## Karl Ekwall

## List of Publications by Year in Descending Order

Source: https://exaly.com/author-pdf/3846222/karl-ekwall-publications-by-year.pdf

Version: 2024-04-28

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

68 56 3,214 29 h-index g-index citations papers 8.5 5.11 72 3,739 avg, IF L-index ext. citations ext. papers

#	Paper	IF	Citations
68	Histone H4 lysine 20 mono-methylation directly facilitates chromatin openness and promotes transcription of housekeeping genes. <i>Nature Communications</i> , <b>2021</b> , 12, 4800	17.4	11
67	Restoration of KMT2C/MLL3 in human colorectal cancer cells reinforces genome-wide H3K4me1 profiles and influences cell growth and gene expression. <i>Clinical Epigenetics</i> , <b>2020</b> , 12, 74	7.7	7
66	AML displays increased CTCF occupancy associated with aberrant gene expression and transcription factor binding. <i>Blood</i> , <b>2020</b> , 136, 339-352	2.2	6
65	Abo1 is required for the H3K9me2 to H3K9me3 transition in heterochromatin. <i>Scientific Reports</i> , <b>2020</b> , 10, 6055	4.9	3
64	High-Throughput Flow Cytometry Combined with Genetic Analysis Brings New Insights into the Understanding of Chromatin Regulation of Cellular Quiescence. <i>International Journal of Molecular Sciences</i> , <b>2020</b> , 21,	6.3	2
63	Comprehensive profiling of the fission yeast transcription start site activity during stress and media response. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, 1671-1691	20.1	19
62	Leo1 is essential for the dynamic regulation of heterochromatin and gene expression during cellular quiescence. <i>Epigenetics and Chromatin</i> , <b>2019</b> , 12, 45	5.8	12
61	H3K14 ubiquitylation promotes H3K9 methylation for heterochromatin assembly. <i>EMBO Reports</i> , <b>2019</b> , 20, e48111	6.5	18
60	Chromatin remodeler Fft3 plays a dual role at blocked DNA replication forks. <i>Life Science Alliance</i> , <b>2019</b> , 2,	5.8	1
59	Histone H2B Ubiquitylation Regulates Histone Gene Expression by Suppressing Antisense Transcription in Fission Yeast. <i>Genetics</i> , <b>2019</b> , 213, 161-172	4	2
58	The binding of Chp2's chromodomain to methylated H3K9 is essential for Chp2's role in heterochromatin assembly in fission yeast. <i>PLoS ONE</i> , <b>2018</b> , 13, e0201101	3.7	3
57	Topokaryotyping demonstrates single cell variability and stress dependent variations in nuclear envelope associated domains. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, e135	20.1	1
56	A second Wpl1 anti-cohesion pathway requires dephosphorylation of fission yeast kleisin Rad21 by PP4. <i>EMBO Journal</i> , <b>2017</b> , 36, 1364-1378	13	10
55	CTG repeat-targeting oligonucleotides for down-regulating Huntingtin expression. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, 5153-5169	20.1	15
54	Cancer-specific changes in DNA methylation reveal aberrant silencing and activation of enhancers in leukemia. <i>Blood</i> , <b>2017</b> , 129, e13-e25	2.2	24
53	Ethyl Methanesulfonate Mutagenesis in. Cold Spring Harbor Protocols, 2017, 2017, pdb.prot091736	1.2	1
52	FANTOM5 CAGE profiles of human and mouse samples. <i>Scientific Data</i> , <b>2017</b> , 4, 170112	8.2	88

51	Mating-Type Determination in. Cold Spring Harbor Protocols, 2017, 2017, pdb.prot091728	1.2	4
50	Genetic Analysis of. <i>Cold Spring Harbor Protocols</i> , <b>2017</b> , 2017, pdb.top079772	1.2	12
49	Selecting Diploids. <i>Cold Spring Harbor Protocols</i> , <b>2017</b> , 2017, pdb.prot091702	1.2	5
48	Spore Analysis and Tetrad Dissection of. <i>Cold Spring Harbor Protocols</i> , <b>2017</b> , 2017, pdb.prot091710	1.2	8
47	Setting up Crosses/Matings. <i>Cold Spring Harbor Protocols</i> , <b>2017</b> , 2017, pdb.prot091694	1.2	7
46	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. <i>Oncotarget</i> , <b>2017</b> , 8, 28812-28825	3.3	28
45	Mutations in histone modulators are associated with prolonged survival during azacitidine therapy. <i>Oncotarget</i> , <b>2016</b> , 7, 22103-15	3.3	35
44	Regulating retrotransposon activity through the use of alternative transcription start sites. <i>EMBO Reports</i> , <b>2016</b> , 17, 753-68	6.5	17
43	Transcription-coupled recruitment of human CHD1 and CHD2 influences chromatin accessibility and histone H3 and H3.3 occupancy at active chromatin regions. <i>Epigenetics and Chromatin</i> , <b>2015</b> , 8, 4	5.8	32
42	Epigenetic Regulation of Chromatin States in Schizosaccharomyces pombe. <i>Cold Spring Harbor Perspectives in Biology</i> , <b>2015</b> , 7, a018770	10.2	113
42 41		10.2	113
	Perspectives in Biology, <b>2015</b> , 7, a018770  The Fun30 chromatin remodeler Fft3 controls nuclear organization and chromatin structure of	_	
41	Perspectives in Biology, 2015, 7, a018770  The Fun30 chromatin remodeler Fft3 controls nuclear organization and chromatin structure of insulators and subtelomeres in fission yeast. <i>PLoS Genetics</i> , 2015, 11, e1005101  A nucleosome turnover map reveals that the stability of histone H4 Lys20 methylation depends on	6	41
41	Perspectives in Biology, 2015, 7, a018770  The Fun30 chromatin remodeler Fft3 controls nuclear organization and chromatin structure of insulators and subtelomeres in fission yeast. PLoS Genetics, 2015, 11, e1005101  A nucleosome turnover map reveals that the stability of histone H4 Lys20 methylation depends on histone recycling in transcribed chromatin. Genome Research, 2015, 25, 872-83  The Paf1 complex factors Leo1 and Paf1 promote local histone turnover to modulate chromatin	6 9·7	41 33
41 40 39	The Fun30 chromatin remodeler Fft3 controls nuclear organization and chromatin structure of insulators and subtelomeres in fission yeast. <i>PLoS Genetics</i> , <b>2015</b> , 11, e1005101  A nucleosome turnover map reveals that the stability of histone H4 Lys20 methylation depends on histone recycling in transcribed chromatin. <i>Genome Research</i> , <b>2015</b> , 25, 872-83  The Paf1 complex factors Leo1 and Paf1 promote local histone turnover to modulate chromatin states in fission yeast. <i>EMBO Reports</i> , <b>2015</b> , 16, 1673-87	6 9·7 6.5	41 33 42
41 40 39 38	Perspectives in Biology, 2015, 7, a018770  The Fun30 chromatin remodeler Fft3 controls nuclear organization and chromatin structure of insulators and subtelomeres in fission yeast. PLoS Genetics, 2015, 11, e1005101  A nucleosome turnover map reveals that the stability of histone H4 Lys20 methylation depends on histone recycling in transcribed chromatin. Genome Research, 2015, 25, 872-83  The Paf1 complex factors Leo1 and Paf1 promote local histone turnover to modulate chromatin states in fission yeast. EMBO Reports, 2015, 16, 1673-87  ABCE1 is a highly conserved RNA silencing suppressor. PLoS ONE, 2015, 10, e0116702  The roles of SNF2/SWI2 nucleosome remodeling enzymes in blood cell differentiation and	6 9·7 6.5	41 33 42 9
41 40 39 38 37	Perspectives in Biology, 2015, 7, a018770  The Fun30 chromatin remodeler Fft3 controls nuclear organization and chromatin structure of insulators and subtelomeres in fission yeast. PLoS Genetics, 2015, 11, e1005101  A nucleosome turnover map reveals that the stability of histone H4 Lys20 methylation depends on histone recycling in transcribed chromatin. Genome Research, 2015, 25, 872-83  The Paf1 complex factors Leo1 and Paf1 promote local histone turnover to modulate chromatin states in fission yeast. EMBO Reports, 2015, 16, 1673-87  ABCE1 is a highly conserved RNA silencing suppressor. PLoS ONE, 2015, 10, e0116702  The roles of SNF2/SWI2 nucleosome remodeling enzymes in blood cell differentiation and leukemia. BioMed Research International, 2015, 2015, 347571  Panspecies small-molecule disruptors of heterochromatin-mediated transcriptional gene silencing.	6 9·7 6.5 3·7	41 33 42 9

33	RNAi mediates post-transcriptional repression of gene expression in fission yeast Schizosaccharomyces pombe. <i>Biochemical and Biophysical Research Communications</i> , <b>2014</b> , 444, 254-9	3.4	15
32	DNA topoisomerase III localizes to centromeres and affects centromeric CENP-A levels in fission yeast. <i>PLoS Genetics</i> , <b>2013</b> , 9, e1003371	6	8
31	Transcriptional regulation at the yeast nuclear envelope. <i>Nucleus</i> , <b>2013</b> , 4, 379-89	3.9	21
30	Telomeric repeats facilitate CENP-A(Cnp1) incorporation via telomere binding proteins. <i>PLoS ONE</i> , <b>2013</b> , 8, e69673	3.7	22
29	CHD1 remodelers regulate nucleosome spacing in vitro and align nucleosomal arrays over gene coding regions in S. pombe. <i>EMBO Journal</i> , <b>2012</b> , 31, 4388-403	13	74
28	The inner nuclear membrane proteins Man1 and Ima1 link to two different types of chromatin at the nuclear periphery in S. pombe. <i>Nucleus</i> , <b>2012</b> , 3, 77-87	3.9	51
27	Comparative functional genomics of the fission yeasts. <i>Science</i> , <b>2011</b> , 332, 930-6	33.3	364
26	The FUN30 chromatin remodeler, Fft3, protects centromeric and subtelomeric domains from euchromatin formation. <i>PLoS Genetics</i> , <b>2011</b> , 7, e1001334	6	61
25	Topoisomerases, chromatin and transcription termination. <i>Transcription</i> , <b>2011</b> , 2, 66-70	4.8	21
24	Heterochromatin and EuchromatinDrganization, Boundaries, and Gene Regulation 2011,		1
23	Podbat: a novel genomic tool reveals Swr1-independent H2A.Z incorporation at gene coding sequences through epigenetic meta-analysis. <i>PLoS Computational Biology</i> , <b>2011</b> , 7, e1002163	5	27
22	Schizosaccharomyces pombe genome-wide nucleosome mapping reveals positioning mechanisms distinct from those of Saccharomyces cerevisiae. <i>Nature Structural and Molecular Biology</i> , <b>2010</b> , 17, 251	- <del>1</del> 7.6	184
21	Topoisomerase I regulates open chromatin and controls gene expression in vivo. <i>EMBO Journal</i> , <b>2010</b> , 29, 2126-34	13	63
20	Fission yeast lec1-ino80-mediated nucleosome eviction regulates nucleotide and phosphate metabolism. <i>Molecular and Cellular Biology</i> , <b>2010</b> , 30, 657-74	4.8	37
19	Chd1 remodelers maintain open chromatin and regulate the epigenetics of differentiation. <i>Experimental Cell Research</i> , <b>2010</b> , 316, 1316-23	4.2	16
18	Histone modification patterns and epigenetic codes. <i>Biochimica Et Biophysica Acta - General Subjects</i> , <b>2009</b> , 1790, 863-8	4	149
17	Genome-wide mapping of nucleosome positions in Schizosaccharomyces pombe. <i>Methods</i> , <b>2009</b> , 48, 218-25	4.6	30
16	Chromatin immunoprecipitation using microarrays. <i>Methods in Molecular Biology</i> , <b>2009</b> , 529, 279-95	1.4	12

## LIST OF PUBLICATIONS

15	The Schizosaccharomyces pombe JmjC-protein, Msc1, prevents H2A.Z localization in centromeric and subtelomeric chromatin domains. <i>PLoS Genetics</i> , <b>2009</b> , 5, e1000726	6	54
14	Molecular biology. The paradox of silent heterochromatin. <i>Science</i> , <b>2008</b> , 320, 624-5	33.3	10
13	Specific functions for the fission yeast Sirtuins Hst2 and Hst4 in gene regulation and retrotransposon silencing. <i>EMBO Journal</i> , <b>2007</b> , 26, 2477-88	13	40
12	A genome-wide role for CHD remodelling factors and Nap1 in nucleosome disassembly. <i>EMBO Journal</i> , <b>2007</b> , 26, 2868-79	13	70
11	Epigenetic control of centromere behavior. <i>Annual Review of Genetics</i> , <b>2007</b> , 41, 63-81	14.5	78
10	Genome-wide studies of histone demethylation catalysed by the fission yeast homologues of mammalian LSD1. <i>PLoS ONE</i> , <b>2007</b> , 2, e386	3.7	29
9	Genomewide analysis of nucleosome density histone acetylation and HDAC function in fission yeast. <i>EMBO Journal</i> , <b>2005</b> , 24, 2906-18	13	116
8	Genome-wide analysis of HDAC function. <i>Trends in Genetics</i> , <b>2005</b> , 21, 608-15	8.5	101
7	RNA Pol II subunit Rpb7 promotes centromeric transcription and RNAi-directed chromatin silencing. <i>Genes and Development</i> , <b>2005</b> , 19, 2301-6	12.6	181
6	Dicer is required for chromosome segregation and gene silencing in fission yeast cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2002</b> , 99, 16648-53	11.5	109
5	Functional divergence between histone deacetylases in fission yeast by distinct cellular localization and in vivo specificity. <i>Molecular and Cellular Biology</i> , <b>2002</b> , 22, 2170-81	4.8	150
4	The domain structure of centromeres is conserved from fission yeast to humans. <i>Molecular Biology of the Cell</i> , <b>2001</b> , 12, 2767-75	3.5	78
3		3·5 56.2	78 341

Comprehensive profiling of the fission yeast transcription start site activity during stress and media response 1