

Lori Anne Passmore

List of Publications by Year in descending order

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Version: 2024-02-01

51
papers

4,128
citations

136740

32
h-index

182168

51
g-index

61
all docs

61
docs citations

61
times ranked

5259
citing authors

#	ARTICLE	IF	CITATIONS
1	Roles of mRNA poly(A) tails in regulation of eukaryotic gene expression. <i>Nature Reviews Molecular Cell Biology</i> , 2022, 23, 93-106.	16.1	188
2	RBBP6 activates the pre-mRNA 3' end processing machinery in humans. <i>Genes and Development</i> , 2022, 36, 210-224.	2.7	31
3	Mpe1 senses the binding of pre-mRNA and controls 3' end processing by CPF. <i>Molecular Cell</i> , 2022, 82, 2490-2504.e12.	4.5	9
4	Gel-Based Analysis of Protein-Nucleic Acid Interactions. <i>Methods in Molecular Biology</i> , 2021, 2263, 321-339.	0.4	1
5	The long and short of it. <i>ELife</i> , 2021, 10, .	2.8	6
6	Three-layered control of mRNA poly(A) tail synthesis in <i>Saccharomyces cerevisiae</i> . <i>Genes and Development</i> , 2021, 35, 1290-1303.	2.7	10
7	Dynamics in Fip1 regulate eukaryotic mRNA 3' end processing. <i>Genes and Development</i> , 2021, 35, 1510-1526.	2.7	13
8	CPSF3-dependent pre-mRNA processing as a druggable node in AML and Ewing's sarcoma. <i>Nature Chemical Biology</i> , 2020, 16, 50-59.	3.9	59
9	FANCD2-FANCI is a clamp stabilized on DNA by monoubiquitination of FANCD2 during DNA repair. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 240-248.	3.6	80
10	Deep learning enables the atomic structure determination of the Fanconi Anemia core complex from cryoEM. <i>IUCr</i> , 2020, 7, 881-892.	1.0	10
11	Interpretation of medium resolution cryoEM maps of multi-protein complexes. <i>Current Opinion in Structural Biology</i> , 2019, 58, 166-174.	2.6	18
12	Mechanistic insights into mRNA 3'-end processing. <i>Current Opinion in Structural Biology</i> , 2019, 59, 143-150.	2.6	83
13	The intrinsic structure of poly(A) RNA determines the specificity of Pan2 and Caf1 deadenylases. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 433-442.	3.6	42
14	Importance of the Conserved Carboxyl-Terminal CNOT1 Binding Domain to Tristetraprolin Activity <i>In Vivo</i> . <i>Molecular and Cellular Biology</i> , 2019, 39, .	1.1	17
15	Activation of the Endonuclease that Defines mRNA 3' Ends Requires Incorporation into an 8-Subunit Core Cleavage and Polyadenylation Factor Complex. <i>Molecular Cell</i> , 2019, 73, 1217-1231.e11.	4.5	70
16	Recognition of Poly(A) RNA through Its Intrinsic Helical Structure. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2019, 84, 21-30.	2.0	11
17	Structure of the Fanconi anaemia monoubiquitin ligase complex. <i>Nature</i> , 2019, 575, 234-237.	13.7	80
18	RNA-binding proteins distinguish between similar sequence motifs to promote targeted deadenylation by Ccr4-Not. <i>ELife</i> , 2019, 8, .	2.8	65

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19	A low-complexity region in the YTH domain protein Mmi1 enhances RNA binding. <i>Journal of Biological Chemistry</i> , 2018, 293, 9210-9222.	1.6	13
20	The APT complex is involved in non-coding RNA transcription and is distinct from CPF. <i>Nucleic Acids Research</i> , 2018, 46, 11528-11538.	6.5	17
21	mRNA Deadenylation Is Coupled to Translation Rates by the Differential Activities of Ccr4-Not Nucleases. <i>Molecular Cell</i> , 2018, 70, 1089-1100.e8.	4.5	182
22	Analysis of mRNA deadenylation by multi-protein complexes. <i>Methods</i> , 2017, 126, 95-104.	1.9	21
23	Architecture of eukaryotic mRNA 3' end processing machinery. <i>Science</i> , 2017, 358, 1056-1059.	6.0	124
24	Ultrastable Gold Substrates Improve the Resolution of 3D Reconstructed Density Maps from Electron Micrographs and Tomograms. <i>Microscopy and Microanalysis</i> , 2016, 22, 1148-1149.	0.2	0
25	Ultrastable gold substrates: Properties of a support for high-resolution electron cryomicroscopy of biological specimens. <i>Journal of Structural Biology</i> , 2016, 193, 33-44.	1.3	78
26	Macromolecular Complexes in Transcription and Co-Transcriptional RNA Processing. <i>Journal of Molecular Biology</i> , 2016, 428, 2539-2541.	2.0	1
27	Specimen Preparation for High-Resolution Cryo-EM. <i>Methods in Enzymology</i> , 2016, 579, 51-86.	0.4	128
28	Reconstitution of Targeted Deadenylation by the Ccr4-Not Complex and the YTH Domain Protein Mmi1. <i>Cell Reports</i> , 2016, 17, 1978-1989.	2.9	59
29	Progress towards an optimal specimen support for electron cryomicroscopy. <i>Current Opinion in Structural Biology</i> , 2016, 37, 81-89.	2.6	73
30	Ubiquitin-SUMO Circuitry Controls Activated Fanconi Anemia ID Complex Dosage in Response to DNA Damage. <i>Molecular Cell</i> , 2015, 57, 150-164.	4.5	106
31	Structural insights into the bacterial carbon-phosphorus lyase machinery. <i>Nature</i> , 2015, 525, 68-72.	13.7	63
32	Advances in Single-Particle Electron Cryomicroscopy Structure Determination applied to Sub-tomogram Averaging. <i>Structure</i> , 2015, 23, 1743-1753.	1.6	189
33	mRNA deadenylation by Pan2-Pan3. <i>Biochemical Society Transactions</i> , 2014, 42, 184-187.	1.6	57
34	Ultrastable gold substrates for electron cryomicroscopy. <i>Science</i> , 2014, 346, 1377-1380.	6.0	346
35	Abundance of the Fanconi anaemia core complex is regulated by the RuvBL1 and RuvBL2 AAA+ ATPases. <i>Nucleic Acids Research</i> , 2014, 42, 13736-13748.	6.5	37
36	RNA polymerase II termination involves C-terminal-domain tyrosine dephosphorylation by CPF subunit Glc7. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 175-179.	3.6	77

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37	Robust evaluation of 3D electron cryomicroscopy data using tilt-pairs. <i>Journal of Structural Biology</i> , 2014, 187, 112-118.	1.3	16
38	Controlling protein adsorption on graphene for cryo-EM using low-energy hydrogen plasmas. <i>Nature Methods</i> , 2014, 11, 649-652.	9.0	172
39	Structural basis for <i>P</i> ^{an3} binding to <i>P</i> ^{an2} and its function in <i>mRNA</i> recruitment and deadenylation. <i>EMBO Journal</i> , 2014, 33, 1514-1526.	3.5	50
40	The Genetic and Biochemical Basis of FANCD2 Monoubiquitination. <i>Molecular Cell</i> , 2014, 54, 858-869.	4.5	109
41	Modifying Graphene Substrates for Imaging Proteins in a Transmission Electron Microscope. <i>Microscopy and Microanalysis</i> , 2014, 20, 1214-1215.	0.2	0
42	The Crystal Structure of the Intact <i>E. coli</i> RelBE Toxin-Antitoxin Complex Provides the Structural Basis for Conditional Cooperativity. <i>Structure</i> , 2012, 20, 1641-1648.	1.6	88
43	Tilt-Pair Analysis of Images from a Range of Different Specimens in Single-Particle Electron Cryomicroscopy. <i>Journal of Molecular Biology</i> , 2011, 413, 1028-1046.	2.0	138
44	Cytoplasmic deadenylation: regulation of mRNA fate. <i>Biochemical Society Transactions</i> , 2010, 38, 1531-1536.	1.6	69
45	The Eukaryotic Translation Initiation Factors eIF1 and eIF1A Induce an Open Conformation of the 40S Ribosome. <i>Molecular Cell</i> , 2007, 26, 41-50.	4.5	289
46	Coactivator functions in a stoichiometric complex with anaphase-promoting complex/cyclosome to mediate substrate recognition. <i>EMBO Reports</i> , 2005, 6, 873-878.	2.0	47
47	Purification and Assay of the Budding Yeast Anaphase-Promoting Complex. <i>Methods in Enzymology</i> , 2005, 398, 195-219.	0.4	19
48	Structural Analysis of the Anaphase-Promoting Complex Reveals Multiple Active Sites and Insights into Polyubiquitylation. <i>Molecular Cell</i> , 2005, 20, 855-866.	4.5	81
49	Getting into position: the catalytic mechanisms of protein ubiquitylation. <i>Biochemical Journal</i> , 2004, 379, 513-525.	1.7	269
50	Doc1 mediates the activity of the anaphase-promoting complex by contributing to substrate recognition. <i>EMBO Journal</i> , 2003, 22, 786-796.	3.5	176
51	Regulation of RasGRP via a Phorbol Ester-Responsive C1 Domain. <i>Molecular and Cellular Biology</i> , 1998, 18, 6995-7008.	1.1	215