

Redundant roles for the TFIID and SAGA complexes in g

Nature

405, 701-704

DOI: [10.1038/35015104](https://doi.org/10.1038/35015104)

Citation Report

#	ARTICLE	IF	CITATIONS
1	Chromatin organisation and human disease. Expert Opinion on Therapeutic Targets, 2000, 4, 665-685.	1.0	22
2	Linking Notch signaling, chromatin remodeling, and T-cell leukemogenesis. Journal of Cellular Biochemistry, 2000, 79, 46-53.	1.2	31
3	Control of gene expression through regulation of the TATA-binding protein. Gene, 2000, 255, 1-14.	1.0	168
4	TAC, a TBP-sans-TAFs Complex Containing the Unprocessed TFIIA ¹ Precursor and the TFIIA ³ Subunit. Molecular Cell, 2000, 6, 527-537.	4.5	43
5	Biomedical Discovery with DNA Arrays. Cell, 2000, 102, 9-15.	13.5	342
6	Transcriptional Coactivator Complexes. Annual Review of Biochemistry, 2001, 70, 475-501.	5.0	506
7	SAGA is an essential in vivo target of the yeast acidic activator Gal4p. Genes and Development, 2001, 15, 1935-1945.	2.7	258
8	Transcription and chromatin converge: lessons from yeast genetics. Current Opinion in Genetics and Development, 2001, 11, 142-147.	1.5	19
9	Transcriptomes, transcription activators and microarrays. FEBS Letters, 2001, 498, 140-144.	1.3	30
10	Progress in the application of DNA microarrays.. Environmental Health Perspectives, 2001, 109, 881-891.	2.8	59
11	SPT Genes: Key Players in the Regulation of Transcription, Chromatin Structure and Other Cellular Processes. Journal of Biochemistry, 2001, 129, 185-191.	0.9	50
12	Mammalian histone acetyltransferases and their complexes. Cellular and Molecular Life Sciences, 2001, 58, 683-692.	2.4	46
13	DNA microarrays: raising the profile. Current Opinion in Biotechnology, 2001, 12, 48-52.	3.3	45
14	New developments in microarray technology. Current Opinion in Biotechnology, 2001, 12, 41-47.	3.3	176
15	Genetic analysis of TAF68/61 reveals links to cell cycle regulators. Yeast, 2001, 18, 1197-1205.	0.8	11
16	Increasing the rate of chromatin remodeling and gene activation—a novel role for the histone acetyltransferase Gcn5. EMBO Journal, 2001, 20, 4944-4951.	3.5	70
17	Distinct requirements for C.elegans TAFs in early embryonic transcription. EMBO Journal, 2001, 20, 5269-5279.	3.5	46
18	Selectivity of chromatin-remodelling cofactors for ligand-activated transcription. Nature, 2001, 414, 924-928.	13.7	238

#	ARTICLE	IF	CITATIONS
19	Chromatin remodeling and transcriptional activation: the cast (in order of appearance). <i>Oncogene</i> , 2001, 20, 2991-3006.	2.6	182
20	A model organism for genomic and postgenomic studies. <i>IEEE Engineering in Medicine and Biology Magazine</i> , 2001, 20, 22-32.	1.1	1
21	The histone fold is a key structural motif of transcription factor TFIID. <i>Trends in Biochemical Sciences</i> , 2001, 26, 250-257.	3.7	127
22	Mutations in the TATA-binding Protein, Affecting Transcriptional Activation, Show Synthetic Lethality with the TAF145 Gene Lacking the TAF N-terminal Domain in <i>Saccharomyces cerevisiae</i> . <i>Journal of Biological Chemistry</i> , 2001, 276, 395-405.	1.6	29
23	Heterozygous Disruption of the TATA-Binding Protein Gene in DT40 Cells Causes Reduced cdc25B Phosphatase Expression and Delayed Mitosis. <i>Molecular and Cellular Biology</i> , 2001, 21, 2435-2448.	1.1	39
24	Two WD Repeat-containing TATA-binding Protein-associated Factors in Fission Yeast That Suppress Defects in the Anaphase-promoting Complex. <i>Journal of Biological Chemistry</i> , 2001, 276, 17117-17124.	1.6	34
25	Fluorescence-based Analyses of the Effects of Full-length Recombinant TAF130p on the Interaction of TATA Box-binding Protein with TATA Box DNA. <i>Journal of Biological Chemistry</i> , 2001, 276, 49100-49109.	1.6	28
26	Altered transcription in yeast expressing expanded polyglutamine. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 13201-13206.	3.3	117
27	Molecular Genetic Dissection of TAF25, an Essential Yeast Gene Encoding a Subunit Shared by TFIID and SAGA Multiprotein Transcription Factors. <i>Molecular and Cellular Biology</i> , 2001, 21, 6668-6680.	1.1	16
28	Analysis of TAF90 Mutants Displaying Allele-Specific and Broad Defects in Transcription. <i>Molecular and Cellular Biology</i> , 2001, 21, 7331-7344.	1.1	39
29	Rvb1p and Rvb2p Are Essential Components of a Chromatin Remodeling Complex That Regulates Transcription of over 5% of Yeast Genes. <i>Journal of Biological Chemistry</i> , 2001, 276, 16279-16288.	1.6	103
30	A Gal4- λ 54 Hybrid Protein That Functions as a Potent Activator of RNA Polymerase II Transcription in Yeast. <i>Journal of Biological Chemistry</i> , 2001, 276, 23881-23887.	1.6	6
31	c-Jun Binds the N Terminus of Human TAFII250 to Derepress RNA Polymerase II Transcription in Vitro. <i>Journal of Biological Chemistry</i> , 2001, 276, 25582-25588.	1.6	37
32	Requirement for Yeast TAF145 Function in Transcriptional Activation of the RPS5 Promoter That Depends on Both Core Promoter Structure and Upstream Activating Sequences. <i>Journal of Biological Chemistry</i> , 2001, 276, 25715-25726.	1.6	19
33	The <i>S. cerevisiae</i> SAGA complex functions in vivo as a coactivator for transcriptional activation by Gal4. <i>Genes and Development</i> , 2001, 15, 1946-1956.	2.7	267
34	Mot1 activates and represses transcription by direct, ATPase-dependent mechanisms. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 2666-2671.	3.3	82
35	Crystal Structure of a Subcomplex of Human Transcription Factor TFIID Formed by TATA Binding Protein-associated Factors hTAF4 (hTAFII135) and hTAF12 (hTAFII20). <i>Journal of Biological Chemistry</i> , 2002, 277, 45502-45509.	1.6	56
36	Distinct Mutations in Yeast TAF II 25 Differentially Affect the Composition of TFIID and SAGA Complexes as Well as Global Gene Expression Patterns. <i>Molecular and Cellular Biology</i> , 2002, 22, 3178-3193.	1.1	31

#	ARTICLE	IF	CITATIONS
37	The Novel SLIK Histone Acetyltransferase Complex Functions in the Yeast Retrograde Response Pathway. <i>Molecular and Cellular Biology</i> , 2002, 22, 8774-8786.	1.1	209
38	Reproducibility of Oligonucleotide Microarray Transcriptome Analyses. <i>Journal of Biological Chemistry</i> , 2002, 277, 37001-37008.	1.6	208
39	Differential Requirement of SAGA Components for Recruitment of TATA-Box-Binding Protein to Promoters In Vivo. <i>Molecular and Cellular Biology</i> , 2002, 22, 7365-7371.	1.1	155
40	Analysis of Spt7 Function in the <i>Saccharomyces cerevisiae</i> SAGA Coactivator Complex. <i>Molecular and Cellular Biology</i> , 2002, 22, 5367-5379.	1.1	121
41	Identification of histone H4-like TAF in <i>Schizosaccharomyces pombe</i> as a protein that interacts with WD repeat-containing TAF. <i>Nucleic Acids Research</i> , 2002, 30, 1952-1958.	6.5	17
42	GDH1 expression is regulated by GLN3, GCN4, and HAP4 under respiratory growth. <i>Biochemical and Biophysical Research Communications</i> , 2002, 293, 79-85.	1.0	43
43	DNA chips for yeast biotechnology. The case of wine yeasts. <i>Journal of Biotechnology</i> , 2002, 98, 227-241.	1.9	59
44	Transcription Activation: Unveiling the Essential Nature of TFIID. <i>Current Biology</i> , 2002, 12, R620-R622.	1.8	32
45	Profiling of retinoid mediated gene expression in synchronized human SCC cells using Atlas? human cDNA expression arrays. <i>Journal of Cellular Physiology</i> , 2002, 190, 345-355.	2.0	11
46	Global Approaches to Chromatin. <i>Chemistry and Biology</i> , 2002, 9, 1167-1173.	6.2	17
47	Multi-protein complexes in eukaryotic gene transcription. <i>Plant Molecular Biology</i> , 2002, 50, 925-947.	2.0	104
48	Systematic analysis of essential yeast TAFs in genome-wide transcription and preinitiation complex assembly. <i>EMBO Journal</i> , 2003, 22, 3395-3402.	3.5	93
49	Artificial recruitment of certain Mediator components affects requirement of basal transcription factor IIE. <i>Genes To Cells</i> , 2003, 8, 41-50.	0.5	7
50	TFIIB and subunits of the SAGA complex are involved in transcriptional activation of phospholipid biosynthetic genes by the regulatory protein Ino2 in the yeast <i>Saccharomyces cerevisiae</i> . <i>Molecular Microbiology</i> , 2003, 48, 1119-1130.	1.2	32
51	NET1 and HFI1 genes of yeast mediate both chromosome maintenance and mitochondrial rho? mutagenesis. <i>Yeast</i> , 2003, 20, 955-971.	0.8	6
52	Roles for BTA1 and Mot1p in dynamics of TATA-binding protein and regulation of RNA polymerase II transcription. <i>Gene</i> , 2003, 315, 1-13.	1.0	47
53	Multiple Mechanistically Distinct Functions of SAGA at the PHO5 Promoter. <i>Molecular and Cellular Biology</i> , 2003, 23, 3468-3476.	1.1	99
54	Mutations in the histone fold domain of the TAF12 gene show synthetic lethality with the TAF1 gene lacking the TAF N-terminal domain (TAND) by different mechanisms from those in the SPT15 gene encoding the TATA box-binding protein (TBP). <i>Nucleic Acids Research</i> , 2003, 31, 1261-1274.	6.5	10

#	ARTICLE	IF	CITATIONS
55	A Multiplicity of Coactivators Is Required by Gcn4p at Individual Promoters In Vivo. <i>Molecular and Cellular Biology</i> , 2003, 23, 2800-2820.	1.1	131
56	Impairment of the DNA Binding Activity of the TATA-binding Protein Renders the Transcriptional Function of Rvb2p/Tih2p, the Yeast RuvB-like Protein, Essential for Cell Growth. <i>Journal of Biological Chemistry</i> , 2003, 278, 14647-14656.	1.6	33
57	The Critical cis-Acting Element Required for IMD2 Feedback Regulation by GDP Is a TATA Box Located 202 Nucleotides Upstream of the Transcription Start Site. <i>Molecular and Cellular Biology</i> , 2003, 23, 6267-6278.	1.1	17
58	Use of a Genetically Introduced Cross-linker to Identify Interaction Sites of Acidic Activators within Native Transcription Factor IID and SAGA. <i>Journal of Biological Chemistry</i> , 2003, 278, 6779-6786.	1.6	35
59	Replication-Independent Assembly of Nucleosome Arrays in a Novel Yeast Chromatin Reconstitution System Involves Antisilencing Factor Asf1p and Chromodomain Protein Chd1p. <i>Molecular and Cellular Biology</i> , 2003, 23, 7937-7946.	1.1	56
60	Mammalian Elongin A Is Not Essential for Cell Viability but Is Required for Proper Cell Cycle Progression with Limited Alteration of Gene Expression. <i>Journal of Biological Chemistry</i> , 2003, 278, 13585-13589.	1.6	17
61	Disruption Mutations of ADA2b and GCN5 Transcriptional Adaptor Genes Dramatically Affect Arabidopsis Growth, Development, and Gene Expression[W]. <i>Plant Cell</i> , 2003, 15, 626-638.	3.1	288
62	A Broad but Restricted Requirement for TAF-5 (Human TAFII100) for Embryonic Transcription in <i>Caenorhabditis elegans</i> . <i>Journal of Biological Chemistry</i> , 2003, 278, 6181-6186.	1.6	9
63	Global Control of Histone Modification by the Anaphase-Promoting Complex. <i>Molecular and Cellular Biology</i> , 2003, 23, 9136-9149.	1.1	30
64	Arabidopsis Histone Acetyltransferase AtGCN5 Regulates the Floral Meristem Activity through the WUSCHEL/AGAMOUS Pathway. <i>Journal of Biological Chemistry</i> , 2003, 278, 28246-28251.	1.6	141
65	TAF10 (TAFII30) Is Necessary for TFIID Stability and Early Embryogenesis in Mice. <i>Molecular and Cellular Biology</i> , 2003, 23, 4307-4318.	1.1	57
66	Functional Analysis of TFIID Components Using Conditional Mutants. <i>Methods in Enzymology</i> , 2003, 370, 415-430.	0.4	12
67	Deubiquitination of Histone H2B by a Yeast Acetyltransferase Complex Regulates Transcription. <i>Journal of Biological Chemistry</i> , 2004, 279, 1867-1871.	1.6	254
68	Barrier Proteins Remodel and Modify Chromatin To Restrict Silenced Domains. <i>Molecular and Cellular Biology</i> , 2004, 24, 1956-1967.	1.1	97
69	Low Affinity Orthophosphate Carriers Regulate PHO Gene Expression Independently of Internal Orthophosphate Concentration in <i>Saccharomyces cerevisiae</i> . <i>Journal of Biological Chemistry</i> , 2004, 279, 35273-35280.	1.6	55
70	An Array of Coactivators Is Required for Optimal Recruitment of TATA Binding Protein and RNA Polymerase II by Promoter-Bound Gcn4p. <i>Molecular and Cellular Biology</i> , 2004, 24, 4104-4117.	1.1	83
71	Redundant Roles for Histone H3 N-Terminal Lysine Residues in Subtelomeric Gene Repression in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2004, 167, 1123-1132.	1.2	65
72	Cluster Analysis of Mass Spectrometry Data Reveals a Novel Component of SAGA. <i>Molecular and Cellular Biology</i> , 2004, 24, 7249-7259.	1.1	127

#	ARTICLE	IF	CITATIONS
73	In vivo target of a transcriptional activator revealed by fluorescence resonance energy transfer. <i>Genes and Development</i> , 2004, 18, 333-343.	2.7	165
74	<i>Drosophila</i> Ada2b Is Required for Viability and Normal Histone H3 Acetylation. <i>Molecular and Cellular Biology</i> , 2004, 24, 8080-8089.	1.1	51
75	Genome-wide Analysis of Pre-mRNA Splicing. <i>Journal of Biological Chemistry</i> , 2004, 279, 52437-52446.	1.6	27
76	Role for Nhp6, Gcn5, and the Swi/Snf Complex in Stimulating Formation of the TATA-Binding Protein-TFIIA-DNA Complex. <i>Molecular and Cellular Biology</i> , 2004, 24, 8312-8321.	1.1	34
77	Positive and negative functions of the SAGA complex mediated through interaction of Spt8 with TBP and the N-terminal domain of TFIIA. <i>Genes and Development</i> , 2004, 18, 1022-1034.	2.7	58
78	An Extensive Requirement for Transcription Factor IID-specific TAF-1 in <i>Caenorhabditis elegans</i> Embryonic Transcription. <i>Journal of Biological Chemistry</i> , 2004, 279, 15339-15347.	1.6	18
79	On the Mechanism of Constitutive Pdr1 Activator-mediated PDR5 Transcription in <i>Saccharomyces cerevisiae</i> . <i>Journal of Biological Chemistry</i> , 2004, 279, 42677-42686.	1.6	34
80	Spt3 and Mot1 cooperate in nucleosome remodeling independently of TBP recruitment. <i>EMBO Journal</i> , 2004, 23, 1943-1948.	3.5	32
81	Structure and mechanism of the RNA polymerase II transcription machinery. <i>Nature Structural and Molecular Biology</i> , 2004, 11, 394-403.	3.6	438
82	mRNA export: an assembly line from genes to nuclear pores. <i>Current Opinion in Cell Biology</i> , 2004, 16, 285-292.	2.6	161
83	RNA polymerase II transcription apparatus in <i>Schizosaccharomyces pombe</i> . <i>Current Genetics</i> , 2004, 44, 287-294.	0.8	20
84	Structure and Function of the TFIID Complex. <i>Advances in Protein Chemistry</i> , 2004, 67, 67-92.	4.4	40
85	A systems view of mRNP biology. <i>Genes and Development</i> , 2004, 18, 2845-2860.	2.7	137
86	Molecular Architecture of the <i>S. cerevisiae</i> SAGA Complex. <i>Molecular Cell</i> , 2004, 15, 199-208.	4.5	141
87	Global Position and Recruitment of HATs and HDACs in the Yeast Genome. <i>Molecular Cell</i> , 2004, 16, 199-209.	4.5	212
88	A Genome-Wide Housekeeping Role for TFIID and a Highly Regulated Stress-Related Role for SAGA in <i>Saccharomyces cerevisiae</i> . <i>Molecular Cell</i> , 2004, 13, 573-585.	4.5	502
89	Sus1, a Functional Component of the SAGA Histone Acetylase Complex and the Nuclear Pore-Associated mRNA Export Machinery. <i>Cell</i> , 2004, 116, 75-86.	13.5	330
90	Identification and Distinct Regulation of Yeast TATA Box-Containing Genes. <i>Cell</i> , 2004, 116, 699-709.	13.5	578

#	ARTICLE	IF	CITATIONS
91	Sp1 and Huntington's Disease. , 2005, , 168-173.		0
92	Chd1 chromodomain links histone H3 methylation with SAGA- and SLIK-dependent acetylation. <i>Nature</i> , 2005, 433, 434-438.	13.7	449
93	Abundant Expression in Vascular Tissue of Plant TAF10, an Orthologous Gene for TATA Box-binding Protein-associated Factor 10, in <i>Flaveria trinervia</i> and Abnormal Morphology of <i>Arabidopsis thaliana</i> Transformants on its Overexpression. <i>Plant and Cell Physiology</i> , 2005, 46, 108-117.	1.5	21
94	Differential Requirement of SAGA Subunits for Mot1p and Taf1p Recruitment in Gene Activation. <i>Molecular and Cellular Biology</i> , 2005, 25, 4863-4872.	1.1	20
95	The <i>Saccharomyces cerevisiae</i> Srb8-Srb11 Complex Functions with the SAGA Complex during Gal4-Activated Transcription. <i>Molecular and Cellular Biology</i> , 2005, 25, 114-123.	1.1	68
96	Transcriptional Activities of Retinoic Acid Receptors. <i>Vitamins and Hormones</i> , 2005, 70, 199-264.	0.7	107
97	Global Regulation by the Yeast Spt10 Protein Is Mediated through Chromatin Structure and the Histone Upstream Activating Sequence Elements. <i>Molecular and Cellular Biology</i> , 2005, 25, 9127-9137.	1.1	58
98	TFIID and Spt-Ada-Gcn5-Acetyltransferase Functions Probed by Genome-wide Synthetic Genetic Array Analysis Using a <i>Saccharomyces cerevisiae</i> taf9-ts Allele. <i>Genetics</i> , 2005, 171, 959-973.	1.2	18
99	TAF9b (Formerly TAF9L) Is a Bona Fide TAF That Has Unique and Overlapping Roles with TAF9. <i>Molecular and Cellular Biology</i> , 2005, 25, 4638-4649.	1.1	60
100	Barrier Function at HMR. <i>Molecular Cell</i> , 2005, 19, 707-716.	4.5	79
101	A role for both wild-type and expanded ataxin-7 in transcriptional regulation. <i>Neurobiology of Disease</i> , 2005, 20, 646-655.	2.1	45
102	Acetylation in Histone H3 Globular Domain Regulates Gene Expression in Yeast. <i>Cell</i> , 2005, 121, 375-385.	13.5	362
104	Sumoylation of the Yeast Gcn5 Protein. <i>Biochemistry</i> , 2006, 45, 1035-1042.	1.2	27
105	The General Transcription Machinery and General Cofactors. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2006, 41, 105-178.	2.3	715
106	The role of chromatin structure in regulating stress-induced transcription in <i>Saccharomyces cerevisiae</i> This paper is one of a selection of papers published in this Special Issue, entitled 27th International West Coast Chromatin and Chromosome Conference, and has undergone the Journal's usual peer review process. <i>Biochemistry and Cell Biology</i> , 2006, 84, 477-489.	0.9	33
107	Engineering Yeast Transcription Machinery for Improved Ethanol Tolerance and Production. <i>Science</i> , 2006, 314, 1565-1568.	6.0	730
108	Nucleocytosolic Acetyl-Coenzyme A Synthetase Is Required for Histone Acetylation and Global Transcription. <i>Molecular Cell</i> , 2006, 23, 207-217.	4.5	386
109	Model-based identification of cis-acting elements from microarray data. <i>Genomics</i> , 2006, 88, 452-461.	1.3	19

#	ARTICLE	IF	CITATIONS
110	SAGA binds TBP via its Spt8 subunit in competition with DNA: implications for TBP recruitment. <i>EMBO Journal</i> , 2006, 25, 3791-3800.	3.5	81
111	SAGA-associated Sgf73p facilitates formation of the preinitiation complex assembly at the promoters either in a HAT-dependent or independent manner in vivo. <i>Nucleic Acids Research</i> , 2006, 34, 6225-6232.	6.5	34
112	Mammalian Gene Expression Program Resiliency: The Roles of Multiple Coactivator Mechanisms in Hypoxia-Responsive Transcription. <i>Cell Cycle</i> , 2006, 5, 142-146.	1.3	44
113	Genome-Wide Relationships between TAF1 and Histone Acetyltransferases in <i>Saccharomyces cerevisiae</i> . <i>Molecular and Cellular Biology</i> , 2006, 26, 2791-2802.	1.1	54
114	Stress-Specific Role of Fission Yeast Gcn5 Histone Acetyltransferase in Programming a Subset of Stress Response Genes. <i>Eukaryotic Cell</i> , 2006, 5, 1337-1346.	3.4	32
115	Genetic Interactions Between Nhp6 and Gcn5 With Mot1 and the Ccr4-Not Complex That Regulate Binding of TATA-Binding Protein in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2006, 172, 837-849.	1.2	20
116	Histone acetylation in gene regulation. <i>Briefings in Functional Genomics & Proteomics</i> , 2006, 5, 209-221.	3.8	190
117	Genome-wide Transcriptional Dependence on TAF1 Functional Domains. <i>Journal of Biological Chemistry</i> , 2006, 281, 6404-6412.	1.6	13
118	Full and partial genome-wide assembly and disassembly of the yeast transcription machinery in response to heat shock. <i>Genes and Development</i> , 2006, 20, 2250-2265.	2.7	100
119	TAF7: A possible transcription initiation check-point regulator. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 602-607.	3.3	36
120	The Essential Gene <i>wda</i> Encodes a WD40 Repeat Subunit of <i>Drosophila</i> SAGA Required for Histone H3 Acetylation. <i>Molecular and Cellular Biology</i> , 2006, 26, 7178-7189.	1.1	30
121	<i>Arabidopsis</i> GCN5, HD1, and TAF1/HAF2 Interact to Regulate Histone Acetylation Required for Light-Responsive Gene Expression. <i>Plant Cell</i> , 2006, 18, 2893-2903.	3.1	302
122	Actively Transcribed GAL Genes Can Be Physically Linked to the Nuclear Pore by the SAGA Chromatin Modifying Complex. <i>Journal of Biological Chemistry</i> , 2007, 282, 3042-3049.	1.6	115
123	PfGCN5-Mediated Histone H3 Acetylation Plays a Key Role in Gene Expression in <i>Plasmodium falciparum</i> . <i>Eukaryotic Cell</i> , 2007, 6, 1219-1227.	3.4	113
124	The New Core Promoter Element XCPE1 (X Core Promoter Element 1) Directs Activator-, Mediator-, and TATA-Binding Protein-Dependent but TFIID-Independent RNA Polymerase II Transcription from TATA-Less Promoters. <i>Molecular and Cellular Biology</i> , 2007, 27, 1844-1858.	1.1	59
125	Characterization of New Spt3 and TATA-Binding Protein Mutants of <i>Saccharomyces cerevisiae</i> : Spt3-TBP Allele-Specific Interactions and Bypass of Spt8. <i>Genetics</i> , 2007, 177, 2007-2017.	1.2	40
126	Pho91 Is a Vacuolar Phosphate Transporter That Regulates Phosphate and Polyphosphate Metabolism in <i>Saccharomyces cerevisiae</i> . <i>Molecular Biology of the Cell</i> , 2007, 18, 4438-4445.	0.9	88
127	Selective Requirement for SAGA in Hog1-Mediated Gene Expression Depending on the Severity of the External Osmostress Conditions. <i>Molecular and Cellular Biology</i> , 2007, 27, 3900-3910.	1.1	82

#	ARTICLE	IF	CITATIONS
128	Plc1p Is Required for SAGA Recruitment and Derepression of Sko1p-regulated Genes. <i>Molecular Biology of the Cell</i> , 2007, 18, 2419-2428.	0.9	19
129	Temporary Expression of the TAF10 Gene and its Requirement for Normal Development of <i>Arabidopsis thaliana</i> . <i>Plant and Cell Physiology</i> , 2007, 48, 134-146.	1.5	19
130	Structural analysis and dimerization potential of the human TAF5 subunit of TFIID. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 1189-1194.	3.3	23
131	Nine-amino-acid transactivation domain: Establishment and prediction utilities. <i>Genomics</i> , 2007, 89, 756-768.	1.3	126
132	A TATA binding protein regulatory network that governs transcription complex assembly. <i>Genome Biology</i> , 2007, 8, R46.	13.9	35
134	Developmental potential of <i>Gcn5</i> ^{+/+} embryonic stem cells in vivo and in vitro. <i>Developmental Dynamics</i> , 2007, 236, 1547-1557.	0.8	55
135	Multi-tasking on chromatin with the SAGA coactivator complexes. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2007, 618, 135-148.	0.4	94
136	Functions of Site-Specific Histone Acetylation and Deacetylation. <i>Annual Review of Biochemistry</i> , 2007, 76, 75-100.	5.0	1,419
137	Isolation and characterization of a GCN5-interacting protein from <i>Arabidopsis thaliana</i> . <i>Planta</i> , 2007, 225, 1367-1379.	1.6	20
138	A genetic screen supports a broad role for the <i>Drosophila</i> insulator proteins BEAF-32A and BEAF-32B in maintaining patterns of gene expression. <i>Molecular Genetics and Genomics</i> , 2007, 277, 273-286.	1.0	21
139	Yeast Rap1 contributes to genomic integrity by activating DNA damage repair genes. <i>EMBO Journal</i> , 2008, 27, 1575-1584.	3.5	30
140	Structure and function of a transcriptional network activated by the MAPK Hog1. <i>Nature Genetics</i> , 2008, 40, 1300-1306.	9.4	197
141	Genome-scale <i>Arabidopsis</i> promoter array identifies targets of the histone acetyltransferase GCN5. <i>Plant Journal</i> , 2008, 56, 493-504.	2.8	120
142	Minimal components of the RNA polymerase II transcription apparatus determine the consensus TATA box. <i>Nucleic Acids Research</i> , 2008, 36, 2906-2916.	6.5	15
143	Nucleosome Positioning and Histone H3 Acetylation Are Independent Processes in the <i>Aspergillus nidulans</i> prnD-prnB Bidirectional Promoter. <i>Eukaryotic Cell</i> , 2008, 7, 656-663.	3.4	58
144	Dissection of Coactivator Requirement at RNR3 Reveals Unexpected Contributions from TFIID and SAGA. <i>Journal of Biological Chemistry</i> , 2008, 283, 27360-27368.	1.6	17
145	Cooperative action of NC2 and Mot1p to regulate TATA-binding protein function across the genome. <i>Genes and Development</i> , 2008, 22, 2359-2369.	2.7	66
146	The <i>S. pombe</i> SAGA complex controls the switch from proliferation to sexual differentiation through the opposing roles of its subunits Gcn5 and Spt8. <i>Genes and Development</i> , 2008, 22, 3184-3195.	2.7	81

#	ARTICLE	IF	CITATIONS
147	Site-specific cross-linking of TBP in vivo and in vitro reveals a direct functional interaction with the SAGA subunit Spt3. <i>Genes and Development</i> , 2008, 22, 2994-3006.	2.7	85
148	Computational Modelling of Genome-Side Transcription Assembly Networks Using a Fluidics Analogy. <i>PLoS ONE</i> , 2008, 3, e3095.	1.1	0
149	Genetic and Genomewide Analysis of Simultaneous Mutations in Acetylated and Methylated Lysine Residues in Histone H3 in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2009, 181, 461-472.	1.2	11
150	TATA-binding Protein Variants That Bypass the Requirement for Mot1 in Vivo. <i>Journal of Biological Chemistry</i> , 2009, 284, 4525-4535.	1.6	9
151	SAGA and Rpd3 Chromatin Modification Complexes Dynamically Regulate Heat Shock Gene Structure and Expression. <i>Journal of Biological Chemistry</i> , 2009, 284, 32914-32931.	1.6	44
152	Differential Cofactor Requirements for Histone Eviction from Two Nucleosomes at the Yeast <i>PHO84</i> Promoter Are Determined by Intrinsic Nucleosome Stability. <i>Molecular and Cellular Biology</i> , 2009, 29, 2960-2981.	1.1	34
153	The Human SPT20-Containing SAGA Complex Plays a Direct Role in the Regulation of Endoplasmic Reticulum Stress-Induced Genes. <i>Molecular and Cellular Biology</i> , 2009, 29, 1649-1660.	1.1	71
154	Genome-wide Mapping of the Coactivator Ada2p Yields Insight into the Functional Roles of SAGA/ADA Complex in <i>Candida albicans</i> . <i>Molecular Biology of the Cell</i> , 2009, 20, 2389-2400.	0.9	86
155	Cryo-EM Reveals Promoter DNA Binding and Conformational Flexibility of the General Transcription Factor TFIID. <i>Structure</i> , 2009, 17, 1442-1452.	1.6	31
156	Yeast Sgf73/Ataxin-7 serves to anchor the deubiquitination module into both SAGA and Slik(SALSA) HAT complexes. <i>Epigenetics and Chromatin</i> , 2009, 2, 2.	1.8	84
157	Histone acetyltransferase GCN5 interferes with the miRNA pathway in Arabidopsis. <i>Cell Research</i> , 2009, 19, 899-909.	5.7	82
158	The involvement of <i>theSchizosaccharomyces pombe sep9/spt8+gene</i> in the regulation of septum cleavage. <i>FEMS Yeast Research</i> , 2009, 9, 757-767.	1.1	5
159	Effect of overexpression of transcription factors on the fermentation properties of <i>Saccharomyces cerevisiae</i> industrial strains. <i>Letters in Applied Microbiology</i> , 2009, 49, 14-19.	1.0	21
160	Genome-Wide Views of Chromatin Structure. <i>Annual Review of Biochemistry</i> , 2009, 78, 245-271.	5.0	292
161	Mitochondria in the elderly: Is acetylcarnitine a rejuvenator? <i>Advanced Drug Delivery Reviews</i> , 2009, 61, 1332-1342.	6.6	75
162	In-Depth Profiling of Post-Translational Modifications on the Related Transcription Factor Complexes TFIID and SAGA. <i>Journal of Proteome Research</i> , 2009, 8, 5020-5030.	1.8	28
163	DNA Arrays. , 2009, , 469-488.		0
164	Biology of Microorganisms on Grapes, in Must and in Wine. , 2009, , .		45

#	ARTICLE	IF	CITATIONS
165	Yeast Biotechnology: Diversity and Applications. , 2009, , .		67
166	Mediator subunits and histone methyltransferase Set2 contribute to Ino2-dependent transcriptional activation of phospholipid biosynthesis in the yeast <i>Saccharomyces cerevisiae</i> . <i>Molecular Genetics and Genomics</i> , 2010, 283, 211-221.	1.0	14
167	Multiple faces of the SAGA complex. <i>Current Opinion in Cell Biology</i> , 2010, 22, 374-382.	2.6	225
168	<i>Saccharomyces cerevisiae</i> Ssd1p promotes <i>CLN2</i> expression by binding to the 5' untranslated region of <i>CLN2</i> mRNA. <i>Genes To Cells</i> , 2010, 15, 1169-1188.	0.5	23
169	Chromatin structure and transcription regulation in <i>Saccharomyces cerevisiae</i> . <i>Molecular Biology</i> , 2010, 44, 856-869.	0.4	3
170	GCN5 Is a Positive Regulator of Origins of DNA Replication in <i>Saccharomyces cerevisiae</i> . <i>PLoS ONE</i> , 2010, 5, e8964.	1.1	29
171	TATA is a modular component of synthetic promoters. <i>Genome Research</i> , 2010, 20, 1391-1397.	2.4	93
172	A Bre1-associated Protein, Large 1 (Lge1), Promotes H2B Ubiquitylation during the Early Stages of Transcription Elongation. <i>Journal of Biological Chemistry</i> , 2010, 285, 2361-2367.	1.6	42
173	TAF4b and Jun/Activating Protein-1 Collaborate to Regulate the Expression of Integrin $\beta 6$ and Cancer Cell Migration Properties. <i>Molecular Cancer Research</i> , 2010, 8, 554-568.	1.5	13
174	Genome-wide localization analysis of a complete set of Tafs reveals a specific effect of the taf1 mutation on Taf2 occupancy and provides indirect evidence for different TFIID conformations at different promoters. <i>Nucleic Acids Research</i> , 2010, 38, 1805-1820.	6.5	14
175	Identification of Pep4p as the Protease Responsible for Formation of the SAGA-related SLIK Protein Complex. <i>Journal of Biological Chemistry</i> , 2010, 285, 22793-22799.	1.6	31
176	Snf1p Regulates Gcn5p Transcriptional Activity by Antagonizing Spt3p. <i>Genetics</i> , 2010, 184, 91-105.	1.2	26
177	<i>Toxoplasma gondii</i> Lysine Acetyltransferase GCN5-A Functions in the Cellular Response to Alkaline Stress and Expression of Cyst Genes. <i>PLoS Pathogens</i> , 2010, 6, e1001232.	2.1	56
178	The <i>Saccharomyces cerevisiae</i> Anaphase-Promoting Complex Interacts with Multiple Histone-Modifying Enzymes To Regulate Cell Cycle Progression. <i>Eukaryotic Cell</i> , 2010, 9, 1418-1431.	3.4	22
179	Histone Acetyltransferase AtGCN5/HAG1 Is a Versatile Regulator of Developmental and Inducible Gene Expression in <i>Arabidopsis</i> . <i>Molecular Plant</i> , 2010, 3, 670-677.	3.9	161
180	Roles for Gcn5 in promoting nucleosome assembly and maintaining genome integrity. <i>Cell Cycle</i> , 2010, 9, 3051-3057.	1.3	29
181	A Role for Gcn5 in Replication-Coupled Nucleosome Assembly. <i>Molecular Cell</i> , 2010, 37, 469-480.	4.5	148
182	Nucleosome Positioning in <i>Saccharomyces cerevisiae</i> . <i>Microbiology and Molecular Biology Reviews</i> , 2011, 75, 301-320.	2.9	108

#	ARTICLE	IF	CITATIONS
183	Distinct regulatory mechanisms of eukaryotic transcriptional activation by SAGA and TFIID. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2011, 1809, 97-108.	0.9	47
184	Transcriptional Regulation in <i>Saccharomyces cerevisiae</i> : Transcription Factor Regulation and Function, Mechanisms of Initiation, and Roles of Activators and Coactivators. <i>Genetics</i> , 2011, 189, 705-736.	1.2	304
185	Antagonistic Gcn5-Hda1 interactions revealed by mutations to the Anaphase Promoting Complex in yeast. <i>Cell Division</i> , 2011, 6, 13.	1.1	18
186	Domains of Tra1 Important for Activator Recruitment and Transcription Coactivator Functions of SAGA and NuA4 Complexes. <i>Molecular and Cellular Biology</i> , 2011, 31, 818-831.	1.1	74
187	The CKH1/EER4 Gene Encoding a TAF12-Like Protein Negatively Regulates Cytokinin Sensitivity in <i>Arabidopsis thaliana</i> . <i>Plant and Cell Physiology</i> , 2011, 52, 629-637.	1.5	20
188	Gcn5 facilitates Pol II progression, rather than recruitment to nucleosome-depleted stress promoters, in <i>Schizosaccharomyces pombe</i> . <i>Nucleic Acids Research</i> , 2011, 39, 6369-6379.	6.5	47
189	Sequential Recruitment of SAGA and TFIID in a Genomic Response to DNA Damage in <i>Saccharomyces cerevisiae</i> . <i>Molecular and Cellular Biology</i> , 2011, 31, 190-202.	1.1	29
190	Sgf29 binds histone H3K4me2/3 and is required for SAGA complex recruitment and histone H3 acetylation. <i>EMBO Journal</i> , 2011, 30, 2829-2842.	3.5	218
191	Tight cooperation between Mot1p and NC2 ² in regulating genome-wide transcription, repression of transcription following heat shock induction and genetic interaction with SAGA. <i>Nucleic Acids Research</i> , 2012, 40, 996-1008.	6.5	14
192	Analysis of Gal4-directed transcription activation using Tra1 mutants selectively defective for interaction with Gal4. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 1997-2002.	3.3	28
193	Acetyl-CoA Carboxylase Regulates Global Histone Acetylation. <i>Journal of Biological Chemistry</i> , 2012, 287, 23865-23876.	1.6	165
194	The 19S proteasome subcomplex promotes the targeting of NuA4 HAT to the promoters of ribosomal protein genes to facilitate the recruitment of TFIID for transcriptional initiation in vivo. <i>Nucleic Acids Research</i> , 2012, 40, 1969-1983.	6.5	38
195	Identification of Pathogenesis-Associated Genes by T-DNA-Mediated Insertional Mutagenesis in <i>Botrytis cinerea</i> : A Type 2A Phosphoprotein Phosphatase and an SPT3 Transcription Factor Have Significant Impact on Virulence. <i>Molecular Plant-Microbe Interactions</i> , 2012, 25, 481-495.	1.4	71
196	Mediator and SAGA Have Distinct Roles in Pol II Preinitiation Complex Assembly and Function. <i>Cell Reports</i> , 2012, 2, 1061-1067.	2.9	28
197	Sgf29p Facilitates the Recruitment of TATA Box Binding Protein but Does Not Alter SAGA's Global Structural Integrity in Vivo. <i>Biochemistry</i> , 2012, 51, 706-714.	1.2	19
198	Cellular stress responses, hormetic phytochemicals and vitagenes in aging and longevity. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2012, 1822, 753-783.	1.8	351
199	mRNA export and gene expression: The SAGA-TREX-2 connection. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2012, 1819, 555-565.	0.9	71
200	Towards the identification of protein complexes and functional modules by integrating PPI network and gene expression data. <i>BMC Bioinformatics</i> , 2012, 13, 109.	1.2	122

#	ARTICLE	IF	CITATIONS
201	Genome-wide structure and organization of eukaryotic pre-initiation complexes. <i>Nature</i> , 2012, 483, 295-301.	13.7	475
202	Chromatin and Transcription in Yeast. <i>Genetics</i> , 2012, 190, 351-387.	1.2	233
203	SAGA function in tissue-specific gene expression. <i>Trends in Cell Biology</i> , 2012, 22, 177-184.	3.6	56
204	<i>Trichoderma reesei</i> Histone Acetyltransferase Gcn5 Regulates Fungal Growth, Conidiation, and Cellulase Gene Expression. <i>Current Microbiology</i> , 2013, 67, 580-589.	1.0	95
205	The Yeast AMPK Homolog SNF1 Regulates Acetyl Coenzyme A Homeostasis and Histone Acetylation. <i>Molecular and Cellular Biology</i> , 2013, 33, 4701-4717.	1.1	71
206	Genome-Wide Organization of Eukaryotic Preinitiation Complex Is Influenced by Nonconsensus Protein-DNA Binding. <i>Biophysical Journal</i> , 2013, 104, 1107-1115.	0.2	23
207	TAF13 interacts with PRC2 members and is essential for Arabidopsis seed development. <i>Developmental Biology</i> , 2013, 379, 28-37.	0.9	22
208	The Spt-Ada-Gcn5 Acetyltransferase (SAGA) Complex in <i>Aspergillus nidulans</i> . <i>PLoS ONE</i> , 2013, 8, e65221.	1.1	18
209	The Histone Acetyltransferase GcnE (GCN5) Plays a Central Role in the Regulation of <i>Aspergillus</i> Asexual Development. <i>Genetics</i> , 2014, 197, 1175-1189.	1.2	79
210	The TAF9 C-Terminal Conserved Region Domain Is Required for SAGA and TFIID Promoter Occupancy To Promote Transcriptional Activation. <i>Molecular and Cellular Biology</i> , 2014, 34, 1547-1563.	1.1	21
211	Cell cycle population effects in perturbation studies. <i>Molecular Systems Biology</i> , 2014, 10, 732.	3.2	118
212	Architecture of the <i>Saccharomyces cerevisiae</i> SAGA transcription coactivator complex. <i>EMBO Journal</i> , 2014, 33, 2534-2546.	3.5	100
213	Structural and functional insight into TAF1-TAF7, a subcomplex of transcription factor II D. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 9103-9108.	3.3	42
214	Protein Acetylation and Acetyl Coenzyme A Metabolism in Budding Yeast. <i>Eukaryotic Cell</i> , 2014, 13, 1472-1483.	3.4	96
215	The N-terminus and Tudor domains of Sgf29 are important for its heterochromatin boundary formation function. <i>Journal of Biochemistry</i> , 2014, 155, 159-171.	0.9	10
216	Mutations on the DNA Binding Surface of TBP Discriminate between Yeast TATA and TATA-Less Gene Transcription. <i>Molecular and Cellular Biology</i> , 2014, 34, 2929-2943.	1.1	18
217	High throughput screening identifies modulators of histone deacetylase inhibitors. <i>BMC Genomics</i> , 2014, 15, 528.	1.2	10
218	The UmGcn5 gene encoding histone acetyltransferase from <i>Ustilago maydis</i> is involved in dimorphism and virulence. <i>Fungal Genetics and Biology</i> , 2014, 71, 86-95.	0.9	60

#	ARTICLE	IF	CITATIONS
219	Global warming impact on rice crop productivity. , 2014, , 212-223.		3
220	Spt-Ada-Gcn5-Acetyltransferase (SAGA) Complex in Plants: Genome Wide Identification, Evolutionary Conservation and Functional Determination. PLoS ONE, 2015, 10, e0134709.	1.1	32
221	Composition of the SAGA complex in plants and its role in controlling gene expression in response to abiotic stresses. Frontiers in Plant Science, 2015, 6, 865.	1.7	53
222	A comparison of whole cell directed evolution approaches in breeding of industrial strain of <i>Saccharomyces cerevisiae</i> . Biotechnology Letters, 2015, 37, 1393-1398.	1.1	5
223	Genetic variants in the ADAMTS13 and SUPT3H genes are associated with ADAMTS13 activity. Blood, 2015, 125, 3949-3955.	0.6	24
224	Eaf1p Is Required for Recruitment of NuA4 in Targeting TFIID to the Promoters of the Ribosomal Protein Genes for Transcriptional Initiation <i>In Vivo</i> . Molecular and Cellular Biology, 2015, 35, 2947-2964.	1.1	23
225	Myc and SAGA rewire an alternative splicing network during early somatic cell reprogramming. Genes and Development, 2015, 29, 803-816.	2.7	73
226	p53 modulates the activity of the GLI1 oncogene through interactions with the shared coactivator TAF9. DNA Repair, 2015, 34, 9-17.	1.3	32
227	Sumoylation and transcription regulation at nuclear pores. Chromosoma, 2015, 124, 45-56.	1.0	26
228	The <i>Aspergillus flavus</i> Histone Acetyltransferase AflGcnE Regulates Morphogenesis, Aflatoxin Biosynthesis, and Pathogenicity. Frontiers in Microbiology, 2016, 7, 1324.	1.5	96
229	Activation of a T-box-Otx2-Gsc gene network independent of TBP and TBP-related factors. Development (Cambridge), 2016, 143, 1340-50.	1.2	10
231	Cooperation between SAGA and SWI/SNF complexes is required for efficient transcriptional responses regulated by the yeast MAPK Slt2. Nucleic Acids Research, 2016, 44, gkw324.	6.5	35
232	Global reorganization of budding yeast chromosome conformation in different physiological conditions. Journal of Cell Biology, 2016, 212, 321-334.	2.3	36
233	Nucleosome repositioning underlies dynamic gene expression. Genes and Development, 2016, 30, 660-672.	2.7	67
234	Protein acetylation in metabolism – metabolites and cofactors. Nature Reviews Endocrinology, 2016, 12, 43-60.	4.3	236
235	Structure and Function of RNA Polymerases and the Transcription Machineries. Sub-Cellular Biochemistry, 2017, 83, 225-270.	1.0	27
236	Macromolecular Protein Complexes. Sub-Cellular Biochemistry, 2017, , .	1.0	5
237	SAGA complex mediates the transcriptional up-regulation of antiviral RNA silencing. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E3499-E3506.	3.3	50

#	ARTICLE	IF	CITATIONS
238	Molecular mechanisms that distinguish TFIID housekeeping from regulatable SAGA promoters. <i>EMBO Journal</i> , 2017, 36, 274-290.	3.5	53
239	TORC1 and TORC2 converge to regulate the SAGA co-activator in response to nutrient availability. <i>EMBO Reports</i> , 2017, 18, 2197-2218.	2.0	39
240	Multiple Taf subunits of TFIID interact with Ino2 activation domains and contribute to expression of genes required for yeast phospholipid biosynthesis. <i>Molecular Microbiology</i> , 2017, 106, 876-890.	1.2	5
241	Transcription of Nearly All Yeast RNA Polymerase II-Transcribed Genes Is Dependent on Transcription Factor TFIID. <i>Molecular Cell</i> , 2017, 68, 118-129.e5.	4.5	142
242	Enzymatic modules of the SAGA chromatin-modifying complex play distinct roles in <i>Drosophila</i> gene expression and development. <i>Genes and Development</i> , 2017, 31, 1588-1600.	2.7	45
243	SAGA Is a General Cofactor for RNA Polymerase II Transcription. <i>Molecular Cell</i> , 2017, 68, 130-143.e5.	4.5	161
244	Functional Genomics in Wine Yeast: DNA Arrays and Next Generation Sequencing. , 2017, , 573-604.		1
245	Transcription factors that influence RNA polymerases I and II: To what extent is mechanism of action conserved?. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2017, 1860, 246-255.	0.9	14
246	Lysine acetyltransferase NuA4 and acetyl-CoA regulate glucose-deprived stress granule formation in <i>Saccharomyces cerevisiae</i> . <i>PLoS Genetics</i> , 2017, 13, e1006626.	1.5	20
247	Mutational analysis of <sc>TAF</sc>6 revealed the essential requirement of the histone- fold domain and the <sc>HEAT</sc> repeat domain for transcriptional activation. <i>FEBS Journal</i> , 2018, 285, 1491-1510.	2.2	2
248	Widespread and precise reprogramming of yeast protein- genome interactions in response to heat shock. <i>Genome Research</i> , 2018, 28, 357-366.	2.4	71
250	Contribution of Surface Thermal Forcing to Mixing in the Ocean. <i>Journal of Geophysical Research: Oceans</i> , 2018, 123, 855-863.	1.0	10
251	Deletion of <i>ADA2</i> Increases Antifungal Drug Susceptibility and Virulence in <i>Candida glabrata</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	1.4	32
252	Improvement of Lead Tolerance of <i>Saccharomyces cerevisiae</i> by Random Mutagenesis of Transcription Regulator SPT3. <i>Applied Biochemistry and Biotechnology</i> , 2018, 184, 155-167.	1.4	3
253	Mechanistic Differences in Transcription Initiation at TATA-Less and TATA-Containing Promoters. <i>Molecular and Cellular Biology</i> , 2018, 38, .	1.1	33
254	Emerging roles of transcriptional enhancers in chromatin looping and promoter-proximal pausing of RNA polymerase II. <i>Journal of Biological Chemistry</i> , 2018, 293, 13786-13794.	1.6	39
255	Plant Biosynthetic Engineering Through Transcription Regulation: An Insight into Molecular Mechanisms During Environmental Stress. <i>Energy, Environment, and Sustainability</i> , 2018, , 51-72.	0.6	10
256	Two Distinct Regulatory Mechanisms of Transcriptional Initiation in Response to Nutrient Signaling. <i>Genetics</i> , 2018, 208, 191-205.	1.2	11

#	ARTICLE	IF	CITATIONS
257	YHMI: a web tool to identify histone modifications and histone/chromatin regulators from a gene list in yeast. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	1.4	1
258	Transcript Buffering: A Balancing Act between mRNA Synthesis and mRNA Degradation. <i>Molecular Cell</i> , 2018, 72, 10-17.	4.5	79
259	<Saccharomyces cerevisiae Metabolic Labeling with 4-thiouracil and the Quantification of Newly Synthesized mRNA As a Proxy for RNA Polymerase II Activity. <i>Journal of Visualized Experiments</i> , 2018, , .	0.2	13
260	A MYST Histone Acetyltransferase Modulates <i>Conidia</i> Development and Secondary Metabolism in <i>Pestalotiopsis microspora</i> , a Taxol Producer. <i>Scientific Reports</i> , 2018, 8, 8199.	1.6	9
261	Epigenetic reprogramming by histone acetyltransferase HAG1/AtGCN5 is required for pluripotency acquisition in <i>Arabidopsis</i> . <i>EMBO Journal</i> , 2018, 37, .	3.5	92
262	Introduction to the Thematic Minireview Series: Chromatin and transcription. <i>Journal of Biological Chemistry</i> , 2018, 293, 13775-13777.	1.6	14
263	Genome-wide expert annotation of the epigenetic machinery of the plant-parasitic nematodes <i>Meloidogyne</i> spp., with a focus on the asexually-reproducing species. <i>BMC Genomics</i> , 2018, 19, 321.	1.2	18
264	Histone Acetyltransferases (HATs) in Chinese Cabbage: Insights from Histone H3 Acetylation and Expression Profiling of HATs in Response to Abiotic Stresses. <i>Journal of the American Society for Horticultural Science</i> , 2018, 143, 296-303.	0.5	13
265	Protein partners of plant ubiquitin-specific proteases (UBPs). <i>Plant Physiology and Biochemistry</i> , 2019, 145, 227-236.	2.8	13
266	Dicer functions transcriptionally and posttranscriptionally in a multilayer antiviral defense. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 2274-2281.	3.3	33
267	Transcription initiation factor TBP: old friend new questions. <i>Biochemical Society Transactions</i> , 2019, 47, 411-423.	1.6	32
268	SAGA DUBm-mediated surveillance regulates prompt export of stress-inducible transcripts for proteostasis. <i>Nature Communications</i> , 2019, 10, 2458.	5.8	11
269	The histone acetyltransferase GcnE regulates conidiation and biofilm formation in <i>Aspergillus fumigatus</i> . <i>Medical Mycology</i> , 2020, 58, 248-259.	0.3	13
270	Aspirin impairs acetyl-coenzyme A metabolism in redox-compromised yeast cells. <i>Scientific Reports</i> , 2019, 9, 6152.	1.6	5
271	Transcriptional activation is weakened when Taf1p N-terminal domain 1 is substituted with its <i>Drosophila</i> counterpart in yeast TFIID. <i>Genes and Genetic Systems</i> , 2019, 94, 51-59.	0.2	2
272	On top of biosynthetic gene clusters: How epigenetic machinery influences secondary metabolism in fungi. <i>Biotechnology Advances</i> , 2019, 37, 107345.	6.0	122
273	Shellfish collection on the westernmost Mediterranean, Bajondillo cave (âˆ¼160-35â€ˆcalâ€ˆkyr BP): A case of behavioral convergence?. <i>Quaternary Science Reviews</i> , 2019, 217, 284-296.	1.4	15
274	Regulated Gene Expression by Synthetic Modulation of the Promoter Architecture in Plants. , 2019, , 235-255.		8

#	ARTICLE	IF	CITATIONS
275	Identification of the gene encoding the TATA box-binding protein-associated factor 1 (TAF1) and its putative role in the heat shock response in the protozoan parasite <i>Entamoeba histolytica</i> . <i>Parasitology Research</i> , 2019, 118, 517-538.	0.6	6
276	Disruption in phosphate transport affects membrane lipid and lipid droplet homeostasis in <i>Saccharomyces cerevisiae</i> . <i>Journal of Bioenergetics and Biomembranes</i> , 2020, 52, 215-227.	1.0	1
277	Kin28 depletion increases association of TFIID subunits Taf1 and Taf4 with promoters in <i>Saccharomyces cerevisiae</i> . <i>Nucleic Acids Research</i> , 2020, 48, 4244-4255.	6.5	9
278	SPT20 Regulates the Hog1-MAPK Pathway and Is Involved in <i>Candida albicans</i> Response to Hyperosmotic Stress. <i>Frontiers in Microbiology</i> , 2020, 11, 213.	1.5	8
279	Analysis of four complete linkage sequence variants within a novel lncRNA located in a growth QTL on chromosome 1 related to growth traits in chickens. <i>Journal of Animal Science</i> , 2020, 98, .	0.2	31
280	Targeting the SAGA and ATAC Transcriptional Coactivator Complexes in MYC-Driven Cancers. <i>Cancer Research</i> , 2020, 80, 1905-1911.	0.4	17
281	SAGA and TFIID: Friends of TBP drifting apart. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2021, 1864, 194604.	0.9	22
282	The SAGA continues: The rise of cis- and trans-histone crosstalk pathways. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2021, 1864, 194600.	0.9	13
283	The biochemical and genetic discovery of the SAGA complex. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2021, 1864, 194669.	0.9	20
284	Deacetylation of H4 lysine16 affects acetylation of lysine residues in histone H3 and H4 and promotes transcription of constitutive genes. <i>Epigenetics</i> , 2021, 16, 597-617.	1.3	8
286	The Histone Acetyltransferase GCN5 and the Associated Coactivators ADA2: From Evolution of the SAGA Complex to the Biological Roles in Plants. <i>Plants</i> , 2021, 10, 308.	1.6	12
287	The Fungi-specific histone Acetyltransferase Rtt109 mediates morphogenesis, Aflatoxin synthesis and pathogenicity in <i>Aspergillus flavus</i> by acetylating H3K9. <i>IMA Fungus</i> , 2021, 12, 9.	1.7	21
288	Updated Mechanisms of GCN5 – The Monkey King of the Plant Kingdom in Plant Development and Resistance to Abiotic Stresses. <i>Cells</i> , 2021, 10, 979.	1.8	16
289	<i>Drosophila</i> USP22/nonstop polarizes the actin cytoskeleton during collective border cell migration. <i>Journal of Cell Biology</i> , 2021, 220, .	2.3	6
290	The SAGA complex regulates early steps in transcription via its deubiquitylase module subunit USP22. <i>EMBO Journal</i> , 2021, 40, e102509.	3.5	9
293	Spt3 Plays Opposite Roles in Filamentous Growth in <i>Saccharomyces cerevisiae</i> and <i>Candida albicans</i> and Is Required for <i>C. albicans</i> Virulence. <i>Genetics</i> , 2002, 161, 509-519.	1.2	43
294	Downstream promoter interactions of TFIID TAFs facilitate transcription reinitiation. <i>Genes and Development</i> , 2017, 31, 2162-2174.	2.7	50
295	The SAGA chromatin-modifying complex: the sum of its parts is greater than the whole. <i>Genes and Development</i> , 2020, 34, 1287-1303.	2.7	38

#	ARTICLE	IF	CITATIONS
296	TAFII250. <i>Journal of Cell Science</i> , 2001, 114, 2895-2902.	1.2	86
297	Adr1 and Cat8 Mediate Coactivator Recruitment and Chromatin Remodeling at Glucose-Regulated Genes. <i>PLoS ONE</i> , 2008, 3, e1436.	1.1	46
298	The Role of <i>Candida albicans</i> SPT20 in Filamentation, Biofilm Formation and Pathogenesis. <i>PLoS ONE</i> , 2014, 9, e94468.	1.1	27
299	SAGA mediates transcription from the TATA-like element independently of Taf1p/TFIID but dependent on core promoter structures in <i>Saccharomyces cerevisiae</i> . <i>PLoS ONE</i> , 2017, 12, e0188435.	1.1	8
300	A class of genes in the HER2 regulon that is poised for transcription in breast cancer cell lines and expressed in human breast tumors. <i>Oncotarget</i> , 2015, 6, 1286-1301.	0.8	8
301	SGF29 and Sry pathway in hepatocarcinogenesis. <i>World Journal of Biological Chemistry</i> , 2015, 6, 139.	1.7	10
302	Two roles for the yeast transcription coactivator SAGA and a set of genes redundantly regulated by TFIID and SAGA. <i>ELife</i> , 2020, 9, .	2.8	79
303	Gene Regulation in Yeast. , 2004, , 129-145.		0
306	A Comparative Study of RNA Polymerase II Transcription Machinery in Yeasts. , 2009, , 405-432.		0
307	The Lysine Acetyltransferases in Cardiovascular Disease. <i>Cardiac and Vascular Biology</i> , 2016, , 147-190.	0.2	0
312	The maize <i>premiere senescence2</i> encodes for <i>PHYTOCHROME-DEPENDENT LATE-FLORERING</i> and its expression modulation improves agronomic traits under abiotic stresses. <i>Plant Direct</i> , 2020, 4, e00295.	0.8	3
314	Control of Gene Expression by mRNA Transport and Turnover. , 0, , 148-188.		1
316	The Novel ReNu Region of TAF12 Regulates Gcn5 Nucleosomal Acetylation. , 2019, 2, .		0
317	Spt20, a Structural Subunit of the SAGA Complex, Regulates <i>Aspergillus fumigatus</i> Biofilm Formation, Asexual Development, and Virulence. <i>Applied and Environmental Microbiology</i> , 2022, 88, AEM0153521.	1.4	6
318	The SAGA of pineapple: genome-wide identification and tissue-specific expression of Spt-Ada-Gcn5-acetyltransferase (SAGA) complex. <i>Euphytica</i> , 2021, 217, 1.	0.6	0
319	Human transcription factor protein interaction networks. <i>Nature Communications</i> , 2022, 13, 766.	5.8	59
320	Control of Gene Expression via the Yeast CWI Pathway. <i>International Journal of Molecular Sciences</i> , 2022, 23, 1791.	1.8	17
321	SAGA Complex Subunits in <i>Candida albicans</i> Differentially Regulate Filamentation, Invasiveness, and Biofilm Formation. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 764711.	1.8	7

#	ARTICLE	IF	CITATIONS
323	SAGA COMPLEX ESSENTIAL FOR THE REGULATION OF GENES INVOLVED IN TREHALOSE METABOLISM. Trakya University Journal of Natural Sciences, 0, , .	0.4	0
324	Effects of environmental stress factors on the actin cytoskeleton of fungi and plants: Ionizing radiation and <scp>ROS</scp>. Cytoskeleton, 2023, 80, 330-355.	1.0	2
325	TFIID dependency of steady-state mRNA transcription altered epigenetically by simultaneous functional loss of Taf1 and Spt3 is Hsp104-dependent. PLoS ONE, 2023, 18, e0281233.	1.1	0
326	Evaluation of reference genes for transcript analyses in Komagataella phaffii (Pichia pastoris). Fungal Biology and Biotechnology, 2023, 10, .	2.5	1