Jurg Bahler

List of Publications by Year
in descending order

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	The Gene Ontology Resource: 20 years and still GOing strong. Nucleic Acids Research, 2019, 47, D330-D338.	14.5	3,474
2	Gene Ontology Consortium: going forward. Nucleic Acids Research, 2015, 43, D1049-D1056.	14.5	2,743
3	The Gene Ontology resource: enriching a GOld mine. Nucleic Acids Research, 2021, 49, D325-D334.	14.5	2,416
4	Heterologous modules for efficient and versatile PCR-based gene targeting inSchizosaccharomyces pombe. Yeast, 1998, 14, 943-951.	1.7	2,105
5	Expansion of the Gene Ontology knowledgebase and resources. Nucleic Acids Research, 2017, 45, D331-D338.	14.5	1,838
6	Dynamic repertoire of a eukaryotic transcriptome surveyed at single-nucleotide resolution. Nature, 2008, 453, 1239-1243.	27.8	888
7	Tuning gene expression to changing environments: from rapid responses to evolutionary adaptation. Nature Reviews Genetics, 2008, 9, 583-593.	16.3	857
8	Global Transcriptional Responses of Fission Yeast to Environmental Stress. Molecular Biology of the Cell, 2003, 14, 214-229.	2.1	726
9	The BioGRID Interaction Database: 2008 update. Nucleic Acids Research, 2007, 36, D637-D640.	14.5	610
10	Quantitative Analysis of Fission Yeast Transcriptomes and Proteomes in Proliferating and Quiescent Cells. Cell, 2012, 151, 671-683.	28.9	513
11	Methylation of Histone H4 Lysine 20 Controls Recruitment of Crb2 to Sites of DNA Damage. Cell, 2004, 119, 603-614.	28.9	512
12	Periodic gene expression program of the fission yeast cell cycle. Nature Genetics, 2004, 36, 809-817.	21.4	472
13	Transient structural variations have strong effects on quantitative traits and reproductive isolation in fission yeast. Nature Communications, 2017, 8, 14061.	12.8	472
14	Gene Ontology Annotations and Resources. Nucleic Acids Research, 2012, 41, D530-D535.	14.5	456
15	The transcriptional program of meiosis and sporulation in fission yeast. Nature Genetics, 2002, 32, 143-147.	21.4	451
16	RNA-seq: from technology to biology. Cellular and Molecular Life Sciences, 2010, 67, 569-579.	5.4	423
17	Rapidly regulated genes are intron poor. Trends in Genetics, 2008, 24, 375-378.	6.7	340
18	Arginine methylation at histone H3R2 controls deposition of H3K4 trimethylation. Nature, 2007, 449, 928-932.	27.8	322

#	Article	IF	Citations
19	Role of Polo Kinase and Mid1p in Determining the Site of Cell Division in Fission Yeast. Journal of Cell Biology, 1998, 143, 1603-1616.	5.2	301
20	PomBase: a comprehensive online resource for fission yeast. Nucleic Acids Research, 2012, 40, D695-D699.	14.5	288
21	Post-transcriptional control of gene expression: a genome-wide perspective. Trends in Biochemical Sciences, 2005, 30, 506-514.	7.5	247
22	Proportionality: A Valid Alternative to Correlation for Relative Data. PLoS Computational Biology, 2015, 11, e1004075.	3.2	232
23	Pom1p, a fission yeast protein kinase that provides positional information for both polarized growth andÂcytokinesis. Genes and Development, 1998, 12, 1356-1370.	5.9	232
24	Cell-Cycle Control of Gene Expression in Budding and Fission Yeast. Annual Review of Genetics, 2005, 39, 69-94.	7.6	199
25	Unusual nuclear structures in meiotic prophase of fission yeast: a cytological analysis.. Journal of Cell Biology, 1993, 121, 241-256.	5.2	197
26	The Gene Ontology: enhancements for 2011. Nucleic Acids Research, 2012, 40, D559-D564.	14.5	191
27	Whole-genome microarrays of fission yeast: characteristics, accuracy, reproducibility, and processing of array data. BMC Genomics, 2003, 4, 27.	2.8	190
28	Genome-wide characterization of fission yeast DNA replication origins. EMBO Journal, 2006, 25, 5171-5179.	7.8	190
29	Coordinating genome expression with cell size. Trends in Genetics, 2012, 28, 560-565.	6.7	188
30	The rec8 gene of Schizosaccharomyces pombe is involved in linear element formation, chromosome pairing and sister-chromatid cohesion during meiosis.. Genetics, 1995, 141, 61-73.	2.9	188
31	A Network of Multiple Regulatory Layers Shapes Gene Expression in Fission Yeast. Molecular Cell, 2007, 26, 145-155.	9.7	184
32	Multiple Pathways Differentially Regulate Global Oxidative Stress Responses in Fission Yeast. Molecular Biology of the Cell, 2008, 19, 308-317.	2.1	184
33	The genomic and phenotypic diversity of Schizosaccharomyces pombe. Nature Genetics, 2015, 47, 235-241.	21.4	174
34	Dynamics of chromosome organization and pairing during meiotic prophase in fission yeast.. Journal of Cell Biology, 1994, 127, 273-285.	5.2	160
35	PomBase 2018: user-driven reimplementation of the fission yeast database provides rapid and intuitive access to diverse, interconnected information. Nucleic Acids Research, 2019, 47, D821-D827.	14.5	157
36	Roles of a Fimbrin and an Î±-Actinin-like Protein in Fission Yeast Cell Polarization and Cytokinesis. Molecular Biology of the Cell, 2001, 12, 1061-1077.	2.1	149

#	Article	IF	Citations
37	Regulation of transcriptome, translation, and proteome in response to environmental stress in fission yeast. Genome Biology, 2012, 13, R25.	9.6	149
38	A histone H3K36 chromatin switch coordinates DNA double-strand break repair pathway choice. Nature Communications, 2014, 5, 4091.	12.8	134
39	Global Effects on Gene Expression in Fission Yeast by Silencing and RNA Interference Machineries. Molecular and Cellular Biology, 2005, 25, 590-601.	2.3	132
40	A Coordinated Global Control over Cellular Transcription. Current Biology, 2010, 20, 2010-2015.	3.9	129
41	Global roles of Ste11p, cell type, and pheromone in the control of gene expression during early sexual differentiation in fission yeast. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 15517-15522.	7.1	122
42	<scp>TORC</scp>1 signaling inhibition by rapamycin and caffeine affect lifespan, global gene expression, and cell proliferation of fission yeast. Aging Cell, 2013, 12, 563-573.	6.7	120
43	The African Swine Fever Virus Transcriptome. Journal of Virology, 2020, 94, .	3.4	118
44	Next-generation sequencing: applications beyond genomes. Biochemical Society Transactions, 2008, 36, 1091-1096.	3.4	111
45	Exploring long non-coding RNAs through sequencing. Seminars in Cell and Developmental Biology, 2012, 23, 200-205.	5.0	108
46	Transcriptional regulatory network for sexual differentiation in fission yeast. Genome Biology, 2007, 8, R217.	9.6	104
47	Synchronized meiosis and recombination in fission yeast: observations with pat1-114 diploid cells. Current Genetics, 1991, 19, 445-451.	1.7	102
48	The Nuclear Poly(A)-Binding Protein Interacts with the Exosome to Promote Synthesis of Noncoding Small Nucleolar RNAs. Molecular Cell, 2010, 37, 34-45.	9.7	99
49	Fission yeast SWI/SNF and RSC complexes show compositional and functional differences from budding yeast. Nature Structural and Molecular Biology, 2008, 15, 873-880.	8.2	97
50	Key Function for the CCAAT-Binding Factor Php4 To Regulate Gene Expression in Response to Iron Deficiency in Fission Yeast. Eukaryotic Cell, 2008, 7, 493-508.	3.4	95
51	PomBase 2015: updates to the fission yeast database. Nucleic Acids Research, 2015, 43, D656-D661.	14.5	95
52	A Pre-mRNA Degradation Pathway that Selectively Targets Intron-Containing Genes Requires the Nuclear Poly(A)-Binding Protein. Molecular Cell, 2011, 44, 108-119.	9.7	93
53	Spt6 Regulates Intragenic and Antisense Transcription, Nucleosome Positioning, and Histone Modifications Genome-Wide in Fission Yeast. Molecular and Cellular Biology, 2013, 33, 4779-4792.	2.3	93
54	A simple method for directional transcriptome sequencing using Illumina technology. Nucleic Acids Research, 2009, 37, e148-e148.	14.5	88

#	Article	IF	Citations
55	The RNA exosome promotes transcription termination of backtracked RNA polymerase II. Nature Structural and Molecular Biology, 2014, 21, 919-926.	8.2	86
56	Global Role for Polyadenylation-Assisted Nuclear RNA Degradation in Posttranscriptional Gene Silencing. Molecular and Cellular Biology, 2008, 28, 656-665.	2.3	85
57	Homologous recombination in fission yeast: Absence of crossover interference and synaptonemal complex. Experientia, 1994, 50, 295-306.	1.2	84
58	Fission yeast Pom1p kinase activity is cell cycle regulated and essential for cellular symmetry during growth and division. EMBO Journal, 2001, 20, 1064-1073.	7.8	84
59	The S. pombe SAGA complex controls the switch from proliferation to sexual differentiation through the opposing roles of its subunits Gcn5 and Spt8. Genes and Development, 2008, 22, 3184-3195.	5.9	81
60	Lithium suppresses AÃŽÂ² pathology by inhibiting translation in an adult Drosophila model of Alzheimer's disease. Frontiers in Aging Neuroscience, 2014, 6, 190.	3.4	81
61	Selected Schizosaccharomyces pombe Strains Have Characteristics That Are Beneficial for Winemaking. PLoS ONE, 2016, 11, e0151102.	2.5	81
62	Hidden in plain sight: what remains to be discovered in the eukaryotic proteome?. Open Biology, 2019, 9, 180241.	3.6	80
63	CENP-B preserves genome integrity at replication forks paused by retrotransposon LTR. Nature, 2011, 469, 112-115.	27.8	79
64	An acetylated form of histone H2A.Z regulates chromosome architecture in Schizosaccharomyces pombe. Nature Structural and Molecular Biology, 2009, 16, 1286-1293.	8.2	77
65	Negative Regulation of Meiotic Gene Expression by the Nuclear Poly(a)-binding Protein in Fission Yeast*. Journal of Biological Chemistry, 2010, 285, 27859-27868.	3.4	72
66	Defining transcribed regions using RNA-seq. Nature Protocols, 2010, 5, 255-266.	12.0	70
67	Microtubule-driven nuclear movements and linear elements as meiosis-specific characteristics of the fission yeasts Schizosaccharomyces versatilis and Schizosaccharomyces pombe. Chromosoma, 1995, 104, 203-214.	2.2	68
68	M26 recombinational hotspot and physical conversion tract analysis in the ade6 gene of Schizosaccharomyces pombe.. Genetics, 1994, 136, 41-51.	2.9	68
69	The Srk1 Protein Kinase Is a Target for the Sty1 Stress-activated MAPK in Fission Yeast. Journal of Biological Chemistry, 2002, 277, 33411-33421.	3.4	67
70	Upf1, an RNA Helicase Required for Nonsense-Mediated mRNA Decay, Modulates the Transcriptional Response to Oxidative Stress in Fission Yeast. Molecular and Cellular Biology, 2006, 26, 6347-6356.	2.3	65
71	Histone H3 Lysine 14 Acetylation Is Required for Activation of a DNA Damage Checkpoint in Fission Yeast. Journal of Biological Chemistry, 2012, 287, 4386-4393.	3.4	65
72	Natural genetic variation impacts expression levels of coding, nonâ€coding, and antisense transcripts in fission yeast. Molecular Systems Biology, 2014, 10, 764.	7.2	65

#	Article	IF	Citations
73	AnGeLi: A Tool for the Analysis of Gene Lists from Fission Yeast. Frontiers in Genetics, 2015, 6, 330.	2.3	65
74	RNA-binding protein Csx1 mediates global control of gene expression in response to oxidative stress. EMBO Journal, 2003, 22, 6256-6266.	7.8	64
75	LaSSO, a strategy for genome-wide mapping of intronic lariats and branch points using RNA-seq. Genome Research, 2014, 24, 1169-1179.	5.5	64
76	Tra1 has specific regulatory roles, rather than global functions, within the SAGA co-activator complex. EMBO Journal, 2011, 30, 2843-2852.	7.8	63
77	Global Gene Expression Responses of Fission Yeast to Ionizing Radiation. Molecular Biology of the Cell, 2004, 15, 851-860.	2.1	62
78	The more the merrier: comparative analysis of microarray studies on cell cycle-regulated genes in fission yeast. Yeast, 2006, 23, 261-277.	1.7	61
79	Fission stories: using PomBase to understand Schizosaccharomyces pombe biology. Genetics, 2022, 220, .	2.9	60
80	SCFPof1-ubiquitin and its target Zip1 transcription factor mediate cadmium response in fission yeast. EMBO Journal, 2005, 24, 599-610.	7.8	58
81	TOR Complex 2 Controls Gene Silencing, Telomere Length Maintenance, and Survival under DNA-Damaging Conditions. Molecular and Cellular Biology, 2009, 29, 4584-4594.	2.3	55
82	In silico characterization and prediction of global proteinâ€“mRNA interactions in yeast. Nucleic Acids Research, 2011, 39, 5826-5836.	14.5	55
83	Elimination of a specific histone H3K14 acetyltransferase complex bypasses the RNAi pathway to regulate pericentric heterochromatin functions. Genes and Development, 2011, 25, 214-219.	5.9	55
84	Systematic screen for mutants resistant to TORC1 inhibition in fission yeast reveals genes involved in cellular ageing and growth. Biology Open, 2014, 3, 161-171.	1.2	55
85	urg1: A Uracil-Regulatable Promoter System for Fission Yeast with Short Induction and Repression Times. PLoS ONE, 2008, 3, e1428.	2.5	55
86	Global transcriptional responses of fission and budding yeast to changes in copper and iron levels: a comparative study. Genome Biology, 2007, 8, R73.	9.6	54
87	The Fission Yeast HIRA Histone Chaperone Is Required for Promoter Silencing and the Suppression of Cryptic Antisense Transcripts. Molecular and Cellular Biology, 2009, 29, 5158-5167.	2.3	54
88	Impairment of the TFIIH-associated CDK-activating Kinase Selectively Affects Cell Cycle-regulated Gene Expression in Fission Yeast. Molecular Biology of the Cell, 2005, 16, 2734-2745.	2.1	53
89	FYPO: the fission yeast phenotype ontology. Bioinformatics, 2013, 29, 1671-1678.	4.1	53
90	Individual letters of the RNA polymerase II CTD code govern distinct gene expression programs in fission yeast. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 4185-4190.	7.1	53

#	Article	IF	Citations
91	Single-cell imaging and RNA sequencing reveal patterns of gene expression heterogeneity during fission yeast growth and adaptation. Nature Microbiology, 2019, 4, 480-491.	13.3	51
92	Expression of a RecQ Helicase Homolog Affects Progression through Crisis in Fission Yeast Lacking Telomerase. Journal of Biological Chemistry, 2005, 280, 5249-5257.	3.4	48
93	General amino acid control in fission yeast is regulated by a nonconserved transcription factor, with functions analogous to Gcn4/Atf4. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E1829-E1838.	7.1	48
94	Chapter 5 Translational Control of Gene Expression. International Review of Cell and Molecular Biology, 2008, 271, 199-251.	3.2	46
95	Failed gene conversion leads to extensive end processing and chromosomal rearrangements in fission yeast. EMBO Journal, 2009, 28, 3400-3412.	7.8	46
96	The Nrd1-like protein Seb1 coordinates cotranscriptional 3â€² end processing and polyadenylation site selection. Genes and Development, 2016, 30, 1558-1572.	5.9	46
97	Long noncoding RNA repertoire and targeting by nuclear exosome, cytoplasmic exonuclease, and RNAi in fission yeast. Rna, 2018, 24, 1195-1213.	3.5	45
98	YOGY: a web-based, integrated database to retrieve protein orthologs and associated Gene Ontology terms. Nucleic Acids Research, 2006, 34, W330-W334.	14.5	44
99	Functional and regulatory profiling of energy metabolism in fission yeast. Genome Biology, 2016, 17, 240.	8.8	44
100	A Transcriptional Pathway for Cell Separation in Fission Yeast. Cell Cycle, 2005, 4, 39-41.	2.6	41
101	Autoregulation of Ribosome Biosynthesis by a Translational Response in Fission Yeast. Molecular and Cellular Biology, 2006, 26, 1731-1742.	2.3	41
102	Role of Ccr4-Not complex in heterochromatin formation at meiotic genes and subtelomeres in fission yeast. Epigenetics and Chromatin, 2015, 8, 28.	3.9	41
103	Saccharomyces cerevisiae cells lacking the homologous pairing protein p175 SEP1 arrest at pachytene during meiotic prophase. Chromosoma, 1994, 103, 129-141.	2.2	39
104	Int6/eIF3e Promotes General Translation and Atf1 Abundance to Modulate Sty1 MAPK-dependent Stress Response in Fission Yeast. Journal of Biological Chemistry, 2008, 283, 22063-22075.	3.4	39
105	The Fission Yeast Homeodomain Protein Yox1p Binds to MBF and Confines MBF-Dependent Cell-Cycle Transcription to G1-S via Negative Feedback. PLoS Genetics, 2009, 5, e1000626.	3.5	39
106	Differential patterns of intronic and exonic DNA regions with respect to RNA polymerase II occupancy, nucleosome density and H3K36me3 marking in fission yeast. Genome Biology, 2011, 12, R82.	9.6	39
107	Fission Yeast MAP Kinase Sty1 Is Recruited to Stress-induced Genes. Journal of Biological Chemistry, 2008, 283, 9945-9956.	3.4	38
108	Role of Septins in the Orientation of Forespore Membrane Extension during Sporulation in Fission Yeast. Molecular and Cellular Biology, 2010, 30, 2057-2074.	2.3	38

#	Article	IF	Citations
109	Parallel Profiling of Fission Yeast Deletion Mutants for Proliferation and for Lifespan During Long-Term Quiescence. G3: Genes, Genomes, Genetics, 2015, 5, 145-155.	1.8	38
110	Increasing extracellular H2O2 produces a bi-phasic response in intracellular H2O2, with peroxiredoxin hyperoxidation only triggered once the cellular H2O2-buffering capacity is overwhelmed. Free Radical Biology and Medicine, 2016, 95, 333-348.	2.9	38
111	Spt6 Is Required for Heterochromatic Silencing in the Fission Yeast Schizosaccharomyces pombe. Molecular and Cellular Biology, 2011, 31, 4193-4204.	2.3	37
112	Genome-wide analysis of poly(A) site selection in Schizosaccharomyces pombe. Rna, 2013, 19, 1617-1631.	3.5	37
113	A Novel Histone Deacetylase Complex in the Control of Transcription and Genome Stability. Molecular and Cellular Biology, 2014, 34, 3500-3514.	2.3	37
114	Widespread exon skipping triggers degradation by nuclear RNA surveillance in fission yeast. Genome Research, 2015, 25, 884-896.	5.5	37
115	Pyphe, a python toolbox for assessing microbial growth and cell viability in high-throughput colony screens. ELife, 2020, 9, .	6.0	37
116	Correlations Between Gene Expression and Gene Conservation in Fission Yeast. Genome Research, 2003, 13, 2686-2690.	5.5	36
117	Response ofSchizosaccharomyces pombeto Zinc Deficiency. Eukaryotic Cell, 2008, 7, 454-464.	3.4	36
118	Meta-analysis of genome regulation and expression variability across hundreds of environmental and genetic perturbations in fission yeast. Molecular BioSystems, 2010, 6, 543-552.	2.9	36
119	Mfc1 Is a Novel Forespore Membrane Copper Transporter in Meiotic and Sporulating Cells. Journal of Biological Chemistry, 2011, 286, 34356-34372.	3.4	36
120	Global expression changes resulting from loss of telomeric DNA in fission yeast. Genome Biology, 2004, 6, R1.	9.6	35
121	Vgl1, a multi-KH domain protein, is a novel component of the fission yeast stress granules required for cell survival under thermal stress. Nucleic Acids Research, 2010, 38, 6555-6566.	14.5	34
122	The Role of Topoisomerase II in Meiotic Chromosome Condensation and Segregation inSchizosaccharomyces pombe. Molecular Biology of the Cell, 1998, 9, 2739-2750.	2.1	33
123	The GATA Transcription Factor Gaf1 Represses tRNAs, Inhibits Growth, and Extends Chronological Lifespan Downstream of Fission Yeast TORC1. Cell Reports, 2020, 30, 3240-3249.e4.	6.4	33
124	De Novo and Bi-allelic Pathogenic Variants in NARS1 Cause Neurodevelopmental Delay Due to Toxic Gain-of-Function and Partial Loss-of-Function Effects. American Journal of Human Genetics, 2020, 107, 311-324.	6.2	32
125	Regulation of spindle pole body assembly and cytokinesis by the centrin-binding protein Sfi1 in fission yeast. Molecular Biology of the Cell, 2014, 25, 2735-2749.	2.1	31
126	Predicting the Fission Yeast Protein Interaction Network. G3: Genes, Genomes, Genetics, 2012, 2, 453-467.	1.8	29

#	Article	IF	Citations
127	H3K9me-Independent Gene Silencing in Fission Yeast Heterochromatin by Clr5 and Histone Deacetylases. PLoS Genetics, 2011, 7, e1001268.	3.5	28
128	Extensive Mass Spectrometry-based Analysis of the Fission Yeast Proteome. Molecular and Cellular Proteomics, 2013, 12, 1741-1751.	3.8	28
129	Mitochondrial respiration is required to provide amino acids during fermentative proliferation of fission yeast. EMBO Reports, 2020, 21, e50845.	4.5	28
130	Cyclin-Dependent Kinase Inhibits Reinitiation of a Normal S-Phase Program during G₂ in Fission Yeast. Molecular and Cellular Biology, 2009, 29, 4025-4032.	2.3	27
131	The DNA damage checkpoint pathway promotes extensive resection and nucleotide synthesis to facilitate homologous recombination repair and genome stability in fission yeast. Nucleic Acids Research, 2014, 42, 5644-5656.	14.5	27
132	A CRISPR/Cas9-based method and primer design tool for seamless genome editing in fission yeast. Wellcome Open Research, 2016, 1, 19.	1.8	27
133	Pyruvate kinase variant of fission yeast tunes carbon metabolism, cell regulation, growth and stress resistance. Molecular Systems Biology, 2020, 16, e9270.	7.2	27
134	Sites of strong Rec12/Spo11 binding in the fission yeast genome are associated with meiotic recombination and with centromeres. Chromosoma, 2008, 117, 431-444.	2.2	26
135	Contributions of transcription and mRNA decay to gene expression dynamics of fission yeast in response to oxidative stress. RNA Biology, 2014, 11, 702-714.	3.1	26
136	Genome-Wide Dynamics of SAPHIRE, an Essential Complex for Gene Activation and Chromatin Boundaries. Molecular and Cellular Biology, 2007, 27, 4058-4069.	2.3	24
137	Identifying genes required for respiratory growth of fission yeast. Wellcome Open Research, 2016, 1, 12.	1.8	24
138	Simplified primer design for PCR-based gene targeting and microarray primer database: two web tools for fission yeast. Yeast, 2006, 23, 921-928.	1.7	23
139	Longevity is determined by ETS transcription factors in multiple tissues and diverse species. PLoS Genetics, 2019, 15, e1008212.	3.5	23
140	C. elegans feed yolk to their young in a form of primitive lactation. Nature Communications, 2021, 12, 5801.	12.8	23
141	The fission yeast Rpb4 subunit of RNA polymerase II plays a specialized role in cell separation. Molecular Genetics and Genomics, 2006, 276, 545-554.	2.1	22
142	The Roles of Stress-Activated Sty1 and Gcn2 Kinases and of the Protooncoprotein Homologue Int6/eIF3e in Responses to Endogenous Oxidative Stress during Histidine Starvation. Journal of Molecular Biology, 2010, 404, 183-201.	4.2	22
143	Abo1, a conserved bromodomain <scp>AAA</scp> â€•<scp>ATP</scp> ase, maintains global nucleosome occupancy and organisation. EMBO Reports, 2016, 17, 79-93.	4.5	22
144	Global gene expression of fission yeast in response to cisplatin. Cellular and Molecular Life Sciences, 2004, 61, 2253-63.	5.4	21

#	Article	IF	Citations
145	Cip1 and Cip2 Are Novel RNA-Recognition-Motif Proteins That Counteract Csx1 Function during Oxidative Stress. Molecular Biology of the Cell, 2006, 17, 1176-1183.	2.1	21
146	Altered nuclear tRNA metabolism in La-deletedSchizosaccharomyces pombeis accompanied by a nutritional stress response involving Atf1p and Pcr1p that is suppressible by Xpo-t/Los1p. Molecular Biology of the Cell, 2012, 23, 480-491.	2.1	21
147	Stress induces remodelling of yeast interaction and co-expression networks. Molecular BioSystems, 2013, 9, 1697.	2.9	21
148	Myb-domain protein Teb1 controls histone levels and centromere assembly in fission yeast. EMBO Journal, 2013, 32, 450-460.	7.8	21
149	Identification of New Players in Cell Division, DNA Damage Response, and Morphogenesis Through Construction of Schizosaccharomyces pombe Deletion Strains. G3: Genes, Genomes, Genetics, 2015, 5, 361-370.	1.8	20
150	Activation of AP-1-Dependent Transcription by a Truncated Translation Initiation Factor. Eukaryotic Cell, 2005, 4, 1840-1850.	3.4	19
151	Barcode sequencing and a high-throughput assay for chronological lifespan uncover ageing-associated genes in fission yeast. Microbial Cell, 2021, 8, 146-160.	3.2	19
152	Fission Yeast CSL Transcription Factors: Mapping Their Target Genes and Biological Roles. PLoS ONE, 2015, 10, e0137820.	2.5	19
153	Genomic expression patterns in cell separation mutants of Schizosaccharomyces pombe defective in the genes sep10 + and sep15 + coding for the Mediator subunits Med31 and Med8. Molecular Genetics and Genomics, 2008, 279, 225-238.	2.1	18
154	A CRISPR/Cas9-based method and primer design tool for seamless genome editing in fission yeast. Wellcome Open Research, 0, 1, 19.	1.8	18
155	Transcriptional and Cellular Responses to Defective Mitochondrial Proteolysis in Fission Yeast. Journal of Molecular Biology, 2011, 408, 222-237.	4.2	17
156	Cuf2 Is a Novel Meiosis-Specific Regulatory Factor of Meiosis Maturation. PLoS ONE, 2012, 7, e36338.	2.5	16
157	Php4 Is a Key Player for Iron Economy in Meiotic and Sporulating Cells. G3: Genes, Genomes, Genetics, 2016, 6, 3077-3095.	1.8	16
158	Cell-based screens and phenomics with fission yeast. Critical Reviews in Biochemistry and Molecular Biology, 2016, 51, 86-95.	5.2	16
159	Preparation of Total RNA from Fission Yeast. Cold Spring Harbor Protocols, 2017, 2017, pdb.prot091629.	0.3	16
160	An essential role for dNTP homeostasis following CDK-induced replication stress. Journal of Cell Science, 2019, 132, .	2.0	16
161	Cdk9 and H2Bub1 signal to Clr6-CII/Rpd3S to suppress aberrant antisense transcription. Nucleic Acids Research, 2020, 48, 7154-7168.	14.5	16
162	The copper transport-associated protein Ctr4 can form prion-like epigenetic determinants in Schizosaccharomyces pombe. Microbial Cell, 2017, 4, 16-28.	3.2	16

#	Article	IF	Citations
163	Improved tools for efficient mapping of fission yeast genes: identification of microtubule nucleation modifier mod22â€1 as an allele of chromatinâ€remodelling factor gene swr1. Yeast, 2008, 25, 913-925.	1.7	15
164	Gene Function Prediction from Functional Association Networks Using Kernel Partial Least Squares Regression. PLoS ONE, 2015, 10, e0134668.	2.5	15
165	Genetic interactions and functional analyses of the fission yeast gsk3 and amk2 single and double mutants defective in TORC1-dependent processes. Scientific Reports, 2017, 7, 44257.	3.3	14
166	RNA metabolism is the primary target of formamide in vivo. Scientific Reports, 2017, 7, 15895.	3.3	14
167	A Multidisciplinary, Open Access Platform for Research on Biomolecules. Biomolecules, 2011, 1, 1-2.	4.0	13
168	CSL protein regulates transcription of genes required to prevent catastrophic mitosis in fission yeast. Cell Cycle, 2016, 15, 3082-3093.	2.6	13
169	A central role for TOR signalling in a yeast model for juvenile CLN3 disease. Microbial Cell, 2015, 2, 466-480.	3.2	13
170	Structural and Functional Characterization of the N Terminus of Schizosaccharomyces pombe Cwf10. Eukaryotic Cell, 2013, 12, 1472-1489.	3.4	12
171	Fitness Landscape of the Fission Yeast Genome. Molecular Biology and Evolution, 2019, 36, 1612-1623.	8.9	12
172	Heterologous modules for efficient and versatile PCR-based gene targeting in Schizosaccharomyces pombe. , 1998, 14, 943.		11
173	Website Review: How to Get the Best From Fission Yeast Genome Data. Comparative and Functional Genomics, 2002, 3, 282-288.	2.0	10
174	Spotsizer: High-throughput quantitative analysis of microbial growth. BioTechniques, 2016, 61, 191-201.	1.8	10
175	Microtubule-driven nuclear movements and linear elements as meiosis-specific characteristics of the fission yeasts Schizosaccharomyces versatilis and Schizosaccharomyces pombe. Chromosoma, 1995, 104, 203-214.	2.2	10
176	Inhibition of TORC1 signaling and increased lifespan: gained in translation?. Aging, 2013, 5, 335-336.	3.1	10
177	Specific replication origins promote DNA amplification in fission yeast. Journal of Cell Science, 2010, 123, 3047-3051.	2.0	9
178	Amino Acids Whose Intracellular Levels Change Most During Aging Alter Chronological Life Span of Fission Yeast. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2021, 76, 205-210.	3.6	9
179	Global network analysis in Schizosaccharomyces pombe reveals three distinct consequences of the common 1-kb deletion causing juvenile CLN3 disease. Scientific Reports, 2021, 11, 6332.	3.3	9
180	A logical circuit for the regulation of fission yeast growth modes. Journal of Theoretical Biology, 2005, 237, 210-218.	1.7	8

#	Article	IF	Citations
181	Uncovering Natural Longevity Alleles from Intercrossed Pools of Aging Fission Yeast Cells. Genetics, 2018, 210, 733-744.	2.9	8
182	N-Termini of Fungal CSL Transcription Factors Are Disordered, Enriched in Regulatory Motifs and Inhibit DNA Binding in Fission Yeast. PLoS ONE, 2011, 6, e23650.	2.5	8
183	Navigating Public Microarray Databases. Comparative and Functional Genomics, 2004, 5, 471-479.	2.0	7
184	A novel function of the mitochondrial transcription factor Mtf1 in fission yeast; Mtf1 regulates the nuclear transcription of srk1. Nucleic Acids Research, 2011, 39, 2690-2700.	14.5	7
185	A metabolic strategy to enhance long-term survival by Phx1 through stationary phase-specific pyruvate decarboxylases in fission yeast. Aging, 2014, 6, 587-601.	3.1	7
186	Identification of nuclear genes affecting 2-Deoxyglucose resistance inSchizosaccharomyces pombe. FEMS Yeast Research, 2016, 16, fow061.	2.3	7
187	Heterologous modules for efficient and versatile PCRâ€based gene targeting in Schizosaccharomyces pombe. Yeast, 1998, 14, 943-951.	1.7	7
188	Functional profiling of long intergenic non-coding RNAs in fission yeast. ELife, 2022, 11, .	6.0	7
189	Transcriptional Activation of the General Amino Acid Permease Gene per1 by the Histone Deacetylase Clr6 Is Regulated by Oca2 Kinase. Molecular and Cellular Biology, 2010, 30, 3396-3410.	2.3	6
190	Saccharomyces cerevisiae cells lacking the homologous pairing protein p175 SEP1 arrest at pachytene during meiotic prophase. Chromosoma, 1994, 103, 129-141.	2.2	6
191	High-Throughput, High-Precision Colony Phenotyping with Pyphe. Methods in Molecular Biology, 2022, 2477, 381-397.	0.9	6
192	Topology of functional networks predicts physical binding of proteins. Bioinformatics, 2012, 28, 2137-2145.	4.1	5
193	A CRISPR/Cas9-based method and primer design tool for seamless genome editing in fission yeast. Wellcome Open Research, 0, 1, 19.	1.8	5
194	Co-Expression Network Models Suggest that Stress Increases Tolerance to Mutations. Scientific Reports, 2015, 5, 16726.	3.3	4
195	The Genome and Beyond. , 2004, , 13-25.		4
196	Ace2 receives helping hand for cell-cycle transcription. Cell Cycle, 2015, 14, 3351-3352.	2.6	2
197	Schizosaccharomyces pombe Polysome Profile Analysis and RNA Purification. Cold Spring Harbor Protocols, 2017, 2017, pdb.prot091637.	0.3	2
198	R-loops and regulatory changes in chronologically ageing fission yeast cells drive non-random patterns of genome rearrangements. PLoS Genetics, 2021, 17, e1009784.	3.5	2

#	Article	IF	Citations
199	Global approaches to study gene regulation. Methods, 2009, 48, 217.	3.8	1
200	The Nuclear Poly(A)-Binding Protein Interacts with the Exosome to Promote Synthesis of Noncoding Small Nucleolar RNAs. Molecular Cell, 2010, 37, 447.	9.7	1
201	Genome regulation and evolution analysed by next-generation sequencing. Seminars in Cell and Developmental Biology, 2012, 23, 191.	5.0	0
202	Gene dosis and the timing of mitosis. Cell Cycle, 2016, 15, 3022-3023.	2.6	0
203	Cell Cycle-regulated Gene Expression. , 2013, , 360-360.		0
204	RNA-seq. , 2013, , 1877-1877.		0
205	Transcriptional Regulatory Network. , 2013, , 2258-2258.		0
206	DNA Microarrays. , 2013, , 609-610.		0
207	Cell Cycle, Synchronization. , 2013, , 359-360.		0
208	Transcriptome. , 2013, , 2259-2259.		0
209	Cell Cycle Analysis, Expression Profiling. , 2013, , 231-233.		0
210	Recombination and biased segregation of mitochondrial genomes during crossing and meiosis of different strains. MicroPublication Biology, 2021, 2021, .	0.1	0