

Liang Tong

List of Publications by Year in descending order

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74
papers

5,800
citations

94415

37
h-index

82542

72
g-index

81
all docs

81
docs citations

81
times ranked

7006
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural basis for signal transduction by the Toll/interleukin-1 receptor domains. <i>Nature</i> , 2000, 408, 111-115.	27.8	714
2	Polyadenylation factor CPSF-73 is the pre-mRNA 3'-end-processing endonuclease. <i>Nature</i> , 2006, 444, 953-956.	27.8	387
3	Structure and function of biotin-dependent carboxylases. <i>Cellular and Molecular Life Sciences</i> , 2013, 70, 863-891.	5.4	321
4	Acetyl-CoA carboxylase inhibition by ND-630 reduces hepatic steatosis, improves insulin sensitivity, and modulates dyslipidemia in rats. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E1796-805.	7.1	223
5	5' End Nicotinamide Adenine Dinucleotide Cap in Human Cells Promotes RNA Decay through DXO-Mediated deNADding. <i>Cell</i> , 2017, 168, 1015-1027.e10.	28.9	184
6	Expression system for structural and functional studies of human glycosylation enzymes. <i>Nature Chemical Biology</i> , 2018, 14, 156-162.	8.0	182
7	Structure and function of the 5' exoribonuclease Rat1 and its activating partner Rai1. <i>Nature</i> , 2009, 458, 784-788.	27.8	177
8	The Cyclic Dinucleotide c-di-AMP Is an Allosteric Regulator of Metabolic Enzyme Function. <i>Cell</i> , 2014, 158, 1389-1401.	28.9	174
9	An HD-domain phosphodiesterase mediates cooperative hydrolysis of c-di-AMP to affect bacterial growth and virulence. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E747-56.	7.1	171
10	Crystal Structure of the Carboxyltransferase Domain of Acetyl-Coenzyme A Carboxylase. <i>Science</i> , 2003, 299, 2064-2067.	12.6	161
11	Nicotinamide adenine dinucleotide metabolism as an attractive target for drug discovery. <i>Expert Opinion on Therapeutic Targets</i> , 2007, 11, 695-705.	3.4	153
12	Identification of a quality-control mechanism for mRNA 5' end capping. <i>Nature</i> , 2010, 467, 608-611.	27.8	150
13	Crystal structure of the human symplekin-Ssu72-CTD phosphopeptide complex. <i>Nature</i> , 2010, 467, 729-733.	27.8	144
14	Crystal structure of the heterotrimer core of <i>Saccharomyces cerevisiae</i> AMPK homologue SNF1. <i>Nature</i> , 2007, 449, 492-495.	27.8	141
15	A Mammalian Pre-mRNA 5' End Capping Quality Control Mechanism and an Unexpected Link of Capping to Pre-mRNA Processing. <i>Molecular Cell</i> , 2013, 50, 104-115.	9.7	129
16	c-di-AMP modulates <i>Listeria monocytogenes</i> central metabolism to regulate growth, antibiotic resistance and osmoregulation. <i>Molecular Microbiology</i> , 2017, 104, 212-233.	2.5	121
17	Molecular basis for the recognition of the human AAUAAA polyadenylation signal. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E1419-E1428.	7.1	121
18	Enzymatic Basis for N-Glycan Sialylation. <i>Journal of Biological Chemistry</i> , 2013, 288, 34680-34698.	3.4	116

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19	Crystal structures of human and <i>Staphylococcus aureus</i> pyruvate carboxylase and molecular insights into the carboxyltransfer reaction. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 295-302.	8.2	111
20	An allosteric mechanism for potent inhibition of human ATP-citrate lyase. <i>Nature</i> , 2019, 568, 566-570.	27.8	105
21	Structure of Histone mRNA Stem-Loop, Human Stem-Loop Binding Protein, and β -Exo Ternary Complex. <i>Science</i> , 2013, 339, 318-321.	12.6	101
22	Dxo1 is a new type of eukaryotic enzyme with both decapping and 5' β - β exoribonuclease activity. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 1011-1017.	8.2	93
23	Cyclic diAMP targets the cystathionine beta-synthase domain of the osmolyte transporter OpuC. <i>Molecular Microbiology</i> , 2016, 102, 233-243.	2.5	89
24	Mechanism for the inhibition of the carboxyltransferase domain of acetyl-coenzyme A carboxylase by pinoxaden. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 22072-22077.	7.1	84
25	Crystal Structure of Murine CstF-77: Dimeric Association and Implications for Polyadenylation of mRNA Precursors. <i>Molecular Cell</i> , 2007, 25, 863-875.	9.7	83
26	Structure of an active human histone pre-mRNA 3'-end processing machinery. <i>Science</i> , 2020, 367, 700-703.	12.6	76
27	COMO: a program for combined molecular replacement. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 1127-1134.	2.5	75
28	Delineating the Structural Blueprint of the Pre-mRNA 3'-End Processing Machinery. <i>Molecular and Cellular Biology</i> , 2014, 34, 1894-1910.	2.3	75
29	Crystal structure of the 500-kDa yeast acetyl-CoA carboxylase holoenzyme dimer. <i>Nature</i> , 2015, 526, 723-727.	27.8	67
30	Integrator subunit 4 is a "Symplekin-like" scaffold that associates with INTS9/11 to form the Integrator cleavage module. <i>Nucleic Acids Research</i> , 2018, 46, 4241-4255.	14.5	65
31	Molecular basis for the interaction between Integrator subunits IntS9 and IntS11 and its functional importance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 4394-4399.	7.1	59
32	Structural Insights into the Human Pre-mRNA 3'-End Processing Machinery. <i>Molecular Cell</i> , 2020, 77, 800-809.e6.	9.7	53
33	Structural and mechanistic basis of mammalian Nudt12 RNA deNADding. <i>Nature Chemical Biology</i> , 2019, 15, 575-582.	8.0	49
34	Cryo-EM as a powerful tool for drug discovery. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2020, 30, 127524.	2.2	48
35	Recent molecular insights into canonical pre-mRNA 3'-end processing. <i>Transcription</i> , 2020, 11, 83-96.	3.1	47
36	Mammalian Nudix proteins cleave nucleotide metabolite caps on RNAs. <i>Nucleic Acids Research</i> , 2020, 48, 6788-6798.	14.5	46

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37	Structural and functional studies of pyruvate carboxylase regulation by cyclic di-AMP in lactic acid bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E7226-E7235.	7.1	44
38	An unexpected binding mode for a Pol II CTD peptide phosphorylated at Ser7 in the active site of the CTD phosphatase Ssu72. <i>Genes and Development</i> , 2012, 26, 2265-2270.	5.9	40
39	Molecular basis for the recognition of cyclic di-AMP by PstA, a P _{II} -like signal transduction protein. <i>MicrobiologyOpen</i> , 2015, 4, 361-374.	3.0	40
40	Structure and Function of Pre-mRNA 5'-End Capping Quality Control and 3'-End Processing. <i>Biochemistry</i> , 2014, 53, 1882-1898.	2.5	33
41	High-resolution structures of inhibitor complexes of human indoleamine 2,3-dioxygenase 1 in a new crystal form. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2018, 74, 717-724.	0.8	32
42	Molecular mechanisms for the regulation of histone mRNA stem-loop binding protein by phosphorylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E2937-46.	7.1	29
43	A unified molecular mechanism for the regulation of acetyl-CoA carboxylase by phosphorylation. <i>Cell Discovery</i> , 2016, 2, 16044.	6.7	29
44	Cryo-EM Analysis Reveals New Insights into the Mechanism of Action of Pyruvate Carboxylase. <i>Structure</i> , 2010, 18, 1300-1310.	3.3	27
45	DXO/Rai1 enzymes remove 5'-end FAD and dephospho-CoA caps on RNAs. <i>Nucleic Acids Research</i> , 2020, 48, 6136-6148.	14.5	27
46	Arabidopsis DXO1 links RNA turnover and chloroplast function independently of its enzymatic activity. <i>Nucleic Acids Research</i> , 2019, 47, 4751-4764.	14.5	26
47	High-Throughput PIXE as an Essential Quantitative Assay for Accurate Metalloprotein Structural Analysis: Development and Application. <i>Journal of the American Chemical Society</i> , 2020, 142, 185-197.	13.7	24
48	Functional Conformations for Pyruvate Carboxylase during Catalysis Explored by Cryoelectron Microscopy. <i>Structure</i> , 2014, 22, 911-922.	3.3	23
49	A serendipitous discovery that in situ proteolysis is essential for the crystallization of yeast CPSF-100 (Ydh1p). <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 1041-1045.	0.7	22
50	Crystal structure of the Rna14-Rna15 complex. <i>Rna</i> , 2012, 18, 1154-1162.	3.5	21
51	A novel 5'-hydroxyl dinucleotide hydrolase activity for the DXO/Rai1 family of enzymes. <i>Nucleic Acids Research</i> , 2020, 48, 349-358.	14.5	21
52	Real-time fluorescence detection of exoribonucleases. <i>Rna</i> , 2009, 15, 2057-2062.	3.5	20
53	Studies with recombinant U7 snRNP demonstrate that CPSF73 is both an endonuclease and a 5'-3' exonuclease. <i>Rna</i> , 2020, 26, 1345-1359.	3.5	20
54	Crystal Structures of Malonyl-Coenzyme A Decarboxylase Provide Insights into Its Catalytic Mechanism and Disease-Causing Mutations. <i>Structure</i> , 2013, 21, 1182-1192.	3.3	17

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55	Biophysical characterizations of the recognition of the AAUAAA polyadenylation signal. <i>Rna</i> , 2019, 25, 1673-1680.	3.5	17
56	The use of in situ proteolysis in the crystallization of murine CstF-77. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 135-138.	0.7	16
57	Structural and biochemical studies of the distinct activity profiles of Rai1 enzymes. <i>Nucleic Acids Research</i> , 2015, 43, 6596-6606.	14.5	16
58	Characterizing the Importance of the Biotin Carboxylase Domain Dimer for <i>Staphylococcus aureus</i> Pyruvate Carboxylase Catalysis. <i>Biochemistry</i> , 2013, 52, 488-496.	2.5	15
59	Molecular mechanism for the inhibition of DXO by adenosine 5'-bisphosphate. <i>Biochemical and Biophysical Research Communications</i> , 2018, 504, 89-95.	2.1	15
60	A distinct holoenzyme organization for two-subunit pyruvate carboxylase. <i>Nature Communications</i> , 2016, 7, 12713.	12.8	14
61	Crystal structure of a <i>Pseudomonas</i> malonate decarboxylase holoenzyme hetero-tetramer. <i>Nature Communications</i> , 2017, 8, 160.	12.8	14
62	Composition and processing activity of a semi-recombinant holo U7 snRNP. <i>Nucleic Acids Research</i> , 2020, 48, 1508-1530.	14.5	13
63	The N-terminal domains of FLASH and Lsm11 form a 2:1 heterotrimer for histone pre-mRNA 3'-end processing. <i>PLoS ONE</i> , 2017, 12, e0186034.	2.5	12
64	Molecular mechanism for the interaction between human CPSF30 and hFip1. <i>Genes and Development</i> , 2020, 34, 1753-1761.	5.9	10
65	A real-time fluorescence assay for CPSF73, the nuclease for pre-mRNA 3'-end processing. <i>Rna</i> , 2021, 27, 1148-1154.	3.5	10
66	Recent insights into noncanonical 5' capping and decapping of RNA. <i>Journal of Biological Chemistry</i> , 2022, 298, 102171.	3.4	10
67	U7 deciphered: the mechanism that forms the unusual 3' end of metazoan replication-dependent histone mRNAs. <i>Biochemical Society Transactions</i> , 2021, 49, 2229-2240.	3.4	8
68	Reconstitution and biochemical assays of an active human histone pre-mRNA 3'-end processing machinery. <i>Methods in Enzymology</i> , 2021, 655, 291-324.	1.0	7
69	Structures of 5' Exoribonucleases. <i>The Enzymes</i> , 2012, 31, 115-129.	1.7	5
70	How Does Polymerization Regulate Human Acetyl-CoA Carboxylase 1?. <i>Biochemistry</i> , 2018, 57, 5495-5496.	2.5	5
71	How to disARM the executioner of axon degeneration. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 10-12.	8.2	5
72	Structural basis for a bacterial Pip system plant effector recognition protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	3

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73	Crystal structure of a thermophilic fungal cyanase and its implications on the catalytic mechanism for bioremediation. Scientific Reports, 2021, 11, 277.	3.3	2
74	Metabolic Regulation by Cyclic di-AMP Signaling. , 2020, , 161-175.		1