

Katsuhiko Shirahige

List of Publications by Year in descending order

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193
papers

18,423
citations

11639

70
h-index

15716

125
g-index

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all docs

207
docs citations

207
times ranked

19843
citing authors

#	ARTICLE	IF	CITATIONS
1	Highly rigid H3.1/H3.2â€“H3K9me3 domains set a barrier for cell fate reprogramming in trophoblast stem cells. <i>Genes and Development</i> , 2022, 36, 84-102.	2.7	10
2	CRISPR/Cas9 Screening for Identification of Genes Required for the Growth of Ovarian Clear Cell Carcinoma Cells. <i>Current Issues in Molecular Biology</i> , 2022, 44, 1587-1596.	1.0	0
3	Cohesin-dependent chromosome loop extrusion is limited by transcription and stalled replication forks. <i>Science Advances</i> , 2022, 8, .	4.7	28
4	Large-scale multi-omics analysis suggests specific roles for intragenic cohesin in transcriptional regulation. <i>Nature Communications</i> , 2022, 13, .	5.8	7
5	Single-cell transcriptional analysis reveals developmental stage-dependent changes in retinal progenitors in the murine early optic vesicle. <i>Biochemical and Biophysical Research Communications</i> , 2021, 543, 80-86.	1.0	6
6	Checkpoint-mediated DNA polymerase δ exonuclease activity curbing counteracts resection-driven fork collapse. <i>Molecular Cell</i> , 2021, 81, 2778-2792.e4.	4.5	14
7	Functional control of Eco1 through the MCM complex in sister chromatid cohesion. <i>Gene</i> , 2021, 784, 145584.	1.0	7
8	Suv4-20h2 protects against influenza virus infection by suppression of chromatin loop formation. <i>IScience</i> , 2021, 24, 102660.	1.9	3
9	Codependency and mutual exclusivity for gene community detection from sparse single-cell transcriptome data. <i>Nucleic Acids Research</i> , 2021, 49, e104-e104.	6.5	3
10	MAB21L1 modulates gene expression and DNA metabolic processes in the lens placode. <i>DMM Disease Models and Mechanisms</i> , 2021, 14, .	1.2	7
11	Transcription-dependent cohesin repositioning rewires chromatin loops in cellular senescence. <i>Nature Communications</i> , 2020, 11, 6049.	5.8	42
12	Bioinformatical dissection of fission yeast DNA replication origins. <i>Open Biology</i> , 2020, 10, 200052.	1.5	1
13	Tet2 and Tet3 in B cells are required to repress CD86 and prevent autoimmunity. <i>Nature Immunology</i> , 2020, 21, 950-961.	7.0	55
14	ATF7-Dependent Epigenetic Changes Are Required for the Intergenerational Effect of a Paternal Low-Protein Diet. <i>Molecular Cell</i> , 2020, 78, 445-458.e6.	4.5	52
15	The Phosphatase PP1 Promotes Mitotic Slippage through Mad3 Dephosphorylation. <i>Current Biology</i> , 2020, 30, 335-343.e5.	1.8	7
16	Combined Cohesinâ€“RUNX1 Deficiency Synergistically Perturbs Chromatin Looping and Causes Myelodysplastic Syndromes. <i>Cancer Discovery</i> , 2020, 10, 836-853.	7.7	51
17	Tex19.1 inhibits the N-end rule pathway and maintains acetylated SMC3 cohesin and sister chromatid cohesion in oocytes. <i>Journal of Cell Biology</i> , 2020, 219, .	2.3	5
18	A common molecular mechanism underlies the role of Mps1 in chromosome biorientation and the spindle assembly checkpoint. <i>EMBO Reports</i> , 2020, 21, e50257.	2.0	21

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19	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
20	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
21	Cux2 refines the forelimb field by controlling expression of <i>Raldh2</i> and <i>Hox</i> genes. Biology Open, 2019, 8, .	0.6	6
22	The novel lncRNA <i>CALIC</i> upregulates <i>AXL</i> to promote colon cancer metastasis. EMBO Reports, 2019, 20, e47052.	2.0	29
23	Comprehensive epigenome characterization reveals diverse transcriptional regulation across human vascular endothelial cells. Epigenetics and Chromatin, 2019, 12, 77.	1.8	34
24	A chromatin integration labelling method enables epigenomic profiling with lower input. Nature Cell Biology, 2019, 21, 287-296.	4.6	121
25	DBTSS/DBKERO for integrated analysis of transcriptional regulation. Nucleic Acids Research, 2018, 46, D229-D238.	6.5	48
26	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
27	Sensitive and robust assessment of ChIP-seq read distribution using a strand-shift profile. Bioinformatics, 2018, 34, 2356-2363.	1.8	21
28	Statistical Analysis and Quality Assessment of ChIP-seq Data with DROMPA. Methods in Molecular Biology, 2018, 1672, 631-643.	0.4	5
29	Identification of Elg1 interaction partners and effects on post-replication chromatin re-formation. PLoS Genetics, 2018, 14, e1007783.	1.5	15
30	Somatic copy number alterations have prognostic impact in patients with ovarian clear cell carcinoma. Oncology Reports, 2018, 40, 309-318.	1.2	16
31	Mapping of histone-binding sites in histone replacement-completed spermatozoa. Nature Communications, 2018, 9, 3885.	5.8	53
32	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
33	Budding yeast Rif1 binds to replication origins and protects DNA at blocked replication forks. EMBO Reports, 2018, 19, .	2.0	29
34	Recent advances in ChIP-seq analysis: from quality management to whole-genome annotation. Briefings in Bioinformatics, 2017, 18, bbw023.	3.2	107
35	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
36	Two Components of Aversive Memory in Drosophila, Anesthesia-Sensitive and Anesthesia-Resistant Memory, Require Distinct Domains Within the Rgl1 Small GTPase. Journal of Neuroscience, 2017, 37, 5496-5510.	1.7	8

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37	Rtt101â€Mms1â€Mms22 coordinates replicationâ€coupled sister chromatid cohesion and nucleosome assembly. EMBO Reports, 2017, 18, 1294-1305.	2.0	31
38	Functional annotation of chemical libraries across diverse biological processes. Nature Chemical Biology, 2017, 13, 982-993.	3.9	76
39	Identification of a variant-specific phosphorylation of TH2A during spermiogenesis. Scientific Reports, 2017, 7, 46228.	1.6	14
40	An InÂVitro Human Liver Model by iPSC-Derived Parenchymal and Non-parenchymal Cells. Stem Cell Reports, 2017, 9, 490-498.	2.3	128
41	The HSF1â€PARP13â€PARP1 complex facilitates DNA repair and promotes mammary tumorigenesis. Nature Communications, 2017, 8, 1638.	5.8	57
42	Cohesin Ubiquitylation and Mobilization Facilitate Stalled Replication Fork Dynamics. Molecular Cell, 2017, 68, 758-772.e4.	4.5	50
43	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
44	ChIP-seq Analysis of Condensin Complex in Cultured Mammalian Cells. Methods in Molecular Biology, 2017, 1515, 257-271.	0.4	5
45	Genome-Wide Target Analyses of Otx2 Homeoprotein in Postnatal Cortex. Frontiers in Neuroscience, 2017, 11, 307.	1.4	25
46	DNMT3A R882 mutants interact with polycomb proteins to block haematopoietic stem and leukaemic cell differentiation. Nature Communications, 2016, 7, 10924.	5.8	64
47	MYU, a Target lncRNA for Wnt/c-Myc Signaling, Mediates Induction of CDK6 to Promote Cell Cycle Progression. Cell Reports, 2016, 16, 2554-2564.	2.9	102
48	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
49	Attaching Accessory Devices to the Replisome. Molecular Cell, 2016, 63, 347-348.	4.5	1
50	Mosaic ratio quantification of isochromosome 12p in Pallisterâ€Killian syndrome using droplet digital <sc>PCR</sc>. Molecular Genetics & Genomic Medicine, 2016, 4, 257-261.	0.6	14
51	ARCNI Mutations Cause a Recognizable Craniofacial Syndrome Due to COPI-Mediated Transport Defects. American Journal of Human Genetics, 2016, 99, 451-459.	2.6	65
52	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. Cell, 2016, 167, 1145-1149.	13.5	404
53	<i>ASBEL</i> â€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
54	Microarray expression analysis of genes involved in innate immune memory in peritoneal macrophages. Genomics Data, 2016, 7, 90-91.	1.3	0

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55	Chromatin determinants of the inner-centromere rely on replication factors with functions that impart cohesion. <i>Oncotarget</i> , 2016, 7, 67934-67947.	0.8	26
56	Assembly of Slx4 signaling complexes behind <sc>DNA</sc> replication forks. <i>EMBO Journal</i> , 2015, 34, 2182-2197.	3.5	40
57	Unique Gene Expression Profile of the Proliferating <i>Xenopus</i> Tadpole Tail Blastema Cells Deciphered by RNA-Sequencing Analysis. <i>PLoS ONE</i> , 2015, 10, e0111655.	1.1	18
58	Sphingolipids regulate telomere clustering by affecting transcriptional levels of genes involved in telomere homeostasis. <i>Journal of Cell Science</i> , 2015, 128, 2454-67.	1.2	11
59	Condensin Relocalization from Centromeres to Chromosome Arms Promotes Top2 Recruitment during Anaphase. <i>Cell Reports</i> , 2015, 13, 2336-2344.	2.9	30
60	Replication-Coupled PCNA Unloading by the Elg1 Complex Occurs Genome-wide and Requires Okazaki Fragment Ligation. <i>Cell Reports</i> , 2015, 12, 774-787.	2.9	100
61	DBTMEE: a database of transcriptome in mouse early embryos. <i>Nucleic Acids Research</i> , 2015, 43, D771-D776.	6.5	71
62	Condensin targets and reduces unwound DNA structures associated with transcription in mitotic chromosome condensation. <i>Nature Communications</i> , 2015, 6, 7815.	5.8	100
63	Esco1 Acetylates Cohesin via a Mechanism Different from That of Esco2. <i>Current Biology</i> , 2015, 25, 1694-1706.	1.8	74
64	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. <i>Molecular Syndromology</i> , 2015, 6, 99-103.	0.3	10
65	Quantitative Dynamics of Chromatin Remodeling during Germ Cell Specification from Mouse Embryonic Stem Cells. <i>Cell Stem Cell</i> , 2015, 16, 517-532.	5.2	166
66	Germline gain-of-function mutations in <i>AFF4</i> cause a developmental syndrome functionally linking the super elongation complex and cohesin. <i>Nature Genetics</i> , 2015, 47, 338-344.	9.4	109
67	The Deubiquitinating Enzyme USP7 Regulates Androgen Receptor Activity by Modulating Its Binding to Chromatin. <i>Journal of Biological Chemistry</i> , 2015, 290, 21713-21723.	1.6	50
68	Rif1 binds to G quadruplexes and suppresses replication over long distances. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 889-897.	3.6	137
69	The transcription factor ATF7 mediates lipopolysaccharide-induced epigenetic changes in macrophages involved in innate immunological memory. <i>Nature Immunology</i> , 2015, 16, 1034-1043.	7.0	149
70	ATF1 Modulates the Heat Shock Response by Regulating the Stress-Inducible Heat Shock Factor 1 Transcription Complex. <i>Molecular and Cellular Biology</i> , 2015, 35, 11-25.	1.1	50
71	The Chromosomal Association of the Smc5/6 Complex Depends on Cohesion and Predicts the Level of Sister Chromatid Entanglement. <i>PLoS Genetics</i> , 2014, 10, e1004680.	1.5	60
72	Dissecting the first and the second meiotic divisions using a marker-less drug-hypersensitive fission yeast. <i>Cell Cycle</i> , 2014, 13, 1327-1334.	1.3	23

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73	Smc5/6-mediated regulation of replication progression contributes to chromosome assembly during mitosis in human cells. <i>Molecular Biology of the Cell</i> , 2014, 25, 302-317.	0.9	61
74	The dynamics of genome replication using deep sequencing. <i>Nucleic Acids Research</i> , 2014, 42, e3-e3.	6.5	113
75	Inactivation of SMC2 shows a synergistic lethal response in MYCN-amplified neuroblastoma cells. <i>Cell Cycle</i> , 2014, 13, 1115-1131.	1.3	30
76	Design, Synthesis, and Biological Activity of NCC149 Derivatives as Histone Deacetylase-selective Inhibitors. <i>ChemMedChem</i> , 2014, 9, 657-664.	1.6	59
77	Temporal and spatial regulation of eukaryotic DNA replication: From regulated initiation to genome-scale timing program. <i>Seminars in Cell and Developmental Biology</i> , 2014, 30, 110-120.	2.3	45
78	The maintenance of chromosome structure: positioning and functioning of SMC complexes. <i>Nature Reviews Molecular Cell Biology</i> , 2014, 15, 601-614.	16.1	191
79	Dimeric combinations of MafB, cFos and cJun control the apoptosis-survival balance in limb morphogenesis. <i>Development (Cambridge)</i> , 2014, 141, 2885-2894.	1.2	27
80	Loss-of-function HDAC8 mutations cause a phenotypic spectrum of Cornelia de Lange syndrome-like features, ocular hypertelorism, large fontanelle and X-linked inheritance. <i>Human Molecular Genetics</i> , 2014, 23, 2888-2900.	1.4	120
81	Genome-wide analysis of murine renal distal convoluted tubular cells for the target genes of mineralocorticoid receptor. <i>Biochemical and Biophysical Research Communications</i> , 2014, 445, 132-137.	1.0	33
82	BRCA2 Coordinates the Activities of Cell-Cycle Kinases to Promote Genome Stability. <i>Cell Reports</i> , 2014, 7, 1547-1559.	2.9	49
83	Histone Variants Enriched in Oocytes Enhance Reprogramming to Induced Pluripotent Stem Cells. <i>Cell Stem Cell</i> , 2014, 14, 217-227.	5.2	130
84	Chromatin Immunoprecipitation Protocol for Mammalian Cells. <i>Methods in Molecular Biology</i> , 2014, 1164, 33-38.	0.4	16
85	Recurrent mutations in multiple components of the cohesin complex in myeloid neoplasms. <i>Nature Genetics</i> , 2013, 45, 1232-1237.	9.4	334
86	Eukaryotic Replisome Components Cooperate to Process Histones During Chromosome Replication. <i>Cell Reports</i> , 2013, 3, 892-904.	2.9	157
87	Sensory-Neuron Subtype-Specific Transcriptional Programs Controlling Dendrite Morphogenesis: Genome-wide Analysis of Abrupt and Knot/Collier. <i>Developmental Cell</i> , 2013, 27, 530-544.	3.1	60
88	A Mesodermal Factor, T, Specifies Mouse Germ Cell Fate by Directly Activating Germline Determinants. <i>Developmental Cell</i> , 2013, 27, 516-529.	3.1	206
89	PRDM14 Ensures Naive Pluripotency through Dual Regulation of Signaling and Epigenetic Pathways in Mouse Embryonic Stem Cells. <i>Cell Stem Cell</i> , 2013, 12, 368-382.	5.2	266
90	Kinetochores Coordinate Pericentromeric Cohesion and Early DNA Replication by Cdc7-Dbf4 Kinase Recruitment. <i>Molecular Cell</i> , 2013, 50, 661-674.	4.5	140

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91	Inferring the choreography of parental genomes during fertilization from ultralarge-scale whole-transcriptome analysis. <i>Genes and Development</i> , 2013, 27, 2736-2748.	2.7	86
92	Importance of PolÎ for Damage-Induced Cohesion Reveals Differential Regulation of Cohesion Establishment at the Break Site and Genome-Wide. <i>PLoS Genetics</i> , 2013, 9, e1003158.	1.5	21
93	<scp>DROMPA</scp>: easyâ€œhandle peak calling and visualization software for the computational analysis and validation of ChIPâ€œseq data. <i>Genes To Cells</i> , 2013, 18, 589-601.	0.5	67
94	Pds5 promotes and protects cohesin acetylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 13020-13025.	3.3	108
95	Telomere-binding protein Taz1 controls global replication timing through its localization near late replication origins in fission yeast. <i>Genes and Development</i> , 2012, 26, 2050-2062.	2.7	68
96	During Replication Stress, Non-Smc Element 5 (Nse5) Is Required for Smc5/6 Protein Complex Functionality at Stalled Forks. <i>Journal of Biological Chemistry</i> , 2012, 287, 11374-11383.	1.6	46
97	Rif1 is a global regulator of timing of replication origin firing in fission yeast. <i>Genes and Development</i> , 2012, 26, 137-150.	2.7	218
98	Rapid Discovery of Highly Potent and Selective Inhibitors of Histone Deacetylase 8 Using Click Chemistry to Generate Candidate Libraries. <i>Journal of Medicinal Chemistry</i> , 2012, 55, 9562-9575.	2.9	135
99	Cohesin Acetylation Promotes Sister Chromatid Cohesion Only in Association with the Replication Machinery. <i>Journal of Biological Chemistry</i> , 2012, 287, 34325-34336.	1.6	53
100	HDAC8 mutations in Cornelia de Lange syndrome affect the cohesin acetylation cycle. <i>Nature</i> , 2012, 489, 313-317.	13.7	488
101	Replisome Stability at Defective DNA Replication Forks Is Independent of S Phase Checkpoint Kinases. <i>Molecular Cell</i> , 2012, 45, 696-704.	4.5	140
102	Endogenous DNA replication stress results in expansion of dNTP pools and a mutator phenotype. <i>EMBO Journal</i> , 2012, 31, 895-907.	3.5	95
103	The Prereplication Complex Recruits XEco2 to Chromatin to Promote Cohesin Acetylation in <i>Xenopus</i> Egg Extracts. <i>Current Biology</i> , 2012, 22, 977-988.	1.8	50
104	Recurrent Mutations of Multiple Components of Cohesin Complex in Myeloid Neoplasms. <i>Blood</i> , 2012, 120, 782-782.	0.6	1
105	The Replication Checkpoint Protects Fork Stability by Releasing Transcribed Genes from Nuclear Pores. <i>Cell</i> , 2011, 146, 233-246.	13.5	204
106	Spo11-Accessory Proteins Link Double-Strand Break Sites to the Chromosome Axis in Early Meiotic Recombination. <i>Cell</i> , 2011, 146, 372-383.	13.5	330
107	The Inheritance of Histone Modifications Depends upon the Location in the Chromosome in <i>Saccharomyces cerevisiae</i> . <i>PLoS ONE</i> , 2011, 6, e28980.	1.1	2
108	A positively charged channel within the Smc1/Smc3 hinge required for sister chromatid cohesion. <i>EMBO Journal</i> , 2011, 30, 364-378.	3.5	69

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109	Chromosome length influences replication-induced topological stress. <i>Nature</i> , 2011, 471, 392-396.	13.7	99
110	ATP Hydrolysis Is Required for Relocating Cohesin from Sites Occupied by Its Scc2/4 Loading Complex. <i>Current Biology</i> , 2011, 21, 12-24.	1.8	173
111	Origin Association of Sld3, Sld7, and Cdc45 Proteins Is a Key Step for Determination of Origin-Firing Timing. <i>Current Biology</i> , 2011, 21, 2055-2063.	1.8	232
112	Genome-wide function of THO/TREX in active genes prevents R-loop-dependent replication obstacles. <i>EMBO Journal</i> , 2011, 30, 3106-3119.	3.5	191
113	Acetylation regulates monopolar attachment at multiple levels during meiosis I in fission yeast. <i>EMBO Reports</i> , 2011, 12, 1189-1195.	2.0	22
114	Rtt107 Is Required for Recruitment of the SMC5/6 Complex to DNA Double Strand Breaks. <i>Journal of Biological Chemistry</i> , 2011, 286, 26250-26257.	1.6	43
115	Both Interaction Surfaces within Cohesin's Hinge Domain Are Essential for Its Stable Chromosomal Association. <i>Current Biology</i> , 2010, 20, 279-289.	1.8	28
116	A Direct Role for Cohesin in Gene Regulation and Ecdysone Response in <i>Drosophila</i> Salivary Glands. <i>Current Biology</i> , 2010, 20, 1787-1798.	1.8	57
117	Receptor for activated C kinase 1 stimulates nascent polypeptide-dependent translation arrest. <i>EMBO Reports</i> , 2010, 11, 956-961.	2.0	151
118	The RSC chromatin-remodeling complex influences mitotic exit and adaptation to the spindle assembly checkpoint by controlling the Cdc14 phosphatase. <i>Journal of Cell Biology</i> , 2010, 191, 981-997.	2.3	44
119	Genome-wide DNA methylation analysis in cohesin mutant human cell lines. <i>Nucleic Acids Research</i> , 2010, 38, 5657-5671.	6.5	22
120	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. <i>Nucleic Acids Research</i> , 2010, 38, 1805-1820.	6.5	14
121	Replication Termination at Eukaryotic Chromosomes Is Mediated by Top2 and Occurs at Genomic Loci Containing Pausing Elements. <i>Molecular Cell</i> , 2010, 39, 595-605.	4.5	131
122	An Smc3 Acetylation Cycle Is Essential for Establishment of Sister Chromatid Cohesion. <i>Molecular Cell</i> , 2010, 39, 689-699.	4.5	149
123	Sororin Mediates Sister Chromatid Cohesion by Antagonizing Wapl. <i>Cell</i> , 2010, 143, 737-749.	13.5	325
124	A wave of nascent transcription on activated human genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 18357-18361.	3.3	145
125	Csm3, Tof1, and Mrc1 Form a Heterotrimeric Mediator Complex That Associates with DNA Replication Forks. <i>Journal of Biological Chemistry</i> , 2009, 284, 34355-34365.	1.6	123
126	Rec8 Guides Canonical Spo11 Distribution along Yeast Meiotic Chromosomes. <i>Molecular Biology of the Cell</i> , 2009, 20, 3064-3076.	0.9	109

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127	Transcriptional Dysregulation in NIPBL and Cohesin Mutant Human Cells. <i>PLoS Biology</i> , 2009, 7, e1000119.	2.6	199
128	Amyloid Precursor Protein Is a Primary Androgen Target Gene That Promotes Prostate Cancer Growth. <i>Cancer Research</i> , 2009, 69, 137-142.	0.4	105
129	The cyclic gene <i>Hes1</i> contributes to diverse differentiation responses of embryonic stem cells. <i>Genes and Development</i> , 2009, 23, 1870-1875.	2.7	226
130	The Direct Binding of Mrc1, a Checkpoint Mediator, to Mcm6, a Replication Helicase, Is Essential for the Replication Checkpoint against Methyl Methanesulfonate-Induced Stress. <i>Molecular and Cellular Biology</i> , 2009, 29, 5008-5019.	1.1	60
131	Budding Yeast Wpl1 (Rad61)-Pds5 Complex Counteracts Sister Chromatid Cohesion-Establishing Reaction. <i>Current Biology</i> , 2009, 19, 492-497.	1.8	200
132	Ctf4 coordinates the progression of helicase and DNA polymerase ϵ . <i>Genes To Cells</i> , 2009, 14, 807-820.	0.5	82
133	SCFDia2 regulates DNA replication forks during S-phase in budding yeast. <i>EMBO Journal</i> , 2009, 28, 3693-3705.	3.5	43
134	Architectural roles of multiple chromatin insulators at the human apolipoprotein gene cluster. <i>EMBO Journal</i> , 2009, 28, 1234-1245.	3.5	185
135	The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. <i>Nature Genetics</i> , 2009, 41, 553-562.	9.4	408
136	Genome-Organizing Factors Top2 and Hmo1 Prevent Chromosome Fragility at Sites of S phase Transcription. <i>Cell</i> , 2009, 138, 870-884.	13.5	101
137	ChIP-on-Chip Analysis of DNA Topoisomerases. <i>Methods in Molecular Biology</i> , 2009, 582, 103-118.	0.4	15
138	Rad51 suppresses gross chromosomal rearrangement at centromere in <i>Schizosaccharomyces pombe</i> . <i>EMBO Journal</i> , 2008, 27, 3036-3046.	3.5	58
139	Cohesin mediates transcriptional insulation by CCCTC-binding factor. <i>Nature</i> , 2008, 451, 796-801.	13.7	1,050
140	Condensin-Dependent rDNA Decatenation Introduces a Temporal Pattern to Chromosome Segregation. <i>Current Biology</i> , 2008, 18, 1084-1089.	1.8	65
141	Mrc1 and DNA Polymerase ϵ Function Together in Linking DNA Replication and the S Phase Checkpoint. <i>Molecular Cell</i> , 2008, 32, 106-117.	4.5	183
142	Balance between Distinct HP1 Family Proteins Controls Heterochromatin Assembly in Fission Yeast. <i>Molecular and Cellular Biology</i> , 2008, 28, 6973-6988.	1.1	100
143	Identification of <i>cis</i> -acting sites for condensin loading onto budding yeast chromosomes. <i>Genes and Development</i> , 2008, 22, 2215-2227.	2.7	302
144	Nutrient-Regulated Antisense and Intragenic RNAs Modulate a Signal Transduction Pathway in Yeast. <i>PLoS Biology</i> , 2008, 6, e326.	2.6	57

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145	A DNA Polymerase δ Accessory Protein, Mcl1, Is Required for Propagation of Centromere Structures in Fission Yeast. <i>PLoS ONE</i> , 2008, 3, e2221.	1.1	20
146	Meiotic recombination-related DNA synthesis and its implications for cross-over and non-cross-over recombinant formation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 5965-5970.	3.3	52
147	Abnormality in Initiation Program of DNA Replication Is Monitored by the Highly Repetitive rRNA Gene Array on Chromosome XII in Budding Yeast. <i>Molecular and Cellular Biology</i> , 2007, 27, 568-578.	1.1	34
148	Assembly of Regulatory Factors on rRNA and Ribosomal Protein Genes in <i>Saccharomyces cerevisiae</i> . <i>Molecular and Cellular Biology</i> , 2007, 27, 6686-6705.	1.1	69
149	Perturbation of the Activity of Replication Origin by Meiosis-specific Transcription. <i>Journal of Biological Chemistry</i> , 2007, 282, 4447-4452.	1.6	37
150	Postreplicative Formation of Cohesion Is Required for Repair and Induced by a Single DNA Break. <i>Science</i> , 2007, 317, 242-245.	6.0	276
151	Top1- and Top2-mediated topological transitions at replication forks ensure fork progression and stability and prevent DNA damage checkpoint activation. <i>Genes and Development</i> , 2007, 21, 1921-1936.	2.7	134
152	Mre11 mediates gene regulation in yeast spore development. <i>Genes and Genetic Systems</i> , 2007, 82, 21-33.	0.2	12
153	An integrated map of p53-binding sites and histone modification in the human ENCODE regions. <i>Genomics</i> , 2007, 89, 178-188.	1.3	50
154	Genome-wide localization of pre-RC sites and identification of replication origins in fission yeast. <i>EMBO Journal</i> , 2007, 26, 1327-1339.	3.5	163
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