

Craig D Kaplan

List of Publications by Year in descending order

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Version: 2024-02-01

51
papers

3,702
citations

279798

23
h-index

189892

50
g-index

67
all docs

67
docs citations

67
times ranked

3789
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural visualization of de novo transcription initiation by <i>Saccharomyces cerevisiae</i> RNA polymerase II. <i>Molecular Cell</i> , 2022, 82, 660-676.e9.	9.7	9
2	Germline mutation in POLR2A: a heterogeneous, multi-systemic developmental disorder characterized by transcriptional dysregulation. <i>Human Genetics and Genomics Advances</i> , 2021, 2, 100014.	1.7	10
3	A genome-wide copper-sensitized screen identifies novel regulators of mitochondrial cytochrome c oxidase activity. <i>Journal of Biological Chemistry</i> , 2021, 296, 100485.	3.4	7
4	Cryo-EM structure of TFIIH/Rad4/Rad23/Rad33 in damaged DNA opening in nucleotide excision repair. <i>Nature Communications</i> , 2021, 12, 3338.	12.8	24
5	A PICture is worth a thousand words (and ten references). <i>Cell</i> , 2021, 184, 3850-3851.	28.9	0
6	Ssl2/TFIIH function in transcription start site scanning by RNA polymerase II in <i>Saccharomyces cerevisiae</i> . <i>ELife</i> , 2021, 10, .	6.0	5
7	Specialized RSC: Substrate Specificities for a Conserved Chromatin Remodeler. <i>BioEssays</i> , 2020, 42, 2000002.	2.5	3
8	Universal promoter scanning by Pol II during transcription initiation in <i>Saccharomyces cerevisiae</i> . <i>Genome Biology</i> , 2020, 21, 132.	8.8	35
9	Organismal benefits of transcription speed control at gene boundaries. <i>EMBO Reports</i> , 2020, 21, e49315.	4.5	28
10	Functional assays for transcription mechanisms in high-throughput. <i>Methods</i> , 2019, 159-160, 115-123.	3.8	9
11	Perturbations of Transcription and Gene Expression-Associated Processes Alter Distribution of Cell Size Values in <i>Saccharomyces cerevisiae</i> . <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 239-250.	1.8	7
12	High-resolution and high-accuracy topographic and transcriptional maps of the nucleosome barrier. <i>ELife</i> , 2019, 8, .	6.0	63
13	Codon-Based Sequence Alignment for Mutation Analysis by High-Throughput Sequencing. , 2018, , .		0
14	Wide-ranging and unexpected consequences of altered Pol II catalytic activity <i>in vivo</i> . <i>Nucleic Acids Research</i> , 2017, 45, gkx037.	14.5	28
15	Relationships Between RNA Polymerase II Activity and Spt Elongation Factors to Spt- Phenotype and Growth in <i>Saccharomyces cerevisiae</i> . <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 2489-2504.	1.8	5
16	RNA Polymerase II Trigger Loop Mobility. <i>Journal of Biological Chemistry</i> , 2016, 291, 14883-14895.	3.4	11
17	The mechanism of RNA 5' capping with NAD ⁺ , NADH and desphospho-CoA. <i>Nature</i> , 2016, 535, 444-447.	27.8	181
18	Pairs of promoter pairs in a web of transcription. <i>Nature Genetics</i> , 2016, 48, 975-976.	21.4	6

#	ARTICLE	IF	CITATIONS
19	High-Resolution Phenotypic Landscape of the RNA Polymerase II Trigger Loop. <i>PLoS Genetics</i> , 2016, 12, e1006321.	3.5	25
20	Relationships of RNA Polymerase II Genetic Interactors to Transcription Start Site Usage Defects and Growth in <i>Saccharomyces cerevisiae</i> . <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 21-33.	1.8	13
21	Uncoupling Promoter Opening from Start-Site Scanning. <i>Molecular Cell</i> , 2015, 59, 133-138.	9.7	37
22	Crystal Structure of a Transcribing RNA Polymerase II Complex Reveals a Complete Transcription Bubble. <i>Molecular Cell</i> , 2015, 59, 258-269.	9.7	98
23	The Histone Chaperones FACT and Spt6 Restrict H2A.Z from Intragenic Locations. <i>Molecular Cell</i> , 2015, 58, 1113-1123.	9.7	108
24	Activation and reactivation of the RNA polymerase II trigger loop for intrinsic RNA cleavage and catalysis. <i>Transcription</i> , 2014, 5, e28869.	3.1	26
25	Transcription factors TFIIF and TFIIIS promote transcript elongation by RNA polymerase II by synergistic and independent mechanisms. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 6642-6647.	7.1	68
26	RNAs nonspecifically inhibit RNA polymerase II by preventing binding to the DNA template. <i>Rna</i> , 2014, 20, 644-655.	3.5	8
27	TFIIF and TFIIIS Enhance the Mechanical Persistence of Transcript Elongation by RNA Polymerase II. <i>Biophysical Journal</i> , 2014, 106, 486a.	0.5	2
28	From Structure to Systems: High-Resolution, Quantitative Genetic Analysis of RNA Polymerase II. <i>Cell</i> , 2013, 154, 775-788.	28.9	132
29	Divergent Contributions of Conserved Active Site Residues to Transcription by Eukaryotic RNA Polymerases I and II. <i>Cell Reports</i> , 2013, 4, 974-984.	6.4	34
30	Basic mechanisms of RNA polymerase II activity and alteration of gene expression in <i>Saccharomyces cerevisiae</i> . <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2013, 1829, 39-54.	1.9	42
31	Dissection of Pol II Trigger Loop Function and Pol II Activity-Dependent Control of Start Site Selection In Vivo. <i>PLoS Genetics</i> , 2012, 8, e1002627.	3.5	93
32	Tfb6, a previously unidentified subunit of the general transcription factor TFIIF, facilitates dissociation of Ssl2 helicase after transcription initiation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 4816-4821.	7.1	23
33	Trigger loop dynamics mediate the balance between the transcriptional fidelity and speed of RNA polymerase II. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 6555-6560.	7.1	118
34	Competing for the Clamp: Promoting RNA Polymerase Processivity and Managing the Transition from Initiation to Elongation. <i>Molecular Cell</i> , 2011, 43, 161-163.	9.7	15
35	The architecture of RNA polymerase fidelity. <i>BMC Biology</i> , 2010, 8, 85.	3.8	13
36	A Dual Interface Determines the Recognition of RNA Polymerase II by RNA Capping Enzyme*. <i>Journal of Biological Chemistry</i> , 2010, 285, 34027-34038.	3.4	29

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37	Revealing the hidden relationship between nucleosomes and splicing. <i>Cell Cycle</i> , 2009, 8, 3631-3635.	2.6	3
38	Evolution, biogenesis and function of promoter-associated RNAs. <i>Cell Cycle</i> , 2009, 8, 2332-2338.	2.6	89
39	Iron Acquisition and Transcriptional Regulation. <i>Chemical Reviews</i> , 2009, 109, 4536-4552.	47.7	248
40	A bridge to transcription by RNA polymerase. <i>Journal of Biology</i> , 2008, 7, 39.	2.7	18
41	The RNA Polymerase II Trigger Loop Functions in Substrate Selection and Is Directly Targeted by Î±-Amanitin. <i>Molecular Cell</i> , 2008, 30, 547-556.	9.7	239
42	Polyadenylation site choice in yeast is affected by competition between Npl3 and polyadenylation factor CFI. <i>Rna</i> , 2007, 13, 1756-1764.	3.5	50
43	Structural basis of RNA polymerase II substrate specificity and catalysis. <i>FASEB Journal</i> , 2007, 21, A656.	0.5	0
44	Structural Basis of Transcription: Role of the Trigger Loop in Substrate Specificity and Catalysis. <i>Cell</i> , 2006, 127, 941-954.	28.9	421
45	Interaction between Transcription Elongation Factors and mRNA 3'â€²-End Formation at the <i>Saccharomyces cerevisiae</i> GAL10-GAL7 Locus. <i>Journal of Biological Chemistry</i> , 2005, 280, 913-922.	3.4	82
46	Regulatory oversight of the iron trade: Posttranscriptional regulation in yeast. <i>Cell Metabolism</i> , 2005, 2, 4-6.	16.2	1
47	Transcription Elongation Factors Repress Transcription Initiation from Cryptic Sites. <i>Science</i> , 2003, 301, 1096-1099.	12.6	526
48	Helicase activity is only partially required for <i>Schizosaccharomyces pombe</i> Rqh1p function. <i>Yeast</i> , 2002, 19, 1381-1398.	1.7	16
49	Spt5 and Spt6 are associated with active transcription and have characteristics of general elongation factors in <i>D. melanogaster</i> . <i>Genes and Development</i> , 2000, 14, 2623-2634.	5.9	204
50	Post-transcriptional Control of Cyclooxygenase-2 Gene Expression. <i>Journal of Biological Chemistry</i> , 2000, 275, 11750-11757.	3.4	314
51	Retinal degeneration characterizes a spinocerebellar ataxia mapping to chromosome 3p. <i>Nature Genetics</i> , 1995, 10, 89-93.	21.4	136