

Timothy Formosa

List of Publications by Year in descending order

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46
papers

3,252
citations

147566
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233125
45
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59
all docs

59
docs citations

59
times ranked

2240
citing authors

#	ARTICLE	IF	CITATIONS
1	Electron microscopy analysis of ATP-independent nucleosome unfolding by FACT. <i>Communications Biology</i> , 2022, 5, 2.	2.0	16
2	The interaction between the Spt6-tSH2 domain and Rpb1 affects multiple functions of RNA Polymerase II. <i>Nucleic Acids Research</i> , 2022, 50, 784-802.	6.5	6
3	The role of FACT in managing chromatin: disruption, assembly, or repair?. <i>Nucleic Acids Research</i> , 2020, 48, 11929-11941.	6.5	74
4	Establishment and Maintenance of Chromatin Architecture Are Promoted Independently of Transcription by the Histone Chaperone FACT and H3-K56 Acetylation in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2019, 211, 877-892.	1.2	16
5	Selective Kinase Inhibition Shows That Bur1 (Cdk9) Phosphorylates the Rpb1 Linker <i>In Vivo</i> . <i>Molecular and Cellular Biology</i> , 2019, 39, .	1.1	20
6	Histone chaperone FACT and curaxins: effects on genome structure and function. <i>Journal of Cancer Metastasis and Treatment</i> , 2019, 2019, .	0.5	10
7	FACT and Ubp10 collaborate to modulate H2B deubiquitination and nucleosome dynamics. <i>ELife</i> , 2019, 8, .	2.8	25
8	Functional roles of the DNA-binding HMGB domain in the histone chaperone FACT in nucleosome reorganization. <i>Journal of Biological Chemistry</i> , 2018, 293, 6121-6133.	1.6	46
9	FACT Inhibition Blocks Induction But Not Maintenance of Pluripotency. <i>Stem Cells and Development</i> , 2018, 27, 1693-1701.	1.1	22
10	A novel SH2 recognition mechanism recruits Spt6 to the doubly phosphorylated RNA polymerase II linker at sites of transcription. <i>ELife</i> , 2017, 6, .	2.8	61
11	Large-scale ATP-independent nucleosome unfolding by a histone chaperone. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 1111-1116.	3.6	85
12	FACT Disrupts Nucleosome Structure by Binding H2A-H2B with Conserved Peptide Motifs. <i>Molecular Cell</i> , 2015, 60, 294-306.	4.5	143
13	The Abundant Histone Chaperones Spt6 and FACT Collaborate to Assemble, Inspect, and Maintain Chromatin Structure in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2015, 201, 1031-1045.	1.2	61
14	Rad52/Rad59-dependent Recombination as a Means to Rectify Faulty Okazaki Fragment Processing. <i>Journal of Biological Chemistry</i> , 2014, 289, 15064-15079.	1.6	18
15	The FACT Histone Chaperone Guides Histone H4 Into Its Nucleosomal Conformation in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2013, 195, 101-113.	1.2	10
16	Structure of the Spt16 Middle Domain Reveals Functional Features of the Histone Chaperone FACT. <i>Journal of Biological Chemistry</i> , 2013, 288, 10188-10194.	1.6	53
17	The role of FACT in making and breaking nucleosomes. <i>Biochimica Et Biophysica Acta</i> , 2013, 1819, 247-55.	1.3	30
18	The role of FACT in making and breaking nucleosomes. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2012, 1819, 247-255.	0.9	178

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19	Structure of a Proteasome Pba1-Pba2 Complex. <i>Journal of Biological Chemistry</i> , 2012, 287, 37371-37382.	1.6	53
20	Crystal Structures of the <i>S. cerevisiae</i> Spt6 Core and C-Terminal Tandem SH2 Domain. <i>Journal of Molecular Biology</i> , 2011, 408, 697-713.	2.0	54
21	Insight Into the Mechanism of Nucleosome Reorganization From Histone Mutants That Suppress Defects in the FACT Histone Chaperone. <i>Genetics</i> , 2011, 188, 835-846.	1.2	38
22	A kinase's work is never done: Rad53 monitors chromatin near replication origins. <i>Cell Cycle</i> , 2011, 10, 573-578.	1.3	0
23	Ubiquitylation of FACT by the Cullin-E3 ligase Rtt101 connects FACT to DNA replication. <i>Genes and Development</i> , 2010, 24, 1485-1490.	2.7	55
24	Structure of a Blm10 Complex Reveals Common Mechanisms for Proteasome Binding and Gate Opening. <i>Molecular Cell</i> , 2010, 37, 728-735.	4.5	138
25	Avoiding a Fatal Attraction: Properties of Nucleosomes and a Histone Chaperone Revealed under Physiological Conditions. <i>Molecular Cell</i> , 2010, 37, 747-748.	4.5	2
26	Structure and Biological Importance of the Spn1-Spt6 Interaction, and Its Regulatory Role in Nucleosome Binding. <i>Molecular Cell</i> , 2010, 40, 725-735.	4.5	66
27	yFACT Induces Global Accessibility of Nucleosomal DNA without H2A-H2B Displacement. <i>Molecular Cell</i> , 2009, 35, 365-376.	4.5	174
28	FACT and the reorganized nucleosome. <i>Molecular BioSystems</i> , 2008, 4, 1085.	2.9	64
29	A Role for Chd1 and Set2 in Negatively Regulating DNA Replication in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2008, 178, 649-659.	1.2	43
30	Structural and Functional Analysis of the Spt16p N-terminal Domain Reveals Overlapping Roles of yFACT Subunits. <i>Journal of Biological Chemistry</i> , 2008, 283, 5058-5068.	1.6	78
31	The Structure of the yFACT Pob3-M Domain, Its Interaction with the DNA Replication Factor RPA, and a Potential Role in Nucleosome Deposition. <i>Molecular Cell</i> , 2007, 27, 171-172.	4.5	1
32	Structure of the Blm10 ^Δ 20 S Proteasome Complex by Cryo-electron Microscopy. Insights into the Mechanism of Activation of Mature Yeast Proteasomes. <i>Journal of Molecular Biology</i> , 2006, 363, 648-659.	2.0	54
33	blm3-1 Is an Allele of UBP3, a Ubiquitin Protease that Appears to Act During Transcription of Damaged DNA. <i>Journal of Molecular Biology</i> , 2006, 363, 660-672.	2.0	10
34	The Structure of the yFACT Pob3-M Domain, Its Interaction with the DNA Replication Factor RPA, and a Potential Role in Nucleosome Deposition. <i>Molecular Cell</i> , 2006, 22, 363-374.	4.5	128
35	Opposing roles for Set2 and yFACT in regulating TBP binding at promoters. <i>EMBO Journal</i> , 2006, 25, 4479-4489.	3.5	64
36	The Yeast FACT Complex Has a Role in Transcriptional Initiation. <i>Molecular and Cellular Biology</i> , 2005, 25, 5812-5822.	1.1	82

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37	Structural Features of Nucleosomes Reorganized by Yeast FACT and Its HMG Box Component, Nhp6. <i>Molecular and Cellular Biology</i> , 2004, 24, 3907-3917.	1.1	72
38	Multiple Nhp6 Molecules Are Required to Recruit Spt16-Pob3 to Form yFACT Complexes and to Reorganize Nucleosomes. <i>Journal of Biological Chemistry</i> , 2003, 278, 45288-45295.	1.6	81
39	Defects in <i>SPT16</i> or <i>POB3</i> (yFACT) in <i>Saccharomyces cerevisiae</i> Cause Dependence on the Hir/Hpc Pathway: Polymerase Passage May Degrade Chromatin Structure. <i>Genetics</i> , 2002, 162, 1557-1571.	1.2	183
40	Spt16-Pob3 and the HMG protein Nhp6 combine to form the nucleosome-binding factor SPN. <i>EMBO Journal</i> , 2001, 20, 3506-3517.	3.5	237
41	<i>POB3</i> Is Required for Both Transcription and Replication in the Yeast <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2000, 155, 1593-1606.	1.2	110
42	Spt16 and Pob3 of <i>Saccharomyces cerevisiae</i> Form an Essential, Abundant Heterodimer That Is Nuclear, Chromatin-Associated, and Copurifies with DNA Polymerase ϵ . <i>Biochemistry</i> , 1999, 38, 8961-8971.	1.2	125
43	Dna2 Mutants Reveal Interactions with Dna Polymerase ϵ and Ctf4, a Pol ϵ Accessory Factor, and Show That Full Dna2 Helicase Activity Is Not Essential for Growth. <i>Genetics</i> , 1999, 151, 1459-1470.	1.2	127
44	[31] Identifying DNA replication complex components using protein affinity chromatography. <i>Methods in Enzymology</i> , 1995, 262, 415-430.	0.4	8
45	[3] Using protein affinity chromatography to probe structure of protein machines. <i>Methods in Enzymology</i> , 1991, 208, 24-45.	0.4	53
46	DNA synthesis dependent on genetic recombination: Characterization of a reaction catalyzed by purified bacteriophage T4 proteins. <i>Cell</i> , 1986, 47, 793-806.	13.5	276