

Jurg Bahler

List of Publications by Year in descending order

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Version: 2024-02-01

210
papers

30,232
citations

14655

66
h-index

5988

160
g-index

348
all docs

348
docs citations

348
times ranked

41556
citing authors

#	ARTICLE	IF	CITATIONS
1	Functional profiling of long intergenic non-coding RNAs in fission yeast. <i>ELife</i> , 2022, 11, .	6.0	7
2	Fission stories: using PomBase to understand <i>Schizosaccharomyces pombe</i> biology. <i>Genetics</i> , 2022, 220, .	2.9	60
3	High-Throughput, High-Precision Colony Phenotyping with Pyphe. <i>Methods in Molecular Biology</i> , 2022, 2477, 381-397.	0.9	6
4	Amino Acids Whose Intracellular Levels Change Most During Aging Alter Chronological Life Span of Fission Yeast. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2021, 76, 205-210.	3.6	9
5	Global network analysis in <i>Schizosaccharomyces pombe</i> reveals three distinct consequences of the common 1-kb deletion causing juvenile CLN3 disease. <i>Scientific Reports</i> , 2021, 11, 6332.	3.3	9
6	Barcode sequencing and a high-throughput assay for chronological lifespan uncover ageing-associated genes in fission yeast. <i>Microbial Cell</i> , 2021, 8, 146-160.	3.2	19
7	R-loops and regulatory changes in chronologically ageing fission yeast cells drive non-random patterns of genome rearrangements. <i>PLoS Genetics</i> , 2021, 17, e1009784.	3.5	2
8	The Gene Ontology resource: enriching a GOld mine. <i>Nucleic Acids Research</i> , 2021, 49, D325-D334.	14.5	2,416
9	<i>C. elegans</i> feed yolk to their young in a form of primitive lactation. <i>Nature Communications</i> , 2021, 12, 5801.	12.8	23
10	Recombination and biased segregation of mitochondrial genomes during crossing and meiosis of different strains. <i>MicroPublication Biology</i> , 2021, 2021, .	0.1	0
11	De Novo and Bi-allelic Pathogenic Variants in NARS1 Cause Neurodevelopmental Delay Due to Toxic Gain-of-Function and Partial Loss-of-Function Effects. <i>American Journal of Human Genetics</i> , 2020, 107, 311-324.	6.2	32
12	Cdk9 and H2Bub1 signal to Clr6-Cli/Rpd3S to suppress aberrant antisense transcription. <i>Nucleic Acids Research</i> , 2020, 48, 7154-7168.	14.5	16
13	The GATA Transcription Factor Gaf1 Represses tRNAs, Inhibits Growth, and Extends Chronological Lifespan Downstream of Fission Yeast TORC1. <i>Cell Reports</i> , 2020, 30, 3240-3249.e4.	6.4	33
14	The African Swine Fever Virus Transcriptome. <i>Journal of Virology</i> , 2020, 94, .	3.4	118
15	Mitochondrial respiration is required to provide amino acids during fermentative proliferation of fission yeast. <i>EMBO Reports</i> , 2020, 21, e50845.	4.5	28
16	Pyruvate kinase variant of fission yeast tunes carbon metabolism, cell regulation, growth and stress resistance. <i>Molecular Systems Biology</i> , 2020, 16, e9270.	7.2	27
17	Pyphe, a python toolbox for assessing microbial growth and cell viability in high-throughput colony screens. <i>ELife</i> , 2020, 9, .	6.0	37
18	Longevity is determined by ETS transcription factors in multiple tissues and diverse species. <i>PLoS Genetics</i> , 2019, 15, e1008212.	3.5	23

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19	An essential role for dNTP homeostasis following CDK-induced replication stress. <i>Journal of Cell Science</i> , 2019, 132, .	2.0	16
20	PomBase 2018: user-driven reimplementaion of the fission yeast database provides rapid and intuitive access to diverse, interconnected information. <i>Nucleic Acids Research</i> , 2019, 47, D821-D827.	14.5	157
21	Fitness Landscape of the Fission Yeast Genome. <i>Molecular Biology and Evolution</i> , 2019, 36, 1612-1623.	8.9	12
22	Hidden in plain sight: what remains to be discovered in the eukaryotic proteome?. <i>Open Biology</i> , 2019, 9, 180241.	3.6	80
23	The Gene Ontology Resource: 20 years and still GOing strong. <i>Nucleic Acids Research</i> , 2019, 47, D330-D338.	14.5	3,474
24	Single-cell imaging and RNA sequencing reveal patterns of gene expression heterogeneity during fission yeast growth and adaptation. <i>Nature Microbiology</i> , 2019, 4, 480-491.	13.3	51
25	General amino acid control in fission yeast is regulated by a nonconserved transcription factor, with functions analogous to Gcn4/Atf4. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E1829-E1838.	7.1	48
26	Uncovering Natural Longevity Alleles from Intercrossed Pools of Aging Fission Yeast Cells. <i>Genetics</i> , 2018, 210, 733-744.	2.9	8
27	Long noncoding RNA repertoire and targeting by nuclear exosome, cytoplasmic exonuclease, and RNAi in fission yeast. <i>Rna</i> , 2018, 24, 1195-1213.	3.5	45
28	Transient structural variations have strong effects on quantitative traits and reproductive isolation in fission yeast. <i>Nature Communications</i> , 2017, 8, 14061.	12.8	472
29	Expansion of the Gene Ontology knowledgebase and resources. <i>Nucleic Acids Research</i> , 2017, 45, D331-D338.	14.5	1,838
30	Genetic interactions and functional analyses of the fission yeast <i>gsk3</i> and <i>amk2</i> single and double mutants defective in TORC1-dependent processes. <i>Scientific Reports</i> , 2017, 7, 44257.	3.3	14
31	Preparation of Total RNA from Fission Yeast. <i>Cold Spring Harbor Protocols</i> , 2017, 2017, pdb.prot091629.	0.3	16
32	<i>Schizosaccharomyces pombe</i> Polysome Profile Analysis and RNA Purification. <i>Cold Spring Harbor Protocols</i> , 2017, 2017, pdb.prot091637.	0.3	2
33	RNA metabolism is the primary target of formamide in vivo. <i>Scientific Reports</i> , 2017, 7, 15895.	3.3	14
34	The copper transport-associated protein Ctr4 can form prion-like epigenetic determinants in <i>Schizosaccharomyces pombe</i> . <i>Microbial Cell</i> , 2017, 4, 16-28.	3.2	16
35	Spotsizer: High-throughput quantitative analysis of microbial growth. <i>BioTechniques</i> , 2016, 61, 191-201.	1.8	10
36	Identification of nuclear genes affecting 2-Deoxyglucose resistance in <i>Schizosaccharomyces pombe</i> . <i>FEMS Yeast Research</i> , 2016, 16, fow061.	2.3	7

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37	Selected <i>Schizosaccharomyces pombe</i> Strains Have Characteristics That Are Beneficial for Winemaking. <i>PLoS ONE</i> , 2016, 11, e0151102.	2.5	81
38	The Nrd1-like protein Seb1 coordinates cotranscriptional 3' end processing and polyadenylation site selection. <i>Genes and Development</i> , 2016, 30, 1558-1572.	5.9	46
39	Gene dosage and the timing of mitosis. <i>Cell Cycle</i> , 2016, 15, 3022-3023.	2.6	0
40	CSL protein regulates transcription of genes required to prevent catastrophic mitosis in fission yeast. <i>Cell Cycle</i> , 2016, 15, 3082-3093.	2.6	13
41	Php4 Is a Key Player for Iron Economy in Meiotic and Sporulating Cells. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 3077-3095.	1.8	16
42	Abo1, a conserved bromodomain AAA domain ATPase, maintains global nucleosome occupancy and organization. <i>EMBO Reports</i> , 2016, 17, 79-93.	4.5	22
43	Functional and regulatory profiling of energy metabolism in fission yeast. <i>Genome Biology</i> , 2016, 17, 240.	8.8	44
44	Cell-based screens and phenomics with fission yeast. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2016, 51, 86-95.	5.2	16
45	Increasing extracellular H ₂ O ₂ produces a bi-phasic response in intracellular H ₂ O ₂ , with peroxiredoxin hyperoxidation only triggered once the cellular H ₂ O ₂ -buffering capacity is overwhelmed. <i>Free Radical Biology and Medicine</i> , 2016, 95, 333-348.	2.9	38
46	A CRISPR/Cas9-based method and primer design tool for seamless genome editing in fission yeast. <i>Wellcome Open Research</i> , 2016, 1, 19.	1.8	27
47	Identifying genes required for respiratory growth of fission yeast. <i>Wellcome Open Research</i> , 2016, 1, 12.	1.8	24
48	Co-Expression Network Models Suggest that Stress Increases Tolerance to Mutations. <i>Scientific Reports</i> , 2015, 5, 16726.	3.3	4
49	Role of Ccr4-Not complex in heterochromatin formation at meiotic genes and subtelomeres in fission yeast. <i>Epigenetics and Chromatin</i> , 2015, 8, 28.	3.9	41
50	AnGeLi: A Tool for the Analysis of Gene Lists from Fission Yeast. <i>Frontiers in Genetics</i> , 2015, 6, 330.	2.3	65
51	Ace2 receives helping hand for cell-cycle transcription. <i>Cell Cycle</i> , 2015, 14, 3351-3352.	2.6	2
52	The genomic and phenotypic diversity of <i>Schizosaccharomyces pombe</i> . <i>Nature Genetics</i> , 2015, 47, 235-241.	21.4	174
53	Parallel Profiling of Fission Yeast Deletion Mutants for Proliferation and for Lifespan During Long-Term Quiescence. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 145-155.	1.8	38
54	Proportionality: A Valid Alternative to Correlation for Relative Data. <i>PLoS Computational Biology</i> , 2015, 11, e1004075.	3.2	232

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55	Identification of New Players in Cell Division, DNA Damage Response, and Morphogenesis Through Construction of <i>Schizosaccharomyces pombe</i> Deletion Strains. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 361-370.	1.8	20
56	PomBase 2015: updates to the fission yeast database. <i>Nucleic Acids Research</i> , 2015, 43, D656-D661.	14.5	95
57	Widespread exon skipping triggers degradation by nuclear RNA surveillance in fission yeast. <i>Genome Research</i> , 2015, 25, 884-896.	5.5	37
58	Gene Ontology Consortium: going forward. <i>Nucleic Acids Research</i> , 2015, 43, D1049-D1056.	14.5	2,743
59	Gene Function Prediction from Functional Association Networks Using Kernel Partial Least Squares Regression. <i>PLoS ONE</i> , 2015, 10, e0134668.	2.5	15
60	Fission Yeast CSL Transcription Factors: Mapping Their Target Genes and Biological Roles. <i>PLoS ONE</i> , 2015, 10, e0137820.	2.5	19
61	A central role for TOR signalling in a yeast model for juvenile CLN3 disease. <i>Microbial Cell</i> , 2015, 2, 466-480.	3.2	13
62	Lithium suppresses A β pathology by inhibiting translation in an adult <i>Drosophila</i> model of Alzheimer's disease. <i>Frontiers in Aging Neuroscience</i> , 2014, 6, 190.	3.4	81
63	A metabolic strategy to enhance long-term survival by Phx1 through stationary phase-specific pyruvate decarboxylases in fission yeast. <i>Aging</i> , 2014, 6, 587-601.	3.1	7
64	Individual letters of the RNA polymerase II CTD code govern distinct gene expression programs in fission yeast. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 4185-4190.	7.1	53
65	Contributions of transcription and mRNA decay to gene expression dynamics of fission yeast in response to oxidative stress. <i>RNA Biology</i> , 2014, 11, 702-714.	3.1	26
66	Systematic screen for mutants resistant to TORC1 inhibition in fission yeast reveals genes involved in cellular ageing and growth. <i>Biology Open</i> , 2014, 3, 161-171.	1.2	55
67	LaSSO, a strategy for genome-wide mapping of intronic lariats and branch points using RNA-seq. <i>Genome Research</i> , 2014, 24, 1169-1179.	5.5	64
68	Regulation of spindle pole body assembly and cytokinesis by the centrin-binding protein Sfi1 in fission yeast. <i>Molecular Biology of the Cell</i> , 2014, 25, 2735-2749.	2.1	31
69	Natural genetic variation impacts expression levels of coding, non-coding, and antisense transcripts in fission yeast. <i>Molecular Systems Biology</i> , 2014, 10, 764.	7.2	65
70	The DNA damage checkpoint pathway promotes extensive resection and nucleotide synthesis to facilitate homologous recombination repair and genome stability in fission yeast. <i>Nucleic Acids Research</i> , 2014, 42, 5644-5656.	14.5	27
71	A Novel Histone Deacetylase Complex in the Control of Transcription and Genome Stability. <i>Molecular and Cellular Biology</i> , 2014, 34, 3500-3514.	2.3	37
72	A histone H3K36 chromatin switch coordinates DNA double-strand break repair pathway choice. <i>Nature Communications</i> , 2014, 5, 4091.	12.8	134

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73	The RNA exosome promotes transcription termination of backtracked RNA polymerase II. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 919-926.	8.2	86
74	Stress induces remodelling of yeast interaction and co-expression networks. <i>Molecular BioSystems</i> , 2013, 9, 1697.	2.9	21
75	Spt6 Regulates Intragenic and Antisense Transcription, Nucleosome Positioning, and Histone Modifications Genome-Wide in Fission Yeast. <i>Molecular and Cellular Biology</i> , 2013, 33, 4779-4792.	2.3	93
76	Extensive Mass Spectrometry-based Analysis of the Fission Yeast Proteome. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 1741-1751.	3.8	28
77	Genome-wide analysis of poly(A) site selection in <i>Schizosaccharomyces pombe</i> . <i>Rna</i> , 2013, 19, 1617-1631.	3.5	37
78	Myb-domain protein Teb1 controls histone levels and centromere assembly in fission yeast. <i>EMBO Journal</i> , 2013, 32, 450-460.	7.8	21
79	FYPO: the fission yeast phenotype ontology. <i>Bioinformatics</i> , 2013, 29, 1671-1678.	4.1	53
80	<scp>TORC</scp>1 signaling inhibition by rapamycin and caffeine affect lifespan, global gene expression, and cell proliferation of fission yeast. <i>Aging Cell</i> , 2013, 12, 563-573.	6.7	120
81	Structural and Functional Characterization of the N Terminus of <i>Schizosaccharomyces pombe</i> Cwf10. <i>Eukaryotic Cell</i> , 2013, 12, 1472-1489.	3.4	12
82	Inhibition of TORC1 signaling and increased lifespan: gained in translation?. <i>Aging</i> , 2013, 5, 335-336.	3.1	10
83	Cell Cycle-regulated Gene Expression. , 2013, , 360-360.		0
84	RNA-seq. , 2013, , 1877-1877.		0
85	Transcriptional Regulatory Network. , 2013, , 2258-2258.		0
86	DNA Microarrays. , 2013, , 609-610.		0
87	Cell Cycle, Synchronization. , 2013, , 359-360.		0
88	Transcriptome. , 2013, , 2259-2259.		0
89	Cell Cycle Analysis, Expression Profiling. , 2013, , 231-233.		0
90	Predicting the Fission Yeast Protein Interaction Network. <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 453-467.	1.8	29

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91	Altered nuclear tRNA metabolism in La-deleted <i>Schizosaccharomyces pombe</i> is accompanied by a nutritional stress response involving Atf1p and Pcr1p that is suppressible by Xpo-t/Los1p. <i>Molecular Biology of the Cell</i> , 2012, 23, 480-491.	2.1	21
92	The Gene Ontology: enhancements for 2011. <i>Nucleic Acids Research</i> , 2012, 40, D559-D564.	14.5	191
93	Histone H3 Lysine 14 Acetylation Is Required for Activation of a DNA Damage Checkpoint in Fission Yeast. <i>Journal of Biological Chemistry</i> , 2012, 287, 4386-4393.	3.4	65
94	Gene Ontology Annotations and Resources. <i>Nucleic Acids Research</i> , 2012, 41, D530-D535.	14.5	456
95	PomBase: a comprehensive online resource for fission yeast. <i>Nucleic Acids Research</i> , 2012, 40, D695-D699.	14.5	288
96	Regulation of transcriptome, translation, and proteome in response to environmental stress in fission yeast. <i>Genome Biology</i> , 2012, 13, R25.	9.6	149
97	Quantitative Analysis of Fission Yeast Transcriptomes and Proteomes in Proliferating and Quiescent Cells. <i>Cell</i> , 2012, 151, 671-683.	28.9	513
98	Exploring long non-coding RNAs through sequencing. <i>Seminars in Cell and Developmental Biology</i> , 2012, 23, 200-205.	5.0	108
99	Genome regulation and evolution analysed by next-generation sequencing. <i>Seminars in Cell and Developmental Biology</i> , 2012, 23, 191.	5.0	0
100	Coordinating genome expression with cell size. <i>Trends in Genetics</i> , 2012, 28, 560-565.	6.7	188
101	Cuf2 Is a Novel Meiosis-Specific Regulatory Factor of Meiosis Maturation. <i>PLoS ONE</i> , 2012, 7, e36338.	2.5	16
102	Topology of functional networks predicts physical binding of proteins. <i>Bioinformatics</i> , 2012, 28, 2137-2145.	4.1	5
103	In silico characterization and prediction of global protein-mRNA interactions in yeast. <i>Nucleic Acids Research</i> , 2011, 39, 5826-5836.	14.5	55
104	Differential patterns of intronic and exonic DNA regions with respect to RNA polymerase II occupancy, nucleosome density and H3K36me3 marking in fission yeast. <i>Genome Biology</i> , 2011, 12, R82.	9.6	39
105	A Pre-mRNA Degradation Pathway that Selectively Targets Intron-Containing Genes Requires the Nuclear Poly(A)-Binding Protein. <i>Molecular Cell</i> , 2011, 44, 108-119.	9.7	93
106	Transcriptional and Cellular Responses to Defective Mitochondrial Proteolysis in Fission Yeast. <i>Journal of Molecular Biology</i> , 2011, 408, 222-237.	4.2	17
107	A Multidisciplinary, Open Access Platform for Research on Biomolecules. <i>Biomolecules</i> , 2011, 1, 1-2.	4.0	13
108	CENP-B preserves genome integrity at replication forks paused by retrotransposon LTR. <i>Nature</i> , 2011, 469, 112-115.	27.8	79

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109	Elimination of a specific histone H3K14 acetyltransferase complex bypasses the RNAi pathway to regulate pericentric heterochromatin functions. <i>Genes and Development</i> , 2011, 25, 214-219.	5.9	55
110	Spt6 Is Required for Heterochromatic Silencing in the Fission Yeast <i>Schizosaccharomyces pombe</i> . <i>Molecular and Cellular Biology</i> , 2011, 31, 4193-4204.	2.3	37
111	Mfc1 Is a Novel Forespore Membrane Copper Transporter in Meiotic and Sporulating Cells. <i>Journal of Biological Chemistry</i> , 2011, 286, 34356-34372.	3.4	36
112	A novel function of the mitochondrial transcription factor Mtf1 in fission yeast; Mtf1 regulates the nuclear transcription of <i>srk1</i> . <i>Nucleic Acids Research</i> , 2011, 39, 2690-2700.	14.5	7
113	Tra1 has specific regulatory roles, rather than global functions, within the SAGA co-activator complex. <i>EMBO Journal</i> , 2011, 30, 2843-2852.	7.8	63
114	H3K9me-Independent Gene Silencing in Fission Yeast Heterochromatin by Clr5 and Histone Deacetylases. <i>PLoS Genetics</i> , 2011, 7, e1001268.	3.5	28
115	N-Termini of Fungal CSL Transcription Factors Are Disordered, Enriched in Regulatory Motifs and Inhibit DNA Binding in Fission Yeast. <i>PLoS ONE</i> , 2011, 6, e23650.	2.5	8
116	RNA-seq: from technology to biology. <i>Cellular and Molecular Life Sciences</i> , 2010, 67, 569-579.	5.4	423
117	A Coordinated Global Control over Cellular Transcription. <i>Current Biology</i> , 2010, 20, 2010-2015.	3.9	129
118	Defining transcribed regions using RNA-seq. <i>Nature Protocols</i> , 2010, 5, 255-266.	12.0	70
119	Specific replication origins promote DNA amplification in fission yeast. <i>Journal of Cell Science</i> , 2010, 123, 3047-3051.	2.0	9
120	Role of Septins in the Orientation of Forespore Membrane Extension during Sporulation in Fission Yeast. <i>Molecular and Cellular Biology</i> , 2010, 30, 2057-2074.	2.3	38
121	Vgl1, a multi-KH domain protein, is a novel component of the fission yeast stress granules required for cell survival under thermal stress. <i>Nucleic Acids Research</i> , 2010, 38, 6555-6566.	14.5	34
122	Negative Regulation of Meiotic Gene Expression by the Nuclear Poly(a)-binding Protein in Fission Yeast*. <i>Journal of Biological Chemistry</i> , 2010, 285, 27859-27868.	3.4	72
123	Transcriptional Activation of the General Amino Acid Permease Gene <i>per1</i> by the Histone Deacetylase Clr6 Is Regulated by Oca2 Kinase. <i>Molecular and Cellular Biology</i> , 2010, 30, 3396-3410.	2.3	6
124	The Nuclear Poly(A)-Binding Protein Interacts with the Exosome to Promote Synthesis of Noncoding Small Nucleolar RNAs. <i>Molecular Cell</i> , 2010, 37, 34-45.	9.7	99
125	The Nuclear Poly(A)-Binding Protein Interacts with the Exosome to Promote Synthesis of Noncoding Small Nucleolar RNAs. <i>Molecular Cell</i> , 2010, 37, 447.	9.7	1
126	The Roles of Stress-Activated Sty1 and Gcn2 Kinases and of the Protooncprotein Homologue Int6/eIF3e in Responses to Endogenous Oxidative Stress during Histidine Starvation. <i>Journal of Molecular Biology</i> , 2010, 404, 183-201.	4.2	22

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127	Meta-analysis of genome regulation and expression variability across hundreds of environmental and genetic perturbations in fission yeast. <i>Molecular BioSystems</i> , 2010, 6, 543-552.	2.9	36
128	The Fission Yeast HIRA Histone Chaperone Is Required for Promoter Silencing and the Suppression of Cryptic Antisense Transcripts. <i>Molecular and Cellular Biology</i> , 2009, 29, 5158-5167.	2.3	54
129	The Fission Yeast Homeodomain Protein Yox1p Binds to MBF and Confines MBF-Dependent Cell-Cycle Transcription to G1-S via Negative Feedback. <i>PLoS Genetics</i> , 2009, 5, e1000626.	3.5	39
130	A simple method for directional transcriptome sequencing using Illumina technology. <i>Nucleic Acids Research</i> , 2009, 37, e148-e148.	14.5	88
131	Cyclin-Dependent Kinase Inhibits Reinitiation of a Normal S-Phase Program during G ₂ in Fission Yeast. <i>Molecular and Cellular Biology</i> , 2009, 29, 4025-4032.	2.3	27
132	TOR Complex 2 Controls Gene Silencing, Telomere Length Maintenance, and Survival under DNA-Damaging Conditions. <i>Molecular and Cellular Biology</i> , 2009, 29, 4584-4594.	2.3	55
133	Failed gene conversion leads to extensive end processing and chromosomal rearrangements in fission yeast. <i>EMBO Journal</i> , 2009, 28, 3400-3412.	7.8	46
134	An acetylated form of histone H2A.Z regulates chromosome architecture in <i>Schizosaccharomyces pombe</i> . <i>Nature Structural and Molecular Biology</i> , 2009, 16, 1286-1293.	8.2	77
135	Global approaches to study gene regulation. <i>Methods</i> , 2009, 48, 217.	3.8	1
136	Genomic expression patterns in cell separation mutants of <i>Schizosaccharomyces pombe</i> defective in the genes <i>sep10+</i> and <i>sep15+</i> coding for the Mediator subunits Med31 and Med8. <i>Molecular Genetics and Genomics</i> , 2008, 279, 225-238.	2.1	18
137	Improved tools for efficient mapping of fission yeast genes: identification of microtubule nucleation modifier <i>mod22</i> as an allele of chromatin remodelling factor gene <i>swr1</i> . <i>Yeast</i> , 2008, 25, 913-925.	1.7	15
138	Dynamic repertoire of a eukaryotic transcriptome surveyed at single-nucleotide resolution. <i>Nature</i> , 2008, 453, 1239-1243.	27.8	888
139	Fission yeast SWI/SNF and RSC complexes show compositional and functional differences from budding yeast. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 873-880.	8.2	97
140	Tuning gene expression to changing environments: from rapid responses to evolutionary adaptation. <i>Nature Reviews Genetics</i> , 2008, 9, 583-593.	16.3	857
141	Rapidly regulated genes are intron poor. <i>Trends in Genetics</i> , 2008, 24, 375-378.	6.7	340
142	Sites of strong Rec12/Spo11 binding in the fission yeast genome are associated with meiotic recombination and with centromeres. <i>Chromosoma</i> , 2008, 117, 431-444.	2.2	26
143	Chapter 5 Translational Control of Gene Expression. <i>International Review of Cell and Molecular Biology</i> , 2008, 271, 199-251.	3.2	46
144	Key Function for the CCAAT-Binding Factor Php4 To Regulate Gene Expression in Response to Iron Deficiency in Fission Yeast. <i>Eukaryotic Cell</i> , 2008, 7, 493-508.	3.4	95

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145	Global Role for Polyadenylation-Assisted Nuclear RNA Degradation in Posttranscriptional Gene Silencing. <i>Molecular and Cellular Biology</i> , 2008, 28, 656-665.	2.3	85
146	Response of <i>Schizosaccharomyces pombe</i> to Zinc Deficiency. <i>Eukaryotic Cell</i> , 2008, 7, 454-464.	3.4	36
147	Fission Yeast MAP Kinase Sty1 Is Recruited to Stress-induced Genes. <i>Journal of Biological Chemistry</i> , 2008, 283, 9945-9956.	3.4	38
148	Multiple Pathways Differentially Regulate Global Oxidative Stress Responses in Fission Yeast. <i>Molecular Biology of the Cell</i> , 2008, 19, 308-317.	2.1	184
149	Int6/eIF3e Promotes General Translation and Atf1 Abundance to Modulate Sty1 MAPK-dependent Stress Response in Fission Yeast. <i>Journal of Biological Chemistry</i> , 2008, 283, 22063-22075.	3.4	39
150	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.	5.9	81
151	Next-generation sequencing: applications beyond genomes. <i>Biochemical Society Transactions</i> , 2008, 36, 1091-1096.	3.4	111
152	urg1: A Uracil-Regulatable Promoter System for Fission Yeast with Short Induction and Repression Times. <i>PLoS ONE</i> , 2008, 3, e1428.	2.5	55
153	The BioGRID Interaction Database: 2008 update. <i>Nucleic Acids Research</i> , 2007, 36, D637-D640.	14.5	610
154	Genome-Wide Dynamics of SAPHIRE, an Essential Complex for Gene Activation and Chromatin Boundaries. <i>Molecular and Cellular Biology</i> , 2007, 27, 4058-4069.	2.3	24
155	A Network of Multiple Regulatory Layers Shapes Gene Expression in Fission Yeast. <i>Molecular Cell</i> , 2007, 26, 145-155.	9.7	184
156	Transcriptional regulatory network for sexual differentiation in fission yeast. <i>Genome Biology</i> , 2007, 8, R217.	9.6	104
157	Global transcriptional responses of fission and budding yeast to changes in copper and iron levels: a comparative study. <i>Genome Biology</i> , 2007, 8, R73.	9.6	54
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