

L Stirling Churchman

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9042674/publications.pdf>

Version: 2024-02-01

34
papers

3,772
citations

361413

20
h-index

414414

32
g-index

46
all docs

46
docs citations

46
times ranked

5576
citing authors

#	ARTICLE	IF	CITATIONS
1	Transcription elongation is finely tuned by dozens of regulatory factors. <i>ELife</i> , 2022, 11, .	6.0	8
2	Revealing nascent RNA processing dynamics with nano-COP. <i>Nature Protocols</i> , 2021, 16, 1343-1375.	12.0	27
3	GeneWalk identifies relevant gene functions for a biological context using network representation learning. <i>Genome Biology</i> , 2021, 22, 55.	8.8	28
4	Essential histone chaperones collaborate to regulate transcription and chromatin integrity. <i>Genes and Development</i> , 2021, 35, 698-712.	5.9	22
5	Hsf1 activation by proteotoxic stress requires concurrent protein synthesis. <i>Molecular Biology of the Cell</i> , 2021, 32, 1800-1806.	2.1	19
6	Splicing Kinetics and Coordination Revealed by Direct Nascent RNA Sequencing through Nanopores. <i>Molecular Cell</i> , 2020, 77, 985-998.e8.	9.7	149
7	The yeast exoribonuclease Xrn1 and associated factors modulate RNA polymerase II processivity in 5' and 3' gene regions. <i>Journal of Biological Chemistry</i> , 2020, 295, 11435-11454.	3.4	25
8	Single-molecule regulatory architectures captured by chromatin fiber sequencing. <i>Science</i> , 2020, 368, 1449-1454.	12.6	106
9	<i>RPS15</i> and <i>TP53</i> Co-Mutation Drives B Cell Malignancy through Altered Translation and MYC Activation in a Murine Model. <i>Blood</i> , 2020, 136, 28-29.	1.4	4
10	The Long and the Short of the RNA Polymerase C-Terminal Domain and Phase Separation. <i>Molecular Cell</i> , 2019, 73, 1087-1088.	9.7	4
11	Proteotoxicity from aberrant ribosome biogenesis compromises cell fitness. <i>ELife</i> , 2019, 8, .	6.0	88
12	Set2 methyltransferase facilitates cell cycle progression by maintaining transcriptional fidelity. <i>Nucleic Acids Research</i> , 2018, 46, 1331-1344.	14.5	23
13	Cell-Cycle Modulation of Transcription Termination Factor Sen1. <i>Molecular Cell</i> , 2018, 70, 312-326.e7.	9.7	18
14	Spt6 Is Required for the Fidelity of Promoter Selection. <i>Molecular Cell</i> , 2018, 72, 687-699.e6.	9.7	58
15	The Multiple Levels of Mitonuclear Coregulation. <i>Annual Review of Genetics</i> , 2018, 52, 511-533.	7.6	43
16	The code and beyond: transcription regulation by the RNA polymerase II carboxy-terminal domain. <i>Nature Reviews Molecular Cell Biology</i> , 2017, 18, 263-273.	37.0	370
17	Subgenic Pol II interactomes identify region-specific transcription elongation regulators. <i>Molecular Systems Biology</i> , 2017, 13, 900.	7.2	34
18	Total RNA-seq to identify pharmacological effects on specific stages of mRNA synthesis. <i>Nature Chemical Biology</i> , 2017, 13, 501-507.	8.0	26

#	ARTICLE	IF	CITATIONS
19	Pause & go: from the discovery of RNA polymerase pausing to its functional implications. <i>Current Opinion in Cell Biology</i> , 2017, 46, 72-80.	5.4	113
20	Not Just Noise: Genomics and Genetics Bring Long Noncoding RNAs into Focus. <i>Molecular Cell</i> , 2017, 65, 1-2.	9.7	18
21	A Detailed Protocol for Subcellular RNA Sequencing (subRNA-seq). <i>Current Protocols in Molecular Biology</i> , 2017, 120, 4.29.1-4.29.18.	2.9	20
22	Mitochondrial Ribosome (Mitoribosome) Profiling for Monitoring Mitochondrial Translation In Vivo. <i>Current Protocols in Molecular Biology</i> , 2017, 119, 4.28.1-4.28.25.	2.9	16
23	The Ground State and Evolution of Promoter Region Directionality. <i>Cell</i> , 2017, 170, 889-898.e10.	28.9	77
24	BET Bromodomain Proteins Function as Master Transcription Elongation Factors Independent of CDK9 Recruitment. <i>Molecular Cell</i> , 2017, 67, 5-18.e19.	9.7	347
25	Synchronized mitochondrial and cytosolic translation programs. <i>Nature</i> , 2016, 533, 499-503.	27.8	267
26	Comprehensive RNA Polymerase II Interactomes Reveal Distinct and Varied Roles for Each Phospho-CTD Residue. <i>Cell Reports</i> , 2016, 15, 2147-2158.	6.4	113
27	Genome-wide profiling of RNA polymerase transcription at nucleotide resolution in human cells with native elongating transcript sequencing. <i>Nature Protocols</i> , 2016, 11, 813-833.	12.0	65
28	Native Elongating Transcript Sequencing Reveals Human Transcriptional Activity at Nucleotide Resolution. <i>Cell</i> , 2015, 161, 541-554.	28.9	342
29	Single Mammalian Cells Compensate for Differences in Cellular Volume and DNA Copy Number through Independent Global Transcriptional Mechanisms. <i>Molecular Cell</i> , 2015, 58, 339-352.	9.7	429
30	Interactome Dynamics of the Transcription Elongation Complex Revealed by Quantitative Proteomics. <i>FASEB Journal</i> , 2015, 29, 562.3.	0.5	0
31	Mitochondrial Ribosome Profiling Reveals Rapid and Dynamic Translation Regulation During Yeast Mitochondrial Biogenesis. <i>FASEB Journal</i> , 2015, 29, 565.3.	0.5	0
32	A Chromatin-Based Mechanism for Limiting Divergent Noncoding Transcription. <i>Cell</i> , 2014, 157, 1712-1723.	28.9	98
33	Native Elongating Transcript Sequencing (NET-seq). <i>Current Protocols in Molecular Biology</i> , 2012, 98, Unit 4.14.1-17.	2.9	67
34	Nascent transcript sequencing visualizes transcription at nucleotide resolution. <i>Nature</i> , 2011, 469, 368-373.	27.8	706