

Christopher D Lima

List of Publications by Year in descending order

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Version: 2024-02-01

32
papers

1,966
citations

430874

18
h-index

501196

28
g-index

32
all docs

32
docs citations

32
times ranked

2811
citing authors

#	ARTICLE	IF	CITATIONS
1	Ubiquitin-like Protein Conjugation: Structures, Chemistry, and Mechanism. <i>Chemical Reviews</i> , 2018, 118, 889-918.	47.7	376
2	Targeting RNA for processing or destruction by the eukaryotic RNA exosome and its cofactors. <i>Genes and Development</i> , 2017, 31, 88-100.	5.9	180
3	The eukaryotic RNA exosome. <i>Current Opinion in Structural Biology</i> , 2014, 24, 132-140.	5.7	148
4	ketu mutant mice uncover an essential meiotic function for the ancient RNA helicase YTHDC2. <i>ELife</i> , 2018, 7, .	6.0	129
5	Enzymology of RNA cap synthesis. <i>Wiley Interdisciplinary Reviews RNA</i> , 2010, 1, 152-172.	6.4	124
6	Recognition of Lys48-Linked Di-ubiquitin and Deubiquitinating Activities of the SARS Coronavirus Papain-like Protease. <i>Molecular Cell</i> , 2016, 62, 572-585.	9.7	122
7	Structure of the Human SENP7 Catalytic Domain and Poly-SUMO Deconjugation Activities for SENP6 and SENP7. <i>Journal of Biological Chemistry</i> , 2008, 283, 32045-32055.	3.4	116
8	Helicase-Dependent RNA Decay Illuminated by a Cryo-EM Structure of a Human Nuclear RNA Exosome-MTR4 Complex. <i>Cell</i> , 2018, 173, 1663-1677.e21.	28.9	116
9	Taking it step by step: mechanistic insights from structural studies of ubiquitin/ubiquitin-like protein modification pathways. <i>Current Opinion in Structural Biology</i> , 2007, 17, 726-735.	5.7	101
10	Nuclear RNA Exosome at 3.1Å... Reveals Substrate Specificities, RNA Paths, and Allosteric Inhibition of Rrp44/Dis3. <i>Molecular Cell</i> , 2016, 64, 734-745.	9.7	84
11	Structure of a Complex between Nedd8 and the Ulp/Senp Protease Family Member Den1. <i>Journal of Molecular Biology</i> , 2005, 345, 141-151.	4.2	76
12	Structural basis for MTR4-ZCCHC8 interactions that stimulate the MTR4 helicase in the nuclear exosome-targeting complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E5506-E5515.	7.1	49
13	Structure and reconstitution of yeast Mpp6-nuclear exosome complexes reveals that Mpp6 stimulates RNA decay and recruits the Mtr4 helicase. <i>ELife</i> , 2017, 6, .	6.0	49
14	The Rrp6 C-terminal domain binds RNA and activates the nuclear RNA exosome. <i>Nucleic Acids Research</i> , 2017, 45, 846-860.	14.5	46
15	Structural basis for adenylation and thioester bond formation in the ubiquitin E1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 15475-15484.	7.1	45
16	Discovery and engineering of enhanced SUMO protease enzymes. <i>Journal of Biological Chemistry</i> , 2018, 293, 13224-13233.	3.4	43
17	Structure and function of the yeast listerin (Ltn1) conserved N-terminal domain in binding to stalled 60S ribosomal subunits. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E4151-60.	7.1	34
18	RNA helicases are hubs that orchestrate exosome-dependent 3'→5' decay. <i>Current Opinion in Structural Biology</i> , 2021, 67, 86-94.	5.7	26

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19	YTHDC2 control of gametogenesis requires helicase activity but not m ⁶ A binding. <i>Genes and Development</i> , 2022, 36, 180-194.	5.9	25
20	Structure and Activities of the Eukaryotic RNA Exosome. <i>The Enzymes</i> , 2012, 31, 53-75.	1.7	18
21	Structural basis for RNA surveillance by the human nuclear exosome targeting (NEXT) complex. <i>Cell</i> , 2022, 185, 2132-2147.e26.	28.9	16
22	Fission yeast RNA triphosphatase reads an Spt5 CTD code. <i>Rna</i> , 2015, 21, 113-123.	3.5	11
23	Substrate selectivity by the exonuclease Rrp6p. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 982-992.	7.1	8
24	DNA asymmetry promotes SUMO modification of the single-stranded DNA-binding protein RPA. <i>EMBO Journal</i> , 2021, 40, e103787.	7.8	8
25	Substrate discrimination and quality control require each catalytic activity of TRAMP and the nuclear RNA exosome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	7
26	Strategies to Trap Enzyme-Substrate Complexes that Mimic Michaelis Intermediates During E3-Mediated Ubiquitin-Like Protein Ligation. <i>Methods in Molecular Biology</i> , 2018, 1844, 169-196.	0.9	5
27	Whole Cell Active Inhibitors of Mycobacterial Lipoamide Dehydrogenase Afford Selectivity over the Human Enzyme through Tight Binding Interactions. <i>ACS Infectious Diseases</i> , 2021, 7, 435-444.	3.8	1
28	Crystal structure of the <i>Schizosaccharomyces pombe</i> U7BR E2-binding region in complex with Ubc7. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2019, 75, 552-560.	0.8	1
29	Reconstitution of the Human Nuclear RNA Exosome. <i>Methods in Molecular Biology</i> , 2020, 2062, 467-489.	0.9	1
30	Reconstitution of <i>S. cerevisiae</i> RNA Exosome Complexes Using Recombinantly Expressed Proteins. <i>Methods in Molecular Biology</i> , 2020, 2062, 427-448.	0.9	1
31	Strategies for Generating RNA Exosome Complexes from Recombinant Expression Hosts. <i>Methods in Molecular Biology</i> , 2020, 2062, 417-425.	0.9	0
32	Reconstitution of the <i>Schizosaccharomyces pombe</i> RNA Exosome. <i>Methods in Molecular Biology</i> , 2020, 2062, 449-465.	0.9	0