Sebastian S Chavez

List of Publications by Year
in descending order

83 papers	4,447 citations	109264 35 h-index	114418 63 g-index
92 all docs	92 docs citations	92 times ranked	5457 citing authors

#	Article	IF	Citations
1	Xrn1 influence on gene transcription results from the combination of general effects on elongating RNA pol II and gene-specific chromatin configuration. RNA Biology, 2021, 18, 1310-1323.	1.5	12
2	Cell volume homeostatically controls the rDNA repeat copy number and rRNA synthesis rate in yeast. PLoS Genetics, 2021, 17, e1009520.	1.5	14
3	Human prefoldin modulates co-transcriptional pre-mRNA splicing. Nucleic Acids Research, 2021, 49, 6267-6280.	6.5	5
4	The total mRNA concentration buffering system in yeast is global rather than gene-specific. Rna, 2021, 27, 1281-1290.	1.6	11
5	Transcriptional Run-on: Measuring Nascent Transcription at Specific Genomic Sites in Yeast. Bio-protocol, 2021, 11, e4064.	0.2	0
6	Overexpression of Canonical Prefoldin Associates with the Risk of Mortality and Metastasis in Non-Small Cell Lung Cancer. Cancers, 2020, 12, 1052.	1.7	8
7	Homeostasis in the Central Dogma of molecular biology: the importance of mRNA instability. RNA Biology, 2019, 16, 1659-1666.	1.5	26
8	The mRNA degradation factor Xrn1 regulates transcription elongation in parallel to Ccr4. Nucleic Acids Research, 2019, 47, 9524-9541.	6.5	26
9	Feedback regulation of ribosome assembly. Current Genetics, 2018, 64, 393-404.	0.8	50
10	Rpb5 modulates the RNA polymerase II transition from initiation to elongation by influencing Spt5 association and backtracking. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2018, 1861, 1-13.	0.9	6
11	Functional Contributions of Prefoldin to Gene Expression. Advances in Experimental Medicine and Biology, 2018, 1106, 1-10.	0.8	13
12	High levels of histones promote whole-genome-duplications and trigger a Swe1WEE1-dependent phosphorylation of Cdc28CDK1. ELife, 2018, 7, .	2.8	10
13	Asymmetric cell division requires specific mechanisms for adjusting global transcription. Nucleic Acids Research, 2017, 45, 12401-12412.	6.5	30
14	The ribosome assembly gene network is controlled by the feedback regulation of transcription elongation. Nucleic Acids Research, 2017, 45, 9302-9318.	6.5	13
15	Subtracting the sequence bias from partially digested MNase-seq data reveals a general contribution of TFIIS to nucleosome positioning. Epigenetics and Chromatin, 2017, 10, 58.	1.8	17
16	Regulation of transcription elongation in response to osmostress. PLoS Genetics, 2017, 13, e1007090.	1.5	19
17	The importance of controlling mRNA turnover during cell proliferation. Current Genetics, 2016, 62, 701-710.	0.8	23
18	Growth rate controls mRNA turnover in steady and non-steady states. RNA Biology, 2016, 13, 1175-1181.	1.5	21

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19	The cellular growth rate controls overall mRNA turnover, and modulates either transcription or degradation rates of particular gene regulons. Nucleic Acids Research, 2016, 44, 3643-3658.	6.5	45
20	<i>Cis</i>- and <i>Trans</i>-Regulatory Mechanisms of Gene Expression in the ASJ Sensory Neuron of <i>Caenorhabditis elegans</i>. Genetics, 2015, 200, 123-134.	1.2	14
21	H3K4 monomethylation dictates nucleosome dynamics and chromatin remodeling at stress-responsive genes. Nucleic Acids Research, 2015, 43, 4937-4949.	6.5	34
22	Chromatin-dependent regulation of RNA polymerases II and III activity throughout the transcription cycle. Nucleic Acids Research, 2015, 43, 787-802.	6.5	23
23	Cytoplasmic 5â€²-3â€² exonuclease Xrn1p is also a genome-wide transcription factor in yeast. Frontiers in Genetics, 2014, 5, 1.	1.1	427
24	The yeast prefoldin-like URI-orthologue Bud27 associates with the RSC nucleosome remodeler and modulates transcription. Nucleic Acids Research, 2014, 42, 9666-9676.	6.5	29
25	Flow Cytometry of Microencapsulated Colonies for Genetics Analysis of Filamentous Fungi. G3: Genes, Genomes, Genetics, 2014, 4, 2271-2278.	0.8	19
26	RNA Polymerase II-Dependent Transcription in Fungi and Its Interplay with mRNA Decay. , 2014, , 1-26.		0
27	Nuclear functions of prefoldin. Open Biology, 2014, 4, 140085.	1.5	103
28	What do you mean by transcription rate?. BioEssays, 2013, 35, 1056-1062.	1.2	19
29	External conditions inversely change the RNA polymerase II elongation rate and density in yeast. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2013, 1829, 1248-1255.	0.9	17
30	Eukaryotic mRNA Decay: Methodologies, Pathways, and Links to Other Stages of Gene Expression. Journal of Molecular Biology, 2013, 425, 3750-3775.	2.0	125
31	Gene Expression Is Circular: Factors for mRNA Degradation Also Foster mRNA Synthesis. Cell, 2013, 153, 1000-1011.	13.5	311
32	Balanced Production of Ribosome Components Is Required for Proper G1/S Transition in Saccharomyces cerevisiae. Journal of Biological Chemistry, 2013, 288, 31689-31700.	1.6	43
33	The Prefoldin Complex Regulates Chromatin Dynamics during Transcription Elongation. PLoS Genetics, 2013, 9, e1003776.	1.5	45
34	A Genome-Wide Screen Identifies Yeast Genes Required for Tolerance to Technical Toxaphene, an Organochlorinated Pesticide Mixture. PLoS ONE, 2013, 8, e81253.	1.1	12
35	The relative importance of transcription rate, cryptic transcription and mRNA stability on shaping stress responses in yeast. Transcription, 2012, 3, 39-44.	1.7	5
36	TFIIS is required for the balanced expression of the genes encoding ribosomal components under transcriptional stress. Nucleic Acids Research, 2012, 40, 6508-6519.	6.5	32

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37	Gene Control during Transcription Elongation. Genetics Research International, 2012, 2012, 1-2.	2.0	0
38	One step back before moving forward: Regulation of transcription elongation by arrest and backtracking. FEBS Letters, 2012, 586, 2820-2825.	1.3	25
39	Genome-wide studies of mRNA synthesis and degradation in eukaryotes. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2012, 1819, 604-615.	0.9	31
40	A Matter of Packaging: Influence of Nucleosome Positioning on Heterologous Gene Expression. Methods in Molecular Biology, 2012, 824, 51-64.	0.4	1
41	Free Histones and the Cell Cycle. , 2011, , .		0
42	Chromatin Reassembly Factors Are Involved in Transcriptional Interference Promoting HIV Latency. Journal of Virology, 2011, 85, 3187-3202.	1.5	71
43	Application of Flow Focusing to the Break-Up of a Magnetite Suspension Jet for the Production of Paramagnetic Microparticles. Journal of Nanomaterials, 2011, 2011, 1-10.	1.5	9
44	FACT Prevents the Accumulation of Free Histones Evicted from Transcribed Chromatin and a Subsequent Cell Cycle Delay in G1. PLoS Genetics, 2010, 6, e1000964.	1.5	59
45	The distribution of active RNA polymerase II along the transcribed region is gene-specific and controlled by elongation factors. Nucleic Acids Research, 2010, 38, 4651-4664.	6.5	40
46	A Complete Set of Nascent Transcription Rates for Yeast Genes. PLoS ONE, 2010, 5, e15442.	1.1	151
47	Yeast Genetic Analysis Reveals the Involvement of Chromatin Reassembly Factors in Repressing HIV-1 Basal Transcription. PLoS Genetics, 2009, 5, e1000339.	1.5	23
48	Genome-Wide Analysis of Factors Affecting Transcription Elongation and DNA Repair: A New Role for PAF and Ccr4-Not in Transcription-Coupled Repair. PLoS Genetics, 2009, 5, e1000364.	1.5	81
49	Regulon-Specific Control of Transcription Elongation across the Yeast Genome. PLoS Genetics, 2009, 5, e1000614.	1.5	59
50	Recruitment of a chromatin remodelling complex by the Hog1 MAP kinase to stress genes. EMBO Journal, 2009, 28, 326-336.	3.5	104
51	Recruitment of a chromatin remodelling complex by the Hog1 MAP kinase to stress genes. EMBO Journal, 2009, 28, 1191-1191.	3.5	1
52	Systems for applied gene control in Saccharomyces cerevisiae. Biotechnology Letters, 2008, 30, 979-987.	1.1	38
53	Different physiological relevance of yeast THO/TREX subunits in gene expression and genome integrity. Molecular Genetics and Genomics, 2008, 279, 123-132.	1.0	32
54	Sus1 is recruited to coding regions and functions during transcription elongation in association with SAGA and TREX2. Genes and Development, 2008, 22, 2811-2822.	2.7	90

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55	An improved system for estradiol-dependent regulation of gene expression in yeast. Microbial Cell Factories, 2007, 6, 10.	1.9	22
56	Structural Characterization of Set1 RNA Recognition Motifs and their Role in Histone H3 Lysine 4 Methylation. Journal of Molecular Biology, 2006, 359, 1170-1181.	2.0	52
57	A simple in vivo assay for measuring the efficiency of gene length-dependent processes in yeast mRNA biogenesis. FEBS Journal, 2006, 273, 756-769.	2.2	52
58	Straightforward production of encoded microbeads by Flow Focusing: Potential applications for biomolecule detection. International Journal of Pharmaceutics, 2006, 324, 19-26.	2.6	24
59	Towards High-Throughput Production of Uniformly Encoded Microparticles. Advanced Materials, 2006, 18, 559-564.	11.1	70
60	A Gene-Specific Requirement for FACT during Transcription Is Related to the Chromatin Organization of the Transcribed Region. Molecular and Cellular Biology, 2006, 26, 8710-8721.	1.1	43
61	Protein Interactions within the Set1 Complex and Their Roles in the Regulation of Histone 3 Lysine 4 Methylation. Journal of Biological Chemistry, 2006, 281, 35404-35412.	1.6	142
62	Flow Focusing: A Versatile Technology to Produce Size-Controlled and Specific-Morphology Microparticles. Small, 2005, 1, 688-692.	5.2	185
63	Hpr1 Is Preferentially Required for Transcription of Either Long or G+C-Rich DNA Sequences in Saccharomyces cerevisiae. Molecular and Cellular Biology, 2001, 21, 7054-7064.	1.1	106
64	Mitotic recombination in yeast: elements controlling its incidence. Yeast, 2000, 16, 731-754.	0.8	78
65	Variegation associated with lacZ in transgenic animals: a warning note. Transgenic Research, 2000, 9, 237-239.	1.3	39
66	A protein complex containing Tho2, Hpr1, Mft1 and a novel protein, Thp2, connects transcription elongation with mitotic recombination in Saccharomyces cerevisiae. EMBO Journal, 2000, 19, 5824-5834.	3.5	267
67	The yeast <i>HPR1</i> gene has a functional role in transcriptional elongation that uncovers a novel source of genomeâ€‰instability. Genes and Development, 1997, 11, 3459-3470.	2.7	156
68	Nucleosome-mediated synergism between transcription factors on the mouse mammary tumor virus promoter. Proceedings of the National Academy of Sciences of the United States of America, 1997, 94, 2885-2890.	3.3	81
69	The Yeast <i>HRS1</i> Gene Is Involved in Positive and Negative Regulation of Transcription and Shows Genetic Characteristics Similar to <i>SIN4</i> and <i>GAL11</i>. Genetics, 1997, 147, 1585-1594.	1.2	52
70	Chromatin Structure and Gene Regulation by Steroid Hormones. , 1997, , 127-144.		0
71	The hormone responsive region of mouse mammary tumor virus positions a nucleosome and precludes access of nuclear factor I to the promoter. Journal of Steroid Biochemistry and Molecular Biology, 1996, 57, 19-31.	1.2	22
72	Interaction of steroid hormone receptors with transcription factors involves chromatin remodelling. Journal of Steroid Biochemistry and Molecular Biology, 1996, 56, 47-59.	1.2	43

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73	Control of Transcription by Steroid Hormones. Annals of the New York Academy of Sciences, 1996, 784, 93-123.	1.8	138
74	Transcriptional regulation by steroid hormones. Steroids, 1996, 61, 240-251.	0.8	217
75	Chromatin structure of the MMTV promoter and its changes during hormonal induction. Cellular and Molecular Neurobiology, 1996, 16, 85-101.	1.7	16
76	Existence of two ferredoxin-glutamate synthases in the cyanobacterium Synechocystis sp. PCC 6803. Isolation and insertional inactivation of gltB and gltS genes. Plant Molecular Biology, 1995, 27, 753-767.	2.0	40
77	The NADP-glutamate dehydrogenase of the cyanobacterium Synechocystis 6803: cloning, transcriptional analysis and disruption of the gdhA gene. Plant Molecular Biology, 1995, 28, 173-188.	2.0	24
78	Light-regulated promoters fromSynechocystisPCC6803 share a consensus motif involved in photoregulation. Molecular Microbiology, 1994, 12, 1005-1012.	1.2	17
79	Cloning and correct expression inE. coliof thepetJ gene encoding cytochromec6fromSynechocystis6803. FEBS Letters, 1994, 347, 173-177.	1.3	41
80	Synechocystis6803 plastocyanin isolated from both the cyanobacterium andE. colitransformed cells are identical. FEBS Letters, 1993, 319, 257-260.	1.3	37
81	Effect of Glucose Utilization on Nitrite Excretion by the Unicellular Cyanobacterium Synechocystis sp. Strain PCC 6803. Applied and Environmental Microbiology, 1993, 59, 3161-3163.	1.4	7
82	An NAD-specific glutamate dehydrogenase from cyanobacteria Identification and properties. FEBS Letters, 1991, 285, 35-38.	1.3	38
83	Point Mutation in the Ligand-Binding Domain of the Progesterone Receptor Generates a Transdominant Negative Phenotype. , 0, .		5