Katsuhiko Shirahige

List of Publications by Year in descending order

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KATSUHIKO SHIDAHICE

#	Article	IF	CITATIONS
1	Cohesin mediates transcriptional insulation by CCCTC-binding factor. Nature, 2008, 451, 796-801.	13.7	1,050
2	S-phase checkpoint proteins Tof1 and Mrc1 form a stable replication-pausing complex. Nature, 2003, 424, 1078-1083.	13.7	614
3	Cohesin relocation from sites of chromosomal loading to places of convergent transcription. Nature, 2004, 430, 573-578.	13.7	544
4	HDAC8 mutations in Cornelia de Lange syndrome affect the cohesin acetylation cycle. Nature, 2012, 489, 313-317.	13.7	488
5	Postreplicative Recruitment of Cohesin to Double-Strand Breaks Is Required for DNA Repair. Molecular Cell, 2004, 16, 1003-1015.	4.5	473
6	Protein phosphatase 2A protects centromeric sister chromatid cohesion during meiosis I. Nature, 2006, 441, 53-61.	13.7	419
7	The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. Nature Genetics, 2009, 41, 553-562.	9.4	408
8	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. Cell, 2016, 167, 1145-1149.	13.5	404
9	Regulation of DNA-replication origins during cell-cycle progression. Nature, 1998, 395, 618-621.	13.7	394
10	Recurrent mutations in multiple components of the cohesin complex in myeloid neoplasms. Nature Genetics, 2013, 45, 1232-1237.	9.4	334
11	Spo11-Accessory Proteins Link Double-Strand Break Sites to the Chromosome Axis in Early Meiotic Recombination. Cell, 2011, 146, 372-383.	13.5	330
12	Sororin Mediates Sister Chromatid Cohesion by Antagonizing Wapl. Cell, 2010, 143, 737-749.	13.5	325
13	Identification of <i>cis</i> -acting sites for condensin loading onto budding yeast chromosomes. Genes and Development, 2008, 22, 2215-2227.	2.7	302
14	Postreplicative Formation of Cohesion Is Required for Repair and Induced by a Single DNA Break. Science, 2007, 317, 242-245.	6.0	276
15	Evidence that Loading of Cohesin Onto Chromosomes Involves Opening of Its SMC Hinge. Cell, 2006, 127, 523-537.	13.5	271
16	Establishment of Sister Chromatid Cohesion at the S. cerevisiae Replication Fork. Molecular Cell, 2006, 23, 787-799.	4.5	268
17	PRDM14 Ensures Naive Pluripotency through Dual Regulation of Signaling and Epigenetic Pathways in Mouse Embryonic Stem Cells. Cell Stem Cell, 2013, 12, 368-382.	5.2	266
18	Origin Association of Sld3, Sld7, and Cdc45 Proteins Is a Key Step for Determination of Origin-Firing Timing. Current Biology, 2011, 21, 2055-2063.	1.8	232

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19	The cyclic gene <i>Hes1</i> contributes to diverse differentiation responses of embryonic stem cells. Genes and Development, 2009, 23, 1870-1875.	2.7	226
20	Rif1 is a global regulator of timing of replication origin firing in fission yeast. Genes and Development, 2012, 26, 137-150.	2.7	218
21	A Mesodermal Factor, T, Specifies Mouse Germ Cell Fate by Directly Activating Germline Determinants. Developmental Cell, 2013, 27, 516-529.	3.1	206
22	The Replication Checkpoint Protects Fork Stability by Releasing Transcribed Genes from Nuclear Pores. Cell, 2011, 146, 233-246.	13.5	204
23	Budding Yeast Wpl1(Rad61)-Pds5 Complex Counteracts Sister Chromatid Cohesion-Establishing Reaction. Current Biology, 2009, 19, 492-497.	1.8	200
24	Transcriptional Dysregulation in NIPBL and Cohesin Mutant Human Cells. PLoS Biology, 2009, 7, e1000119.	2.6	199
25	Chromosomal Association of the Smc5/6 Complex Reveals that It Functions in Differently Regulated Pathways. Molecular Cell, 2006, 22, 755-767.	4.5	197
26	Genome-wide function of THO/TREX in active genes prevents R-loop-dependent replication obstacles. EMBO Journal, 2011, 30, 3106-3119.	3.5	191
27	The maintenance of chromosome structure: positioning and functioning of SMC complexes. Nature Reviews Molecular Cell Biology, 2014, 15, 601-614.	16.1	191
28	Architectural roles of multiple chromatin insulators at the human apolipoprotein gene cluster. EMBO Journal, 2009, 28, 1234-1245.	3.5	185
29	Mrc1 and DNA Polymerase É> Function Together in Linking DNA Replication and the S Phase Checkpoint. Molecular Cell, 2008, 32, 106-117.	4.5	183
30	ATP Hydrolysis Is Required for Relocating Cohesin from Sites Occupied by Its Scc2/4 Loading Complex. Current Biology, 2011, 21, 12-24.	1.8	173
31	Monopolar Attachment of Sister Kinetochores at Meiosis I Requires Casein Kinase 1. Cell, 2006, 126, 1049-1064.	13.5	168
32	Quantitative Dynamics of Chromatin Remodeling during Germ Cell Specification from Mouse Embryonic Stem Cells. Cell Stem Cell, 2015, 16, 517-532.	5.2	166
33	Genome-wide localization of pre-RC sites and identification of replication origins in fission yeast. EMBO Journal, 2007, 26, 1327-1339.	3.5	163
34	Eukaryotic Replisome Components Cooperate to Process Histones During Chromosome Replication. Cell Reports, 2013, 3, 892-904.	2.9	157
35	Receptor for activated C kinase 1 stimulates nascent polypeptideâ€dependent translation arrest. EMBO Reports, 2010, 11, 956-961.	2.0	151
36	An Smc3 Acetylation Cycle Is Essential for Establishment of Sister Chromatid Cohesion. Molecular Cell, 2010, 39, 689-699.	4.5	149

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37	The transcription factor ATF7 mediates lipopolysaccharide-induced epigenetic changes in macrophages involved in innate immunological memory. Nature Immunology, 2015, 16, 1034-1043.	7.0	149
38	A wave of nascent transcription on activated human genes. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 18357-18361.	3.3	145
39	Replisome Stability at Defective DNA Replication Forks Is Independent of S Phase Checkpoint Kinases. Molecular Cell, 2012, 45, 696-704.	4.5	140
40	Kinetochores Coordinate Pericentromeric Cohesion and Early DNA Replication by Cdc7-Dbf4 Kinase Recruitment. Molecular Cell, 2013, 50, 661-674.	4.5	140
41	Rif1 binds to G quadruplexes and suppresses replication over long distances. Nature Structural and Molecular Biology, 2015, 22, 889-897.	3.6	137
42	Rapid Discovery of Highly Potent and Selective Inhibitors of Histone Deacetylase 8 Using Click Chemistry to Generate Candidate Libraries. Journal of Medicinal Chemistry, 2012, 55, 9562-9575.	2.9	135
43	Top1- and Top2-mediated topological transitions at replication forks ensure fork progression and stability and prevent DNA damage checkpoint activation. Genes and Development, 2007, 21, 1921-1936.	2.7	134
44	Replication Termination at Eukaryotic Chromosomes Is Mediated by Top2 and Occurs at Genomic Loci Containing Pausing Elements. Molecular Cell, 2010, 39, 595-605.	4.5	131
45	Histone Variants Enriched in Oocytes Enhance Reprogramming to Induced Pluripotent Stem Cells. Cell Stem Cell, 2014, 14, 217-227.	5.2	130
46	An InÂVitro Human Liver Model by iPSC-Derived Parenchymal and Non-parenchymal Cells. Stem Cell Reports, 2017, 9, 490-498.	2.3	128
47	Csm3, Tof1, and Mrc1 Form a Heterotrimeric Mediator Complex That Associates with DNA Replication Forks. Journal of Biological Chemistry, 2009, 284, 34355-34365.	1.6	123
48	The efficiency and timing of initiation of replication of multiple replicons ofSaccharomyces cerevisiaechromosome VI. Genes To Cells, 1997, 2, 655-665.	0.5	122
49	A chromatin integration labelling method enables epigenomic profiling with lower input. Nature Cell Biology, 2019, 21, 287-296.	4.6	121
50	Loss-of-function HDAC8 mutations cause a phenotypic spectrum of Cornelia de Lange syndrome-like features, ocular hypertelorism, large fontanelle and X-linked inheritance. Human Molecular Genetics, 2014, 23, 2888-2900.	1.4	120
51	The dynamics of genome replication using deep sequencing. Nucleic Acids Research, 2014, 42, e3-e3.	6.5	113
52	Rec8 Guides Canonical Spo11 Distribution along Yeast Meiotic Chromosomes. Molecular Biology of the Cell, 2009, 20, 3064-3076.	0.9	109
53	Germline gain-of-function mutations in AFF4 cause a developmental syndrome functionally linking the super elongation complex and cohesin. Nature Genetics, 2015, 47, 338-344.	9.4	109
54	Pds5 promotes and protects cohesin acetylation. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 13020-13025.	3.3	108

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55	Recent advances in ChIP-seq analysis: from quality management to whole-genome annotation. Briefings in Bioinformatics, 2017, 18, bbw023.	3.2	107
56	Amyloid Precursor Protein Is a Primary Androgen Target Gene That Promotes Prostate Cancer Growth. Cancer Research, 2009, 69, 137-142.	0.4	105
57	MYU, a Target IncRNA for Wnt/c-Myc Signaling, Mediates Induction of CDK6 to Promote Cell Cycle Progression. Cell Reports, 2016, 16, 2554-2564.	2.9	102
58	Genome-Organizing Factors Top2 and Hmo1 Prevent Chromosome Fragility at Sites of S phase Transcription. Cell, 2009, 138, 870-884.	13.5	101
59	Balance between Distinct HP1 Family Proteins Controls Heterochromatin Assembly in Fission Yeast. Molecular and Cellular Biology, 2008, 28, 6973-6988.	1.1	100
60	Replication-Coupled PCNA Unloading by the Elg1 Complex Occurs Genome-wide and Requires Okazaki Fragment Ligation. Cell Reports, 2015, 12, 774-787.	2.9	100
61	Condensin targets and reduces unwound DNA structures associated with transcription in mitotic chromosome condensation. Nature Communications, 2015, 6, 7815.	5.8	100
62	Chromosome length influences replication-induced topological stress. Nature, 2011, 471, 392-396.	13.7	99
63	The Kinetochore Proteins Pcs1 and Mde4 and Heterochromatin Are Required to Prevent Merotelic Orientation. Current Biology, 2007, 17, 1190-1200.	1.8	98
64	Endogenous DNA replication stress results in expansion of dNTP pools and a mutator phenotype. EMBO Journal, 2012, 31, 895-907.	3.5	95
65	Spo13 Facilitates Monopolin Recruitment to Kinetochores and Regulates Maintenance of Centromeric Cohesion during Yeast Meiosis. Current Biology, 2004, 14, 2183-2196.	1.8	91
66	Meiotic cohesins modulate chromosome compaction during meiotic prophase in fission yeast. Journal of Cell Biology, 2006, 174, 499-508.	2.3	91
67	Inferring the choreography of parental genomes during fertilization from ultralarge-scale whole-transcriptome analysis. Genes and Development, 2013, 27, 2736-2748.	2.7	86
68	Reciprocal Association of the Budding Yeast ATM-Related Proteins Tel1 and Mec1 with Telomeres In Vivo. Molecular Cell, 2004, 14, 515-522.	4.5	82
69	Ctf4 coordinates the progression of helicase and DNA polymerase α. Genes To Cells, 2009, 14, 807-820.	0.5	82
70	Functional annotation of chemical libraries across diverse biological processes. Nature Chemical Biology, 2017, 13, 982-993.	3.9	76
71	Esco1 Acetylates Cohesin via a Mechanism Different from That of Esco2. Current Biology, 2015, 25, 1694-1706.	1.8	74
72	A member of the YER057c/yjgf/Uk114 family links isoleucine biosynthesis and intact mitochondria maintenance inSaccharomyces cerevisiae. Genes To Cells, 2001, 6, 507-517.	0.5	72

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73	DBTMEE: a database of transcriptome in mouse early embryos. Nucleic Acids Research, 2015, 43, D771-D776.	6.5	71
74	Assembly of Regulatory Factors on rRNA and Ribosomal Protein Genes in <i>Saccharomyces cerevisiae</i> . Molecular and Cellular Biology, 2007, 27, 6686-6705.	1.1	69
75	A positively charged channel within the Smc1/Smc3 hinge required for sister chromatid cohesion. EMBO Journal, 2011, 30, 364-378.	3.5	69
76	Telomere-binding protein Taz1 controls global replication timing through its localization near late replication origins in fission yeast. Genes and Development, 2012, 26, 2050-2062.	2.7	68
77	<scp>DROMPA</scp> : easyâ€toâ€handle peak calling and visualization software for the computational analysis and validation of ChIPâ€seq data. Genes To Cells, 2013, 18, 589-601.	0.5	67
78	Condensin-Dependent rDNA Decatenation Introduces a Temporal Pattern to Chromosome Segregation. Current Biology, 2008, 18, 1084-1089.	1.8	65
79	ARCN1 Mutations Cause a Recognizable Craniofacial Syndrome Due to COPI-Mediated Transport Defects. American Journal of Human Genetics, 2016, 99, 451-459.	2.6	65
80	DNMT3A R882 mutants interact with polycomb proteins to block haematopoietic stem and leukaemic cell differentiation. Nature Communications, 2016, 7, 10924.	5.8	64
81	Genome-wide expression analysis of NAP1 in Saccharomyces cerevisiae. Biochemical and Biophysical Research Communications, 2003, 306, 5-9.	1.0	62
82	Smc5/6-mediated regulation of replication progression contributes to chromosome assembly during mitosis in human cells. Molecular Biology of the Cell, 2014, 25, 302-317.	0.9	61
83	Genomic Approach for the Understanding of Dynamic Aspect of Chromosome Behavior. Methods in Enzymology, 2006, 409, 389-410.	0.4	60
84	The Direct Binding of Mrc1, a Checkpoint Mediator, to Mcm6, a Replication Helicase, Is Essential for the Replication Checkpoint against Methyl Methanesulfonate-Induced Stress. Molecular and Cellular Biology, 2009, 29, 5008-5019.	1.1	60
85	Sensory-Neuron Subtype-Specific Transcriptional Programs Controlling Dendrite Morphogenesis: Genome-wide Analysis of Abrupt and Knot/Collier. Developmental Cell, 2013, 27, 530-544.	3.1	60
86	The Chromosomal Association of the Smc5/6 Complex Depends on Cohesion and Predicts the Level of Sister Chromatid Entanglement. PLoS Genetics, 2014, 10, e1004680.	1.5	60
87	Design, Synthesis, and Biological Activity of NCC149 Derivatives as Histone Deacetylaseâ€8â€5elective Inhibitors. ChemMedChem, 2014, 9, 657-664.	1.6	59
88	Rad51 suppresses gross chromosomal rearrangement at centromere in Schizosaccharomyces pombe. EMBO Journal, 2008, 27, 3036-3046.	3.5	58
89	Nutrient-Regulated Antisense and Intragenic RNAs Modulate a Signal Transduction Pathway in Yeast. PLoS Biology, 2008, 6, e326.	2.6	57
90	A Direct Role for Cohesin in Gene Regulation and Ecdysone Response in Drosophila Salivary Glands. Current Biology, 2010, 20, 1787-1798.	1.8	57

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91	The HSF1–PARP13–PARP1 complex facilitates DNA repair and promotes mammary tumorigenesis. Nature Communications, 2017, 8, 1638.	5.8	57
92	Tet2 and Tet3 in B cells are required to repress CD86 and prevent autoimmunity. Nature Immunology, 2020, 21, 950-961.	7.0	55
93	Cohesin Acetylation Promotes Sister Chromatid Cohesion Only in Association with the Replication Machinery. Journal of Biological Chemistry, 2012, 287, 34325-34336.	1.6	53
94	Mapping of histone-binding sites in histone replacement-completed spermatozoa. Nature Communications, 2018, 9, 3885.	5.8	53
95	Meiotic recombination-related DNA synthesis and its implications for cross-over and non-cross-over recombinant formation. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 5965-5970.	3.3	52
96	<i>ASBEL</i> –TCF3 complex is required for the tumorigenicity of colorectal cancer cells. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 12739-12744.	3.3	52
97	ATF7-Dependent Epigenetic Changes Are Required for the Intergenerational Effect of a Paternal Low-Protein Diet. Molecular Cell, 2020, 78, 445-458.e6.	4.5	52
98	Combined Cohesin–RUNX1 Deficiency Synergistically Perturbs Chromatin Looping and Causes Myelodysplastic Syndromes. Cancer Discovery, 2020, 10, 836-853.	7.7	51
99	An integrated map of p53-binding sites and histone modification in the human ENCODE regions. Genomics, 2007, 89, 178-188.	1.3	50
100	The Prereplication Complex Recruits XEco2 to Chromatin to Promote Cohesin Acetylation in Xenopus Egg Extracts. Current Biology, 2012, 22, 977-988.	1.8	50
101	The Deubiquitinating Enzyme USP7 Regulates Androgen Receptor Activity by Modulating Its Binding to Chromatin. Journal of Biological Chemistry, 2015, 290, 21713-21723.	1.6	50
102	ATF1 Modulates the Heat Shock Response by Regulating the Stress-Inducible Heat Shock Factor 1 Transcription Complex. Molecular and Cellular Biology, 2015, 35, 11-25.	1.1	50
103	Cohesin Ubiquitylation and Mobilization Facilitate Stalled Replication Fork Dynamics. Molecular Cell, 2017, 68, 758-772.e4.	4.5	50
104	BRCA2 Coordinates the Activities of Cell-Cycle Kinases to Promote Genome Stability. Cell Reports, 2014, 7, 1547-1559.	2.9	49
105	DBTSS/DBKERO for integrated analysis of transcriptional regulation. Nucleic Acids Research, 2018, 46, D229-D238.	6.5	48
106	Molecular cloning, genetic characterization and DNA sequence analysis of therecM region ofBacillus subtilis. Nucleic Acids Research, 1990, 18, 6771-6777.	6.5	46
107	During Replication Stress, Non-Smc Element 5 (Nse5) Is Required for Smc5/6 Protein Complex Functionality at Stalled Forks. Journal of Biological Chemistry, 2012, 287, 11374-11383.	1.6	46
108	Temporal and spatial regulation of eukaryotic DNA replication: From regulated initiation to genome-scale timing program. Seminars in Cell and Developmental Biology, 2014, 30, 110-120.	2.3	45

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109	MRG15-mediated tethering of PALB2 to unperturbed chromatin protects active genes from genotoxic stress. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 7671-7676.	3.3	45
110	The RSC chromatin-remodeling complex influences mitotic exit and adaptation to the spindle assembly checkpoint by controlling the Cdc14 phosphatase. Journal of Cell Biology, 2010, 191, 981-997.	2.3	44
111	Decreased cohesin in the brain leads to defective synapse development and anxiety-related behavior. Journal of Experimental Medicine, 2017, 214, 1431-1452.	4.2	44
112	Association of Human Origin Recognition Complex 1 with Chromatin DNA and Nuclease-resistant Nuclear Structures. Journal of Biological Chemistry, 2000, 275, 5904-5910.	1.6	43
113	A checkpoint control linking meiotic S phase and recombination initiation in fission yeast. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 5797-5801.	3.3	43
114	SCFDia2 regulates DNA replication forks during S-phase in budding yeast. EMBO Journal, 2009, 28, 3693-3705.	3.5	43
115	Rtt107 Is Required for Recruitment of the SMC5/6 Complex to DNA Double Strand Breaks. Journal of Biological Chemistry, 2011, 286, 26250-26257.	1.6	43
116	Displacement and re-accumulation of centromeric cohesin during transient pre-anaphase centromere splitting. Chromosoma, 2007, 116, 531-544.	1.0	42
117	Transcription-dependent cohesin repositioning rewires chromatin loops in cellular senescence. Nature Communications, 2020, 11, 6049.	5.8	42
118	Relationship between G+C content, ORF-length and mRNA concentration inSaccharomyces cerevisiae. Yeast, 2003, 20, 703-711.	0.8	40
119	Assembly of Slx4 signaling complexes behind <scp>DNA</scp> replication forks. EMBO Journal, 2015, 34, 2182-2197.	3.5	40
120	Aging of spermatogonial stem cells by Jnk-mediated glycolysis activation. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 16404-16409.	3.3	39
121	Involvement of RAD9 -Dependent Damage Checkpoint Control in Arrest of Cell Cycle, Induction of Cell Death, and Chromosome Instability Caused by Defects in Origin Recognition Complex in Saccharomyces cerevisiae. Eukaryotic Cell, 2002, 1, 200-212.	3.4	37
122	Perturbation of the Activity of Replication Origin by Meiosis-specific Transcription. Journal of Biological Chemistry, 2007, 282, 4447-4452.	1.6	37
123	Abnormality in Initiation Program of DNA Replication Is Monitored by the Highly Repetitive rRNA Gene Array on Chromosome XII in Budding Yeast. Molecular and Cellular Biology, 2007, 27, 568-578.	1.1	34
124	Comprehensive epigenome characterization reveals diverse transcriptional regulation across human vascular endothelial cells. Epigenetics and Chromatin, 2019, 12, 77.	1.8	34
125	Genome-wide analysis of murine renal distal convoluted tubular cells for the target genes of mineralocorticoid receptor. Biochemical and Biophysical Research Communications, 2014, 445, 132-137.	1.0	33
126	Genome-wide expression analysis of genes affected by amino acid sensor Ssy1p in Saccharomyces cerevisiae. Current Genetics, 2002, 41, 63-72.	0.8	31

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127	Rtt101â€Mms1â€Mms22 coordinates replicationâ€eoupled sister chromatid cohesion and nucleosome assembly. EMBO Reports, 2017, 18, 1294-1305.	2.0	31
128	Different requirements for the association of ATR–ATRIP and 9-1-1 to the stalled replication forks. Gene, 2006, 377, 88-95.	1.0	30
129	Inactivation of SMC2 shows a synergistic lethal response inMYCN-amplified neuroblastoma cells. Cell Cycle, 2014, 13, 1115-1131.	1.3	30
130	Condensin Relocalization from Centromeres to Chromosome Arms Promotes Top2 Recruitment during Anaphase. Cell Reports, 2015, 13, 2336-2344.	2.9	30
131	Temporal Regulation of ESCO2 Degradation by the MCM Complex, the CUL4-DDB1-VPRBP Complex, and the Anaphase-Promoting Complex. Current Biology, 2018, 28, 2665-2672.e5.	1.8	30
132	Budding yeast Rif1 binds to replication origins and protects <scp>DNA</scp> at blocked replication forks. EMBO Reports, 2018, 19, .	2.0	29
133	The novel lnc <scp>RNA</scp> <i> <scp>CALIC</scp> </i> upregulates <scp>AXL</scp> to promote colon cancer metastasis. EMBO Reports, 2019, 20, e47052.	2.0	29
134	Screening for candidate genes involved in tolerance to organic solvents in yeast. Applied Microbiology and Biotechnology, 2006, 71, 75-79.	1.7	28
135	Both Interaction Surfaces within Cohesin's Hinge Domain Are Essential for Its Stable Chromosomal Association. Current Biology, 2010, 20, 279-289.	1.8	28
136	Cohesin-dependent chromosome loop extrusion is limited by transcription and stalled replication forks. Science Advances, 2022, 8, .	4.7	28
137	Dimeric combinations of MafB, cFos and cJun control the apoptosis-survival balance in limb morphogenesis. Development (Cambridge), 2014, 141, 2885-2894.	1.2	27
138	Progression of cell cycle monitored by dielectric spectroscopy and flow-cytometric analysis of DNA content. Yeast, 2000, 16, 1359-1363.	0.8	26
139	Chromatin determinants of the inner-centromere rely on replication factors with functions that impart cohesion. Oncotarget, 2016, 7, 67934-67947.	0.8	26
140	Genome-Wide Target Analyses of Otx2 Homeoprotein in Postnatal Cortex. Frontiers in Neuroscience, 2017, 11, 307.	1.4	25
141	Glucose-dependent cell size is regulated by a G protein-coupled receptor system in yeastSaccharomyces cerevisiae. Genes To Cells, 2005, 10, 193-206.	0.5	24
142	Dissecting the first and the second meiotic divisions using a marker-less drug-hypersensitive fission yeast. Cell Cycle, 2014, 13, 1327-1334.	1.3	23
143	Combined Loss of JMJD1A and JMJD1B Reveals Critical Roles for H3K9 Demethylation in the Maintenance of Embryonic Stem Cells and Early Embryogenesis. Stem Cell Reports, 2018, 10, 1340-1354.	2.3	23
144	Genome-wide DNA methylation analysis in cohesin mutant human cell lines. Nucleic Acids Research, 2010, 38, 5657-5671.	6.5	22

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145	Acetylation regulates monopolar attachment at multiple levels during meiosis I in fission yeast. EMBO Reports, 2011, 12, 1189-1195.	2.0	22
146	Yeast Pho85 kinase is required for proper gene expression during the diauxic shift. Yeast, 2004, 21, 903-918.	0.8	21
147	Importance of Polî· for Damage-Induced Cohesion Reveals Differential Regulation of Cohesion Establishment at the Break Site and Genome-Wide. PLoS Genetics, 2013, 9, e1003158.	1.5	21
148	Sensitive and robust assessment of ChIP-seq read distribution using a strand-shift profile. Bioinformatics, 2018, 34, 2356-2363.	1.8	21
149	A common molecular mechanism underlies the role of Mps1 in chromosome biorientation and the spindle assembly checkpoint. EMBO Reports, 2020, 21, e50257.	2.0	21
150	A DNA Polymerase α Accessory Protein, Mcl1, Is Required for Propagation of Centromere Structures in Fission Yeast. PLoS ONE, 2008, 3, e2221.	1.1	20
151	Cell cycle dependent topological changes of chromosomal replication origins in Saccharomyces cerevisiae. Genes To Cells, 1998, 3, 737-749.	0.5	19
152	The cloning and characterization of theCDC50 gene family inSaccharomyces cerevisiae. Yeast, 2001, 18, 195-205.	0.8	19
153	Unique Gene Expression Profile of the Proliferating Xenopus Tadpole Tail Blastema Cells Deciphered by RNA-Sequencing Analysis. PLoS ONE, 2015, 10, e0111655.	1.1	18
154	Chromatin Immunoprecipitation Protocol for Mammalian Cells. Methods in Molecular Biology, 2014, 1164, 33-38.	0.4	16
155	Somatic copy number alterations have prognostic impact in patients with ovarian clear cell carcinoma. Oncology Reports, 2018, 40, 309-318.	1.2	16
156	Identification of Elg1 interaction partners and effects on post-replication chromatin re-formation. PLoS Genetics, 2018, 14, e1007783.	1.5	15
157	ChIP-on-Chip Analysis of DNA Topoisomerases. Methods in Molecular Biology, 2009, 582, 103-118.	0.4	15
158	Genome-wide localization analysis of a complete set of Tafs reveals a specific effect of the taf1 mutation on Taf2 occupancy and provides indirect evidence for different TFIID conformations at different promoters. Nucleic Acids Research, 2010, 38, 1805-1820.	6.5	14
159	Mosaic ratio quantification of isochromosome 12p in Pallister–Killian syndrome using droplet digital <scp>PCR</scp> . Molecular Genetics & Genomic Medicine, 2016, 4, 257-261.	0.6	14
160	Identification of a variant-specific phosphorylation of TH2A during spermiogenesis. Scientific Reports, 2017, 7, 46228.	1.6	14
161	Checkpoint-mediated DNA polymerase ε exonuclease activity curbing counteracts resection-driven fork collapse. Molecular Cell, 2021, 81, 2778-2792.e4.	4.5	14
162	Anatomy of the stimulative sequences flanking the ARS consensus sequence of chromosome VI in Saccharomyces cerevisiae. Gene, 1994, 150, 213-220.	1.0	12

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163	Mre11 mediates gene regulation in yeast spore development. Genes and Genetic Systems, 2007, 82, 21-33.	0.2	12
164	Sphingolipids regulate telomere clustering by affecting transcriptional levels of genes involved in telomere homeostasis. Journal of Cell Science, 2015, 128, 2454-67.	1.2	11
165	Missense Mutations in NKAP Cause a Disorder of Transcriptional Regulation Characterized by Marfanoid Habitus and Cognitive Impairment. American Journal of Human Genetics, 2019, 105, 987-995.	2.6	11
166	Exome Sequencing Identification of <i>EP300</i> Mutation in a Proband with Coloboma and Imperforate Anus: Possible Expansion of the Phenotypic Spectrum of Rubinstein-Taybi Syndrome. Molecular Syndromology, 2015, 6, 99-103.	0.3	10
167	Highly rigid H3.1/H3.2–H3K9me3 domains set a barrier for cell fate reprogramming in trophoblast stem cells. Genes and Development, 2022, 36, 84-102.	2.7	10
168	The direct cloning of the yeast genome using the gap-filling method and the complete physical mapping of Saccharomyces cerevisiae chromosome VI. Gene, 1991, 109, 81-87.	1.0	9
169	Physical Association of Saccharomyces cerevisiae Polo-like Kinase Cdc5 with Chromosomal Cohesin Facilitates DNA Damage Response. Journal of Biological Chemistry, 2016, 291, 17228-17246.	1.6	9
170	Two Components of Aversive Memory in Drosophila, Anesthesia-Sensitive and Anesthesia-Resistant Memory, Require Distinct Domains Within the Rgk1 Small GTPase. Journal of Neuroscience, 2017, 37, 5496-5510.	1.7	8
171	Genome-wide localization of pre-RC sites and identification of replication origins in fission yeast. EMBO Journal, 2007, 26, 2821-2821.	3.5	7
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