Karl Ekwall

List of Publications by Year in descending order

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KADI EKMALI

#	Article	IF	CITATIONS
1	Comparative Functional Genomics of the Fission Yeasts. Science, 2011, 332, 930-936.	12.6	458
2	Transient Inhibition of Histone Deacetylation Alters the Structural and Functional Imprint at Fission Yeast Centromeres. Cell, 1997, 91, 1021-1032.	28.9	368
3	Schizosaccharomyces pombe genome-wide nucleosome mapping reveals positioning mechanisms distinct from those of Saccharomyces cerevisiae. Nature Structural and Molecular Biology, 2010, 17, 251-257.	8.2	215
4	RNA Pol II subunit Rpb7 promotes centromeric transcription and RNAi-directed chromatin silencing. Genes and Development, 2005, 19, 2301-2306.	5.9	199
5	FANTOM5 CAGE profiles of human and mouse samples. Scientific Data, 2017, 4, 170112.	5.3	195
6	Histone modification patterns and epigenetic codes. Biochimica Et Biophysica Acta - General Subjects, 2009, 1790, 863-868.	2.4	184
7	Functional Divergence between Histone Deacetylases in Fission Yeast by Distinct Cellular Localization and In Vivo Specificity. Molecular and Cellular Biology, 2002, 22, 2170-2181.	2.3	174
8	Epigenetic Regulation of Chromatin States in <i>Schizosaccharomyces pombe</i> . Cold Spring Harbor Perspectives in Biology, 2015, 7, a018770.	5.5	161
9	Genomewide analysis of nucleosome density histone acetylation and HDAC function in fission yeast. EMBO Journal, 2005, 24, 2906-2918.	7.8	150
10	Dicer is required for chromosome segregation and gene silencing in fission yeast cells. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 16648-16653.	7.1	123
11	Genome-wide analysis of HDAC function. Trends in Genetics, 2005, 21, 608-615.	6.7	111
12	Epigenetic Control of Centromere Behavior. Annual Review of Genetics, 2007, 41, 63-81.	7.6	89
13	The Domain Structure of Centromeres Is Conserved from Fission Yeast to Humans. Molecular Biology of the Cell, 2001, 12, 2767-2775.	2.1	83
14	CHD1 remodelers regulate nucleosome spacing <i>in vitro</i> and align nucleosomal arrays over gene coding regions in <i>S. pombe</i> . EMBO Journal, 2012, 31, 4388-4403.	7.8	82
15	A genome-wide role for CHD remodelling factors and Nap1 in nucleosome disassembly. EMBO Journal, 2007, 26, 2868-2879.	7.8	78
16	Centromeric histone H2B monoubiquitination promotes noncoding transcription and chromatin integrity. Nature Structural and Molecular Biology, 2014, 21, 236-243.	8.2	75
17	Topoisomerase I regulates open chromatin and controls gene expression in vivo. EMBO Journal, 2010, 29, 2126-2134.	7.8	73
18	The FUN30 Chromatin Remodeler, Fft3, Protects Centromeric and Subtelomeric Domains from Euchromatin Formation. PLoS Genetics, 2011, 7, e1001334.	3.5	71

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19	The <scp>P</scp> af1 complex factors <scp>L</scp> eo1 and <scp>P</scp> af1 promote local histone turnover to modulate chromatin states in fission yeast. EMBO Reports, 2015, 16, 1673-1687.	4.5	69
20	The Schizosaccharomyces pombe JmjC-Protein, Msc1, Prevents H2A.Z Localization in Centromeric and Subtelomeric Chromatin Domains. PLoS Genetics, 2009, 5, e1000726.	3.5	61
21	The inner nuclear membrane proteins Man1 and Ima1 link to two different types of chromatin at the nuclear periphery in <i>S. pombe</i> . Nucleus, 2012, 3, 77-87.	2.2	60
22	Histone H4 lysine 20 mono-methylation directly facilitates chromatin openness and promotes transcription of housekeeping genes. Nature Communications, 2021, 12, 4800.	12.8	56
23	The Fun30 Chromatin Remodeler Fft3 Controls Nuclear Organization and Chromatin Structure of Insulators and Subtelomeres in Fission Yeast. PLoS Genetics, 2015, 11, e1005101.	3.5	52
24	A nucleosome turnover map reveals that the stability of histone H4 Lys20 methylation depends on histone recycling in transcribed chromatin. Genome Research, 2015, 25, 872-883.	5.5	51
25	Specific functions for the fission yeast Sirtuins Hst2 and Hst4 in gene regulation and retrotransposon silencing. EMBO Journal, 2007, 26, 2477-2488.	7.8	47
26	Fission Yeast lec1-Ino80-Mediated Nucleosome Eviction Regulates Nucleotide and Phosphate Metabolism. Molecular and Cellular Biology, 2010, 30, 657-674.	2.3	45
27	Genome-Wide Studies of Histone Demethylation Catalysed by the Fission Yeast Homologues of Mammalian LSD1. PLoS ONE, 2007, 2, e386.	2.5	44
28	Transcription-coupled recruitment of human CHD1 and CHD2 influences chromatin accessibility and histone H3 and H3.3 occupancy at active chromatin regions. Epigenetics and Chromatin, 2015, 8, 4.	3.9	42
29	Comprehensive mapping of the effects of azacitidine on DNA methylation, repressive/permissive histone marks and gene expression in primary cells from patients with MDS and MDS-related disease. Oncotarget, 2017, 8, 28812-28825.	1.8	42
30	Mutations in histone modulators are associated with prolonged survival during azacitidine therapy. Oncotarget, 2016, 7, 22103-22115.	1.8	37
31	Genome-wide mapping of nucleosome positions in Schizosaccharomyces pombe. Methods, 2009, 48, 218-225.	3.8	36
32	H3K14 ubiquitylation promotes H3K9 methylation for heterochromatin assembly. EMBO Reports, 2019, 20, e48111.	4.5	35
33	Comprehensive profiling of the fission yeast transcription start site activity during stress and media response. Nucleic Acids Research, 2019, 47, 1671-1691.	14.5	34
34	Podbat: A Novel Genomic Tool Reveals Swr1-Independent H2A.Z Incorporation at Gene Coding Sequences through Epigenetic Meta-Analysis. PLoS Computational Biology, 2011, 7, e1002163.	3.2	29
35	Telomeric Repeats Facilitate CENP-ACnp1 Incorporation via Telomere Binding Proteins. PLoS ONE, 2013, 8, e69673.	2.5	27
36	Cancer-specific changes in DNA methylation reveal aberrant silencing and activation of enhancers in leukemia. Blood, 2017, 129, e13-e25.	1.4	27

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37	The Roles of SNF2/SWI2 Nucleosome Remodeling Enzymes in Blood Cell Differentiation and Leukemia. BioMed Research International, 2015, 2015, 1-17.	1.9	23
38	Topoisomerases, chromatin and transcription termination. Transcription, 2011, 2, 66-70.	3.1	22
39	Transcriptional regulation at the yeast nuclear envelope. Nucleus, 2013, 4, 379-389.	2.2	22
40	Restoration of KMT2C/MLL3 in human colorectal cancer cells reinforces genome-wide H3K4me1 profiles and influences cell growth and gene expression. Clinical Epigenetics, 2020, 12, 74.	4.1	22
41	Regulating retrotransposon activity through the use of alternative transcription start sites. EMBO Reports, 2016, 17, 753-768.	4.5	21
42	Budding yeastCAN1gene as a selection marker in fission yeast. Nucleic Acids Research, 1991, 19, 1150-1150.	14.5	19
43	CTG repeat-targeting oligonucleotides for down-regulating Huntingtin expression. Nucleic Acids Research, 2017, 45, 5153-5169.	14.5	19
44	Spore Analysis and Tetrad Dissection of <i>Schizosaccharomyces pombe</i> . Cold Spring Harbor Protocols, 2017, 2017, pdb.prot091710.	0.3	19
45	Chd1 remodelers maintain open chromatin and regulate the epigenetics of differentiation. Experimental Cell Research, 2010, 316, 1316-1323.	2.6	18
46	RNAi mediates post-transcriptional repression of gene expression in fission yeast Schizosaccharomyces pombe. Biochemical and Biophysical Research Communications, 2014, 444, 254-259.	2.1	18
47	Leo1 is essential for the dynamic regulation of heterochromatin and gene expression during cellular quiescence. Epigenetics and Chromatin, 2019, 12, 45.	3.9	17
48	AML displays increased CTCF occupancy associated with aberrant gene expression and transcription factor binding. Blood, 2020, 136, 339-352.	1.4	17
49	Setting up <i>Schizosaccharomyces pombe</i> Crosses/Matings. Cold Spring Harbor Protocols, 2017, 2017, pdb.prot091694.	0.3	16
50	Genetic Analysis of <i>Schizosaccharomyces pombe</i> . Cold Spring Harbor Protocols, 2017, 2017, pdb.top079772.	0.3	15
51	ABCE1 Is a Highly Conserved RNA Silencing Suppressor. PLoS ONE, 2015, 10, e0116702.	2.5	14
52	A second Wpl1 antiâ€cohesion pathway requires dephosphorylation of fission yeast kleisin Rad21 by PP 4. EMBO Journal, 2017, 36, 1364-1378.	7.8	13
53	Chromatin Immunoprecipitation Using Microarrays. Methods in Molecular Biology, 2009, 529, 279-295.	0.9	12
54	The Paradox of Silent Heterochromatin. Science, 2008, 320, 624-625.	12.6	11

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55	DNA Topoisomerase III Localizes to Centromeres and Affects Centromeric CENP-A Levels in Fission Yeast. PLoS Genetics, 2013, 9, e1003371.	3.5	11
56	Histone H2B Ubiquitylation Regulates Histone Gene Expression by Suppressing Antisense Transcription in Fission Yeast. Genetics, 2019, 213, 161-172.	2.9	11
57	High-Throughput Flow Cytometry Combined with Genetic Analysis Brings New Insights into the Understanding of Chromatin Regulation of Cellular Quiescence. International Journal of Molecular Sciences, 2020, 21, 9022.	4.1	10
58	Abo1 is required for the H3K9me2 to H3K9me3 transition in heterochromatin. Scientific Reports, 2020, 10, 6055.	3.3	8
59	Selecting Schizosaccharomyces pombe Diploids. Cold Spring Harbor Protocols, 2017, 2017, pdb.prot091702.	0.3	7
60	Mating-Type Determination in <i>Schizosaccharomyces pombe</i> . Cold Spring Harbor Protocols, 2017, 2017, pdb.prot091728.	0.3	6
61	The binding of Chp2's chromodomain to methylated H3K9 is essential for Chp2's role in heterochromatin assembly in fission yeast. PLoS ONE, 2018, 13, e0201101.	2.5	5
62	The CDK Pef1 and protein phosphatase 4 oppose each other for regulating cohesin binding to fission yeast chromosomes. ELife, 2020, 9, .	6.0	5
63	Panspecies Small-Molecule Disruptors of Heterochromatin-Mediated Transcriptional Gene Silencing. Molecular and Cellular Biology, 2015, 35, 662-674.	2.3	3
64	Topokaryotyping demonstrates single cell variability and stress dependent variations in nuclear envelope associated domains. Nucleic Acids Research, 2018, 46, e135-e135.	14.5	3
65	Chromatin remodeler Fft3 plays a dual role at blocked DNA replication forks. Life Science Alliance, 2019, 2, e201900433.	2.8	3
66	Ethyl Methanesulfonate Mutagenesis in <i>Schizosaccharomyces pombe</i> . Cold Spring Harbor Protocols, 2017, 2017, pdb.prot091736.	0.3	1
67	The Role of Non-Catalytic Domains of Hrp3 in Nucleosome Remodeling. International Journal of Molecular Sciences, 2021, 22, 1793.	4.1	0
68	Mutations in Histone Modulators Are Associated with Prolonged Survival during Azacitidine Therapy. Blood, 2015, 126, 2839-2839.	1.4	0