutamine to the Genetic Code. <i>Science</i> , 2006, 312, 1950-1954.	12.6	80
76	Structural basis for anticodon recognition by methionyl-tRNA synthetase. <i>Nature Structural and Molecular Biology</i> , 2005, 12, 931-932.	8.2	67
77	Roles of Conserved Amino Acid Sequence Motifs in the SpoU (TrmH) RNA Methyltransferase Family. <i>Journal of Biological Chemistry</i> , 2005, 280, 10368-10377.	3.4	59
78	Structural basis for lysidine formation by ATP pyrophosphatase accompanied by a lysine-specific loop and a tRNA-recognition domain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 7487-7492.	7.1	47
79	Crystal Structures of the CP1 Domain from <i>Thermus thermophilus</i> Isoleucyl-tRNA Synthetase and Its Complex with L-Valine. <i>Journal of Biological Chemistry</i> , 2004, 279, 8396-8402.	3.4	50
80	A short peptide insertion crucial for angiostatic activity of human tryptophanyl-tRNA synthetase. <i>Nature Structural and Molecular Biology</i> , 2004, 11, 149-156.	8.2	69
81	Structural basis for template-independent RNA polymerization. <i>Nature</i> , 2004, 430, 700-704.	27.8	96
82	Deep Knot Structure for Construction of Active Site and Cofactor Binding Site of tRNA Modification Enzyme. <i>Structure</i> , 2004, 12, 593-602.	3.3	107
83	Structural basis of the interaction between RalA and Sec5, a subunit of the sec6/8 complex. <i>EMBO Journal</i> , 2003, 22, 3267-3278.	7.8	103
84	Mechanism of molecular interactions for tRNA ^{Val} recognition by valyl-tRNA synthetase. <i>Rna</i> , 2003, 9, 100-111.	3.5	59
85	Crystal Structure of the Complex of Human Epidermal Growth Factor and Receptor Extracellular Domains. <i>Cell</i> , 2002, 110, 775-787.	28.9	1,013
86	Crystal Structure of Archaeosine tRNA-guanine Transglycosylase. <i>Journal of Molecular Biology</i> , 2002, 318, 665-677.	4.2	59
87	Mutational Separation of Two Pathways for Editing by a Class I tRNA Synthetase. <i>Molecular Cell</i> , 2002, 9, 353-362.	9.7	71
88	Crystal Structure of the Homologous-Pairing Domain from the Human Rad52 Recombinase in the Undecameric Form. <i>Molecular Cell</i> , 2002, 10, 359-371.	9.7	210
89	Crystal Structure of Human AUH Protein, a Single-Stranded RNA Binding Homolog of Enoyl-CoA Hydratase. <i>Structure</i> , 2001, 9, 1253-1263.	3.3	31
90	Structural Basis for Double-Sieve Discrimination of L-Valine from L-Isoleucine and L-Threonine by the Complex of tRNA ^{Val} and Valyl-tRNA Synthetase. <i>Cell</i> , 2000, 103, 793-803.	28.9	268

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91	Functional Structures of Class-I Aminoacyl-tRNA Synthetases. , 1999, , 149-158.		0
92	Enzyme Structure with Two Catalytic Sites for Double-Sieve Selection of Substrate. Science, 1998, 280, 578-582.	12.6	347
93	Features of Aminoacyl-tRNA Synthesis Unique to Archaea. , 0, , 198-208.		1