

Sebastian S Chavez

List of Publications by Year in descending order

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83
papers

4,447
citations

109264

35
h-index

114418

63
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92
all docs

92
docs citations

92
times ranked

5457
citing authors

#	ARTICLE	IF	CITATIONS
1	Cytoplasmic 5â€²-3â€² exonuclease Xrn1p is also a genome-wide transcription factor in yeast. <i>Frontiers in Genetics</i> , 2014, 5, 1.	1.1	427
2	Gene Expression Is Circular: Factors for mRNA Degradation Also Foster mRNA Synthesis. <i>Cell</i> , 2013, 153, 1000-1011.	13.5	311
3	A protein complex containing Tho2, Hpr1, Mft1 and a novel protein, Thp2, connects transcription elongation with mitotic recombination in <i>Saccharomyces cerevisiae</i> . <i>EMBO Journal</i> , 2000, 19, 5824-5834.	3.5	267
4	Transcriptional regulation by steroid hormones. <i>Steroids</i> , 1996, 61, 240-251.	0.8	217
5	Flow Focusing: A Versatile Technology to Produce Size-Controlled and Specific-Morphology Microparticles. <i>Small</i> , 2005, 1, 688-692.	5.2	185
6	The yeast <i>HPR1</i> gene has a functional role in transcriptional elongation that uncovers a novel source of genome instability. <i>Genes and Development</i> , 1997, 11, 3459-3470.	2.7	156
7	A Complete Set of Nascent Transcription Rates for Yeast Genes. <i>PLoS ONE</i> , 2010, 5, e15442.	1.1	151
8	Protein Interactions within the Set1 Complex and Their Roles in the Regulation of Histone 3 Lysine 4 Methylation. <i>Journal of Biological Chemistry</i> , 2006, 281, 35404-35412.	1.6	142
9	Control of Transcription by Steroid Hormones. <i>Annals of the New York Academy of Sciences</i> , 1996, 784, 93-123.	1.8	138
10	Eukaryotic mRNA Decay: Methodologies, Pathways, and Links to Other Stages of Gene Expression. <i>Journal of Molecular Biology</i> , 2013, 425, 3750-3775.	2.0	125
11	Hpr1 Is Preferentially Required for Transcription of Either Long or G+C-Rich DNA Sequences in <i>Saccharomyces cerevisiae</i> . <i>Molecular and Cellular Biology</i> , 2001, 21, 7054-7064.	1.1	106
12	Recruitment of a chromatin remodelling complex by the Hog1 MAP kinase to stress genes. <i>EMBO Journal</i> , 2009, 28, 326-336.	3.5	104
13	Nuclear functions of prefoldin. <i>Open Biology</i> , 2014, 4, 140085.	1.5	103
14	Sus1 is recruited to coding regions and functions during transcription elongation in association with SAGA and TREX2. <i>Genes and Development</i> , 2008, 22, 2811-2822.	2.7	90
15	Nucleosome-mediated synergism between transcription factors on the mouse mammary tumor virus promoter. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1997, 94, 2885-2890.	3.3	81
16	Genome-Wide Analysis of Factors Affecting Transcription Elongation and DNA Repair: A New Role for PAF and Ccr4-Not in Transcription-Coupled Repair. <i>PLoS Genetics</i> , 2009, 5, e1000364.	1.5	81
17	Mitotic recombination in yeast: elements controlling its incidence. <i>Yeast</i> , 2000, 16, 731-754.	0.8	78
18	Chromatin Reassembly Factors Are Involved in Transcriptional Interference Promoting HIV Latency. <i>Journal of Virology</i> , 2011, 85, 3187-3202.	1.5	71

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19	Towards High-Throughput Production of Uniformly Encoded Microparticles. <i>Advanced Materials</i> , 2006, 18, 559-564.	11.1	70
20	Regulon-Specific Control of Transcription Elongation across the Yeast Genome. <i>PLoS Genetics</i> , 2009, 5, e1000614.	1.5	59
21	FACT Prevents the Accumulation of Free Histones Evicted from Transcribed Chromatin and a Subsequent Cell Cycle Delay in G1. <i>PLoS Genetics</i> , 2010, 6, e1000964.	1.5	59
22	Structural Characterization of Set1 RNA Recognition Motifs and their Role in Histone H3 Lysine 4 Methylation. <i>Journal of Molecular Biology</i> , 2006, 359, 1170-1181.	2.0	52
23	A simple in vivo assay for measuring the efficiency of gene length-dependent processes in yeast mRNA biogenesis. <i>FEBS Journal</i> , 2006, 273, 756-769.	2.2	52
24	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> . <i>Genetics</i> , 1997, 147, 1585-1594.	1.2	52
25	Feedback regulation of ribosome assembly. <i>Current Genetics</i> , 2018, 64, 393-404.	0.8	50
26	The Prefoldin Complex Regulates Chromatin Dynamics during Transcription Elongation. <i>PLoS Genetics</i> , 2013, 9, e1003776.	1.5	45
27	The cellular growth rate controls overall mRNA turnover, and modulates either transcription or degradation rates of particular gene regulons. <i>Nucleic Acids Research</i> , 2016, 44, 3643-3658.	6.5	45
28	Interaction of steroid hormone receptors with transcription factors involves chromatin remodelling. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 1996, 56, 47-59.	1.2	43
29	A Gene-Specific Requirement for FACT during Transcription Is Related to the Chromatin Organization of the Transcribed Region. <i>Molecular and Cellular Biology</i> , 2006, 26, 8710-8721.	1.1	43
30	Balanced Production of Ribosome Components Is Required for Proper G1/S Transition in <i>Saccharomyces cerevisiae</i> . <i>Journal of Biological Chemistry</i> , 2013, 288, 31689-31700.	1.6	43
31	Cloning and correct expression in <i>E. coli</i> of the <i>petJ</i> gene encoding cytochrome <i>c6</i> from <i>Synechocystis</i> 6803. <i>FEBS Letters</i> , 1994, 347, 173-177.	1.3	41
32	Existence of two ferredoxin-glutamate synthases in the cyanobacterium <i>Synechocystis</i> sp. PCC 6803. Isolation and insertional inactivation of <i>gltB</i> and <i>gltS</i> genes. <i>Plant Molecular Biology</i> , 1995, 27, 753-767.	2.0	40
33	The distribution of active RNA polymerase II along the transcribed region is gene-specific and controlled by elongation factors. <i>Nucleic Acids Research</i> , 2010, 38, 4651-4664.	6.5	40
34	Variegation associated with <i>lacZ</i> in transgenic animals: a warning note. <i>Transgenic Research</i> , 2000, 9, 237-239.	1.3	39
35	An NAD-specific glutamate dehydrogenase from cyanobacteria Identification and properties. <i>FEBS Letters</i> , 1991, 285, 35-38.	1.3	38
36	Systems for applied gene control in <i>Saccharomyces cerevisiae</i> . <i>Biotechnology Letters</i> , 2008, 30, 979-987.	1.1	38

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37	Synechocystis6803 plastocyanin isolated from both the cyanobacterium and E. coli transformed cells are identical. <i>FEBS Letters</i> , 1993, 319, 257-260.	1.3	37
38	H3K4 monomethylation dictates nucleosome dynamics and chromatin remodeling at stress-responsive genes. <i>Nucleic Acids Research</i> , 2015, 43, 4937-4949.	6.5	34
39	Different physiological relevance of yeast THO/TREX subunits in gene expression and genome integrity. <i>Molecular Genetics and Genomics</i> , 2008, 279, 123-132.	1.0	32
40	TFIIS is required for the balanced expression of the genes encoding ribosomal components under transcriptional stress. <i>Nucleic Acids Research</i> , 2012, 40, 6508-6519.	6.5	32
41	Genome-wide studies of mRNA synthesis and degradation in eukaryotes. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2012, 1819, 604-615.	0.9	31
42	Asymmetric cell division requires specific mechanisms for adjusting global transcription. <i>Nucleic Acids Research</i> , 2017, 45, 12401-12412.	6.5	30
43	The yeast prefoldin-like URI-orthologue Bud27 associates with the RSC nucleosome remodeler and modulates transcription. <i>Nucleic Acids Research</i> , 2014, 42, 9666-9676.	6.5	29
44	Homeostasis in the Central Dogma of molecular biology: the importance of mRNA instability. <i>RNA Biology</i> , 2019, 16, 1659-1666.	1.5	26
45	The mRNA degradation factor Xrn1 regulates transcription elongation in parallel to Ccr4. <i>Nucleic Acids Research</i> , 2019, 47, 9524-9541.	6.5	26
46	One step back before moving forward: Regulation of transcription elongation by arrest and backtracking. <i>FEBS Letters</i> , 2012, 586, 2820-2825.	1.3	25
47	The NADP-glutamate dehydrogenase of the cyanobacterium <i>Synechocystis</i> 6803: cloning, transcriptional analysis and disruption of the <i>gdhA</i> gene. <i>Plant Molecular Biology</i> , 1995, 28, 173-188.	2.0	24
48	Straightforward production of encoded microbeads by Flow Focusing: Potential applications for biomolecule detection. <i>International Journal of Pharmaceutics</i> , 2006, 324, 19-26.	2.6	24
49	Yeast Genetic Analysis Reveals the Involvement of Chromatin Reassembly Factors in Repressing HIV-1 Basal Transcription. <i>PLoS Genetics</i> , 2009, 5, e1000339.	1.5	23
50	Chromatin-dependent regulation of RNA polymerases II and III activity throughout the transcription cycle. <i>Nucleic Acids Research</i> , 2015, 43, 787-802.	6.5	23
51	The importance of controlling mRNA turnover during cell proliferation. <i>Current Genetics</i> , 2016, 62, 701-710.	0.8	23
52	The hormone responsive region of mouse mammary tumor virus positions a nucleosome and precludes access of nuclear factor I to the promoter. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 1996, 57, 19-31.	1.2	22
53	An improved system for estradiol-dependent regulation of gene expression in yeast. <i>Microbial Cell Factories</i> , 2007, 6, 10.	1.9	22
54	Growth rate controls mRNA turnover in steady and non-steady states. <i>RNA Biology</i> , 2016, 13, 1175-1181.	1.5	21

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55	What do you mean by transcription rate?. <i>BioEssays</i> , 2013, 35, 1056-1062.	1.2	19
56	Flow Cytometry of Microencapsulated Colonies for Genetics Analysis of Filamentous Fungi. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 2271-2278.	0.8	19
57	Regulation of transcription elongation in response to osmotic stress. <i>PLoS Genetics</i> , 2017, 13, e1007090.	1.5	19
58	Light-regulated promoters from <i>Synechocystis</i> PCC6803 share a consensus motif involved in photoregulation. <i>Molecular Microbiology</i> , 1994, 12, 1005-1012.	1.2	17
59	External conditions inversely change the RNA polymerase II elongation rate and density in yeast. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2013, 1829, 1248-1255.	0.9	17
60	Subtracting the sequence bias from partially digested MNase-seq data reveals a general contribution of TFIIIS to nucleosome positioning. <i>Epigenetics and Chromatin</i> , 2017, 10, 58.	1.8	17
61	Chromatin structure of the MMTV promoter and its changes during hormonal induction. <i>Cellular and Molecular Neurobiology</i> , 1996, 16, 85-101.	1.7	16
62	<i>Cis</i> - and <i>Trans</i> -Regulatory Mechanisms of Gene Expression in the ASJ Sensory Neuron of <i>Caenorhabditis elegans</i> . <i>Genetics</i> , 2015, 200, 123-134.	1.2	14
63	Cell volume homeostatically controls the rDNA repeat copy number and rRNA synthesis rate in yeast. <i>PLoS Genetics</i> , 2021, 17, e1009520.	1.5	14
64	The ribosome assembly gene network is controlled by the feedback regulation of transcription elongation. <i>Nucleic Acids Research</i> , 2017, 45, 9302-9318.	6.5	13
65	Functional Contributions of Prefoldin to Gene Expression. <i>Advances in Experimental Medicine and Biology</i> , 2018, 1106, 1-10.	0.8	13
66	Xrn1 influence on gene transcription results from the combination of general effects on elongating RNA pol II and gene-specific chromatin configuration. <i>RNA Biology</i> , 2021, 18, 1310-1323.	1.5	12
67	A Genome-Wide Screen Identifies Yeast Genes Required for Tolerance to Technical Toxaphene, an Organochlorinated Pesticide Mixture. <i>PLoS ONE</i> , 2013, 8, e81253.	1.1	12
68	The total mRNA concentration buffering system in yeast is global rather than gene-specific. <i>Rna</i> , 2021, 27, 1281-1290.	1.6	11
69	High levels of histones promote whole-genome-duplications and trigger a Swe1WEE1-dependent phosphorylation of Cdc28CDK1. <i>ELife</i> , 2018, 7, .	2.8	10
70	Application of Flow Focusing to the Break-Up of a Magnetite Suspension Jet for the Production of Paramagnetic Microparticles. <i>Journal of Nanomaterials</i> , 2011, 2011, 1-10.	1.5	9
71	Overexpression of Canonical Prefoldin Associates with the Risk of Mortality and Metastasis in Non-Small Cell Lung Cancer. <i>Cancers</i> , 2020, 12, 1052.	1.7	8
72	Effect of Glucose Utilization on Nitrite Excretion by the Unicellular Cyanobacterium <i>Synechocystis</i> sp. Strain PCC 6803. <i>Applied and Environmental Microbiology</i> , 1993, 59, 3161-3163.	1.4	7

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73	Rpb5 modulates the RNA polymerase II transition from initiation to elongation by influencing Spt5 association and backtracking. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2018, 1861, 1-13.	0.9	6
74	The relative importance of transcription rate, cryptic transcription and mRNA stability on shaping stress responses in yeast. <i>Transcription</i> , 2012, 3, 39-44.	1.7	5
75	Human prefoldin modulates co-transcriptional pre-mRNA splicing. <i>Nucleic Acids Research</i> , 2021, 49, 6267-6280.	6.5	5
76	Point Mutation in the Ligand-Binding Domain of the Progesterone Receptor Generates a Transdominant Negative Phenotype. , 0, .		5
77	Recruitment of a chromatin remodelling complex by the Hog1 MAP kinase to stress genes. <i>EMBO Journal</i> , 2009, 28, 1191-1191.	3.5	1
78	A Matter of Packaging: Influence of Nucleosome Positioning on Heterologous Gene Expression. <i>Methods in Molecular Biology</i> , 2012, 824, 51-64.	0.4	1
79	Free Histones and the Cell Cycle. , 2011, , .		0
80	Gene Control during Transcription Elongation. <i>Genetics Research International</i> , 2012, 2012, 1-2.	2.0	0
81	RNA Polymerase II-Dependent Transcription in Fungi and Its Interplay with mRNA Decay. , 2014, , 1-26.		0
82	Transcriptional Run-on: Measuring Nascent Transcription at Specific Genomic Sites in Yeast. <i>Bio-protocol</i> , 2021, 11, e4064.	0.2	0
83	Chromatin Structure and Gene Regulation by Steroid Hormones. , 1997, , 127-144.		0