

Liang Tong

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

72
papers

4,315
citations

31
h-index

65
g-index

81
ext. papers

5,170
ext. citations

16.5
avg. IF

5.74
L-index

#	Paper	IF	Citations
72	How to diSARM the executioner of axon degeneration. <i>Nature Structural and Molecular Biology</i> , 2021 , 28, 10-12	17.6	2
71	A real-time fluorescence assay for CPSF73, the nuclease for pre-mRNA 3' end processing. <i>Rna</i> , 2021 , 27, 1148-1154	5.8	1
70	Reconstitution and biochemical assays of an active human histone pre-mRNA 3' end processing machinery. <i>Methods in Enzymology</i> , 2021 , 655, 291-324	1.7	1
69	Crystal structure of a thermophilic fungal cyanase and its implications on the catalytic mechanism for bioremediation. <i>Scientific Reports</i> , 2021 , 11, 277	4.9	1
68	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	5.1	0
67	DXO/Rai1 enzymes remove 5' end FAD and dephospho-CoA caps on RNAs. <i>Nucleic Acids Research</i> , 2020 , 48, 6136-6148	20.1	12
66	Mammalian Nudix proteins cleave nucleotide metabolite caps on RNAs. <i>Nucleic Acids Research</i> , 2020 , 48, 6788-6798	20.1	17
65	Recent molecular insights into canonical pre-mRNA 3' end processing. <i>Transcription</i> , 2020 , 11, 83-96	4.8	20
64	Studies with recombinant U7 snRNP demonstrate that CPSF73 is both an endonuclease and a 5' 3' exonuclease. <i>Rna</i> , 2020 , 26, 1345-1359	5.8	9
63	Structure of an active human histone pre-mRNA 3' end processing machinery. <i>Science</i> , 2020 , 367, 700-703	33.3	37
62	Metabolic Regulation by Cyclic di-AMP Signaling 2020 , 161-175		0
61	Composition and processing activity of a semi-recombinant holo U7 snRNP. <i>Nucleic Acids Research</i> , 2020 , 48, 1508-1530	20.1	8
60	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	16.4	10
59	A novel 5' hydroxyl dinucleotide hydrolase activity for the DXO/Rai1 family of enzymes. <i>Nucleic Acids Research</i> , 2020 , 48, 349-358	20.1	15
58	Structural Insights into the Human Pre-mRNA 3' End Processing Machinery. <i>Molecular Cell</i> , 2020 , 77, 800-809.e6	17.6	23
57	Cryo-EM as a powerful tool for drug discovery. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2020 , 30, 1275-1279	2.4	19
56	Molecular mechanism for the interaction between human CPSF30 and hFip1. <i>Genes and Development</i> , 2020 , 34, 1753-1761	12.6	4

55	Biophysical characterizations of the recognition of the AAUAAA polyadenylation signal. <i>Rna</i> , 2019 , 25, 1673-1680	5.8	7
54	Structural and mechanistic basis of mammalian Nudt12 RNA deNADding. <i>Nature Chemical Biology</i> , 2019 , 15, 575-582	11.7	20
53	Arabidopsis DXO1 links RNA turnover and chloroplast function independently of its enzymatic activity. <i>Nucleic Acids Research</i> , 2019 , 47, 4751-4764	20.1	13
52	An allosteric mechanism for potent inhibition of human ATP-citrate lyase. <i>Nature</i> , 2019 , 568, 566-570	50.4	52
51	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	20.1	28
50	Expression system for structural and functional studies of human glycosylation enzymes. <i>Nature Chemical Biology</i> , 2018 , 14, 156-162	11.7	114
49	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	11.5	84
48	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	1.1	21
47	How Does Polymerization Regulate Human Acetyl-CoA Carboxylase 1?. <i>Biochemistry</i> , 2018 , 57, 5495-5496	6.2	2
46	Molecular mechanism for the inhibition of DXO by adenosine 3'Sbisphosphate. <i>Biochemical and Biophysical Research Communications</i> , 2018 , 504, 89-95	3.4	6
45	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	4.1	68
44	5'End Nicotinamide Adenine Dinucleotide Cap in Human Cells Promotes RNA Decay through DXO-Mediated deNADding. <i>Cell</i> , 2017 , 168, 1015-1027.e10	56.2	114
43	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	11.5	28
42	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	3.7	9
41	Crystal structure of a <i>Pseudomonas</i> malonate decarboxylase holoenzyme hetero-tetramer. <i>Nature Communications</i> , 2017 , 8, 160	17.4	8
40	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	11.5	30
39	A distinct holoenzyme organization for two-subunit pyruvate carboxylase. <i>Nature Communications</i> , 2016 , 7, 12713	17.4	10
38	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	11.5	169

37	A unified molecular mechanism for the regulation of acetyl-CoA carboxylase by phosphorylation. <i>Cell Discovery</i> , 2016 , 2, 16044	22.3	23
36	Cyclic di-AMP targets the cystathionine beta-synthase domain of the osmolyte transporter OpuC. <i>Molecular Microbiology</i> , 2016 , 102, 233-243	4.1	59
35	Molecular basis for the recognition of cyclic-di-AMP by PstA, a PII-like signal transduction protein. <i>MicrobiologyOpen</i> , 2015 , 4, 361-74	3.4	31
34	Crystal structure of the 500-kDa yeast acetyl-CoA carboxylase holoenzyme dimer. <i>Nature</i> , 2015 , 526, 723-7	50.4	49
33	Structural and biochemical studies of the distinct activity profiles of Rai1 enzymes. <i>Nucleic Acids Research</i> , 2015 , 43, 6596-606	20.1	12
32	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	11.5	132
31	Delineating the structural blueprint of the pre-mRNA 3Send processing machinery. <i>Molecular and Cellular Biology</i> , 2014 , 34, 1894-910	4.8	57
30	The cyclic dinucleotide c-di-AMP is an allosteric regulator of metabolic enzyme function. <i>Cell</i> , 2014 , 158, 1389-1401	56.2	136
29	Structure and function of pre-mRNA 5Send capping quality control and 3Send processing. <i>Biochemistry</i> , 2014 , 53, 1882-98	3.2	24
28	Functional conformations for pyruvate carboxylase during catalysis explored by cryoelectron microscopy. <i>Structure</i> , 2014 , 22, 911-22	5.2	19
27	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	11.5	22
26	Structure and function of biotin-dependent carboxylases. <i>Cellular and Molecular Life Sciences</i> , 2013 , 70, 863-91	10.3	231
25	A mammalian pre-mRNA 5Send capping quality control mechanism and an unexpected link of capping to pre-mRNA processing. <i>Molecular Cell</i> , 2013 , 50, 104-15	17.6	104
24	Enzymatic basis for N-glycan sialylation: structure of rat α 6-sialyltransferase (ST6GAL1) reveals conserved and unique features for glycan sialylation. <i>Journal of Biological Chemistry</i> , 2013 , 288, 34680-98	5.4	85
23	Structure of histone mRNA stem-loop, human stem-loop binding protein, and 3SendExo ternary complex. <i>Science</i> , 2013 , 339, 318-21	33.3	85
22	Crystal structures of malonyl-coenzyme A decarboxylase provide insights into its catalytic mechanism and disease-causing mutations. <i>Structure</i> , 2013 , 21, 1182-92	5.2	16
21	Characterizing the importance of the biotin carboxylase domain dimer for Staphylococcus aureus pyruvate carboxylase catalysis. <i>Biochemistry</i> , 2013 , 52, 488-96	3.2	13
20	Dxo1 is a new type of eukaryotic enzyme with both decapping and 5SendExoribonuclease activity. <i>Nature Structural and Molecular Biology</i> , 2012 , 19, 1011-7	17.6	76

19	Structures of 5S3SExoribonucleases. <i>The Enzymes</i> , 2012 , 31, 115-29	2.3	4
18	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, 2265-70	12.6	36
17	Crystal structure of the Rna14-Rna15 complex. <i>Rna</i> , 2012 , 18, 1154-62	5.8	20
16	Identification of a quality-control mechanism for mRNA 5Send capping. <i>Nature</i> , 2010 , 467, 608-11	50.4	127
15	Crystal structure of the human symplekin-Ssu72-CTD phosphopeptide complex. <i>Nature</i> , 2010 , 467, 729-33	50.4	119
14	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, 22072-7	11.5	69
13	Cryo-EM analysis reveals new insights into the mechanism of action of pyruvate carboxylase. <i>Structure</i> , 2010 , 18, 1300-10	5.2	25
12	Real-time fluorescence detection of exoribonucleases. <i>Rna</i> , 2009 , 15, 2057-62	5.8	18
11	Structure and function of the 5S->3Sexoribonuclease Rat1 and its activating partner Rai1. <i>Nature</i> , 2009 , 458, 784-8	50.4	148
10	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	17.6	97
9	Nicotinamide adenine dinucleotide metabolism as an attractive target for drug discovery. <i>Expert Opinion on Therapeutic Targets</i> , 2007 , 11, 695-705	6.4	126
8	The use of in situ proteolysis in the crystallization of murine CstF-77. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007 , 63, 135-8		16
7	Crystal structure of the heterotrimer core of <i>Saccharomyces cerevisiae</i> AMPK homologue SNF1. <i>Nature</i> , 2007 , 449, 492-5	50.4	127
6	Crystal structure of murine CstF-77: dimeric association and implications for polyadenylation of mRNA precursors. <i>Molecular Cell</i> , 2007 , 25, 863-75	17.6	75
5	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, 1041-5		19
4	Polyadenylation factor CPSF-73 is the pre-mRNA 3Send-processing endonuclease. <i>Nature</i> , 2006 , 444, 953-6	50.4	316
3	Crystal structure of the carboxyltransferase domain of acetyl-coenzyme A carboxylase. <i>Science</i> , 2003 , 299, 2064-7	33.3	147
2	COMO: a program for combined molecular replacement. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001 , 57, 1127-34		75

1 Structural basis for signal transduction by the Toll/interleukin-1 receptor domains. *Nature*, **2000**, 408, 111-5

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