

Joseph C Reese

List of Publications by Year in descending order

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42
papers

2,377
citations

236925

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37
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43
all docs

43
docs citations

43
times ranked

1994
citing authors

#	ARTICLE	IF	CITATIONS
1	DEF1: Much more than an RNA polymerase degradation factor. <i>DNA Repair</i> , 2021, 107, 103202.	2.8	4
2	Single-molecule FRET method to investigate the dynamics of transcription elongation through the nucleosome by RNA polymerase II. <i>Methods</i> , 2019, 159-160, 51-58.	3.8	19
3	Biochemical methods to characterize RNA polymerase II elongation complexes. <i>Methods</i> , 2019, 159-160, 70-81.	3.8	4
4	Analysis of RNAPII complexes. <i>Methods</i> , 2019, 159-160, 1-3.	3.8	1
5	Ccr4 Not maintains genomic integrity by controlling the ubiquitylation and degradation of arrested RNAPII. <i>Genes and Development</i> , 2019, 33, 705-717.	5.9	23
6	Regulation of tRNA synthesis and modification in physiological conditions and disease. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2018, 1861, 283-284.	1.9	0
7	Genome-Wide Mapping of Decay Factor mRNA Interactions in Yeast Identifies Nutrient-Responsive Transcripts as Targets of the Deadenylase Ccr4. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 315-330.	1.8	27
8	The elongation factor Spt4/5 regulates RNA polymerase II transcription through the nucleosome. <i>Nucleic Acids Research</i> , 2017, 45, 6362-6374.	14.5	60
9	Biochemical Analysis of Yeast Suppressor of Ty 4/5 (Spt4/5) Reveals the Importance of Nucleic Acid Interactions in the Prevention of RNA Polymerase II Arrest. <i>Journal of Biological Chemistry</i> , 2016, 291, 9853-9870.	3.4	49
10	Ccr4-Not and TFIIIS Function Cooperatively To Rescue Arrested RNA Polymerase II. <i>Molecular and Cellular Biology</i> , 2015, 35, 1915-1925.	2.3	47
11	The Rpb4/7 Module of RNA Polymerase II Is Required for Carbon Catabolite Repressor Protein 4-Negative on TATA (Ccr4-Not) Complex to Promote Elongation. <i>Journal of Biological Chemistry</i> , 2014, 289, 33125-33130.	3.4	32
12	The control of elongation by the yeast Ccr4 Not complex. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2013, 1829, 127-133.	1.9	41
13	Ccr4-Not complex: the control freak of eukaryotic cells. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2012, 47, 315-333.	5.2	161
14	Intermolecular Interactions within the Abundant DEAD-box Protein Dhh1 Regulate Its Activity in Vivo. <i>Journal of Biological Chemistry</i> , 2011, 286, 27454-27470.	3.4	47
15	The multifunctional Ccr4 Not complex directly promotes transcription elongation. <i>Genes and Development</i> , 2011, 25, 581-593.	5.9	144
16	Ccr4 Not complex directly regulates transcription elongation. <i>FASEB Journal</i> , 2010, 24, 186.2.	0.5	0
17	Roles of the yeast Ccr4 Not complex in regulating transcription. <i>FASEB Journal</i> , 2010, 24, 833.8.	0.5	0
18	The histone H2A N-terminal tail regulates H2B monoubiquitylation and H3 K4 methylation via a novel trans tail pathway. <i>FASEB Journal</i> , 2010, 24, 457.8.	0.5	0

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19	Set2-Dependent K36 Methylation Is Regulated by Novel Intratail Interactions within H3. <i>Molecular and Cellular Biology</i> , 2009, 29, 6413-6426.	2.3	16
20	Yeast Rap1 contributes to genomic integrity by activating DNA damage repair genes. <i>EMBO Journal</i> , 2008, 27, 1575-1584.	7.8	30
21	Histone Deacetylases RPD3 and HOS2 Regulate the Transcriptional Activation of DNA Damage-Inducible Genes. <i>Molecular and Cellular Biology</i> , 2008, 28, 1427-1427.	2.3	0
22	Dissection of Coactivator Requirement at RNR3 Reveals Unexpected Contributions from TFIID and SAGA. <i>Journal of Biological Chemistry</i> , 2008, 283, 27360-27368.	3.4	17
23	Isolation of Highly Purified Yeast Nuclei for Nuclease Mapping of Chromatin Structure. <i>Methods in Molecular Biology</i> , 2008, 463, 43-53.	0.9	5
24	Exposing the core promoter is sufficient to activate transcription and alter coactivator requirement at RNR3. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 8833-8838.	7.1	29
25	Histone Deacetylases RPD3 and HOS2 Regulate the Transcriptional Activation of DNA Damage-Inducible Genes. <i>Molecular and Cellular Biology</i> , 2007, 27, 3199-3210.	2.3	100
26	Isolation of Yeast Nuclei and Micrococcal Nuclease Mapping of Nucleosome Positioning. , 2006, 313, 245-256.		15
27	Molecular Genetic Analysis of the Yeast Repressor Rfx1/Crt1 Reveals a Novel Two-Step Regulatory Mechanism. <i>Molecular and Cellular Biology</i> , 2005, 25, 7399-7411.	2.3	35
28	An Essential Role for the <i>Saccharomyces cerevisiae</i> DEAD-Box Helicase DHH1 in G1/S DNA-Damage Checkpoint Recovery. <i>Genetics</i> , 2004, 167, 21-33.	2.9	30
29	Redundant Mechanisms Are Used by Ssn6-Tup1 in Repressing Chromosomal Gene Transcription in <i>Saccharomyces cerevisiae</i> . <i>Journal of Biological Chemistry</i> , 2004, 279, 39240-39250.	3.4	81
30	Ssn6-Tup1 requires the ISW2 complex to position nucleosomes in <i>Saccharomyces cerevisiae</i> . <i>EMBO Journal</i> , 2004, 23, 2246-2257.	7.8	74
31	Basal transcription factors. <i>Current Opinion in Genetics and Development</i> , 2003, 13, 114-118.	3.3	51
32	SWI/SNF-dependent chromatin remodeling of RNR3 requires TAFII and the general transcription machinery. <i>Genes and Development</i> , 2003, 17, 502-515.	5.9	74
33	Functional Analysis of TFIID Components Using Conditional Mutants. <i>Methods in Enzymology</i> , 2003, 370, 415-430.	1.0	12
34	Genetic analysis of TAF68/61 reveals links to cell cycle regulators. <i>Yeast</i> , 2001, 18, 1197-1205.	1.7	11
35	Analysis of TAF90 Mutants Displaying Allele-Specific and Broad Defects in Transcription. <i>Molecular and Cellular Biology</i> , 2001, 21, 7331-7344.	2.3	39
36	Ssn6-Tup1 Regulates RNR3 by Positioning Nucleosomes and Affecting the Chromatin Structure at the Upstream Repression Sequence. <i>Journal of Biological Chemistry</i> , 2001, 276, 33788-33797.	3.4	67

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37	Derepression of DNA damage-regulated genes requires yeast TAFII. <i>EMBO Journal</i> , 2000, 19, 4091-4100.	7.8	30
38	Identification of a Yeast Transcription Factor IID Subunit, TSG2/TAF48. <i>Journal of Biological Chemistry</i> , 2000, 275, 17391-17398.	3.4	38
39	A Subset of TAFII Are Integral Components of the SAGA Complex Required for Nucleosome Acetylation and Transcriptional Stimulation. <i>Cell</i> , 1998, 94, 45-53.	28.9	411
40	Yeast TAFII145 Required for Transcription of G1/S Cyclin Genes and Regulated by the Cellular Growth State. <i>Cell</i> , 1997, 90, 607-614.	28.9	143
41	Transcription activation in cells lacking TAFII. <i>Nature</i> , 1996, 383, 185-188.	27.8	241
42	Yeast TAF IIS in a multisubunit complex required for activated transcription. <i>Nature</i> , 1994, 371, 523-527.	27.8	163