Susan M Gasser

List of Publications by Year
in descending order

253 papers	26,149 citations	4658 85 h-index	7744 150 g-index
267 all docs	267 docs citations	267 times ranked	15159 citing authors

#	Article	IF	Citations
1	Histone H3 and H4 N-termini interact with SIR3 and SIR4 proteins: A molecular model for the formation of heterochromatin in yeast. Cell, 1995, 80, 583-592.	28.9	799
2	Cohabitation of scaffold binding regions with upstream/enhancer elements of three developmentally regulated genes of D. melanogaster. Cell, 1986, 46, 521-530.	28.9	621
3	Metaphase chromosome structure. Journal of Molecular Biology, 1986, 188, 613-629.	4.2	543
4	Recruitment of the INO80 Complex by H2A Phosphorylation Links ATP-Dependent Chromatin Remodeling with DNA Double-Strand Break Repair. Cell, 2004, 119, 777-788.	28.9	538
5	Step-Wise Methylation of Histone H3K9 Positions Heterochromatin at the Nuclear Periphery. Cell, 2012, 150, 934-947.	28.9	524
6	Crosstalk between histone modifications during the DNA damage response. Trends in Cell Biology, 2009, 19, 207-217.	7.9	457
7	The clustering of telomeres and colocalization with Rap1, Sir3, and Sir4 proteins in wild-type Saccharomyces cerevisiae.. Journal of Cell Biology, 1996, 134, 1349-1363.	5.2	440
8	Relocalization of Telomeric Ku and SIR Proteins in Response to DNA Strand Breaks in Yeast. Cell, 1999, 97, 621-633.	28.9	438
9	Chromosome Dynamics in the Yeast Interphase Nucleus. Science, 2001, 294, 2181-2186.	12.6	431
10	How mitochondria import proteins. BBA - Biomembranes, 1984, 779, 65-87.	8.0	415
11	Functional Targeting of DNA Damage to a Nuclear Pore-Associated SUMO-Dependent Ubiquitin Ligase. Science, 2008, 322, 597-602.	12.6	401
12	SIR3 and SIR4 proteins are required for the positioning and integrity of yeast telomeres. Cell, 1993, 75, 543-555.	28.9	397
13	The nuclear envelope and transcriptional control. Nature Reviews Genetics, 2007, 8, 507-517.	16.3	396
14	Automatic tracking of individual fluorescence particles: application to the study of chromosome dynamics. IEEE Transactions on Image Processing, 2005, 14, 1372-1383.	9.8	391
15	Redistribution of Silencing Proteins from Telomeres to the Nucleolus Is Associated with Extension of Life Span in S. cerevisiae. Cell, 1997, 89, 381-391.	28.9	368
16	Nuclear pore association confers optimal expression levels for an inducible yeast gene. Nature, 2006, 441, 774-778.	27.8	357
17	Mutation of yeast Ku genes disrupts the subnuclear organization of telomeres. Current Biology, 1998, 8, 653-657.	3.9	330
18	Localization of RAP1 and topoisomerase II in nuclei and meiotic chromosomes of yeast. Journal of Cell Biology, 1992, 117, 935-948.	5.2	301

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19	DNA polymerase stabilization at stalled replication forks requires Mec1 and the RecQ helicase Sgs1. EMBO Journal, 2003, 22, 4325-4336.	7.8	301
20	Visualizing Chromatin Dynamics in Interphase Nuclei. Science, 2002, 296, 1412-1416.	12.6	300
21	Distinct roles for SWR1 and INO80 chromatin remodeling complexes at chromosomal double-strand breaks. EMBO Journal, 2007, 26, 4113-4125.	7.8	292
22	Increased mobility of double-strand breaks requires Mec1, Rad9 and the homologous recombination machinery. Nature Cell Biology, 2012, 14, 502-509.	10.3	286
23	Chromosomal ARS and CEN elements bind specifically to the yeast nuclear scaffold. Cell, 1988, 54, 967-978.	28.9	282
24	Live Imaging of Telomeres. Current Biology, 2002, 12, 2076-2089.	3.9	276
25	Long-range compaction and flexibility of interphase chromatin in budding yeast analyzed by high-resolution imaging techniques. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 16495-16500.	7.1	274
26	The histone code at DNA breaks: a guide to repair?. Nature Reviews Molecular Cell Biology, 2005, 6, 757-765.	37.0	270
27	The molecular biology of the SIR proteins. Gene, 2001, 279, 1-16.	2.2	257
28	Evidence for silencing compartments within the yeast nucleus: a role for telomere proximity and Sir protein concentration in silencer-mediated repression.. Genes and Development, 1996, 10, 1796-1811.	5.9	256
29	Chromatin and nucleosome dynamics in DNA damage and repair. Genes and Development, 2017, 31, 2204-2221.	5.9	254
30	Nuclear compartments and gene regulation. Current Opinion in Genetics and Development, 1999, 9, 199-205.	3.3	238
31	Separation of silencing from perinuclear anchoring functions in yeast Ku80, Sir4 and Esc1 proteins. EMBO Journal, 2004, 23, 1301-1312.	7.8	237
32	Localization of Sir2p: the nucleolus as a compartment for silent information regulators. EMBO Journal, 1997, 16, 3243-3255.	7.8	229
33	The yeast Sgs1p helicase acts upstream of Rad53p in the DNA replication checkpoint and colocalizes with Rad53p in S-phase-specific foci. Genes and Development, 2000, 14, 81-96.	5.9	229
34	Histone degradation in response to DNA damage enhances chromatin dynamics and recombination rates. Nature Structural and Molecular Biology, 2017, 24, 99-107.	8.2	220
35	The Telobox, a Myb-Related Telomeric DNA Binding Motif Found in Proteins from Yeast, Plants and Human. Nucleic Acids Research, 1996, 24, 1294-1303.	14.5	218
36	Gene regulation through nuclear organization. Nature Structural and Molecular Biology, 2007, 14, 1049-1055.	8.2	215

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37	RAP-1 factor is necessary for DNA loop formation in vitro at the silent mating type locus HML. Cell, 1989, 57, 725-737.	28.9	208
38	Chromatin Movement in the Maintenance of Genome Stability. Cell, 2013, 152, 1355-1364.	28.9	202
39	Distortion of the DNA Double Helix by RAP1 at Silencers and Multiple Telomeric Binding Sites. Journal of Molecular Biology, 1993, 231, 293-310.	4.2	201
40	Imported mitochondrial proteins cytochrome b2 and cytochrome c1 are processed in two steps.. Proceedings of the National Academy of Sciences of the United States of America, 1982, 79, 267-271.	7.1	200
41	The Function of Nuclear Architecture: A Genetic Approach. Annual Review of Genetics, 2004, 38, 305-345.	7.6	200
42	ORC and the intra-S-phase checkpoint: a threshold regulates Rad53p activation in S phase. Genes and Development, 2002, 16, 3236-3252.	5.9	188
43	Chromosome looping in yeast. Journal of Cell Biology, 2005, 168, 375-387.	5.2	186
44	Structure and Function in the Budding Yeast Nucleus. Genetics, 2012, 192, 107-129.	2.9	183
45	The carboxy termini of Sir4 and Rap1 affect Sir3 localization: evidence for a multicomponent complex required for yeast telomeric silencing.. Journal of Cell Biology, 1995, 129, 909-924.	5.2	181
46	The spatial dynamics of tissue-specific promoters during <i>C. elegans</i> development. Genes and Development, 2010, 24, 766-782.	5.9	180
47	The Positioning and Dynamics of Origins of Replication in the Budding Yeast Nucleus. Journal of Cell Biology, 2001, 152, 385-400.	5.2	178
48	Histone H3K9 methylation is dispensable for Caenorhabditis elegans development but suppresses RNA:DNA hybrid-associated repeat instability. Nature Genetics, 2016, 48, 1385-1395.	21.4	173
49	Replisome instability, fork collapse, and gross chromosomal rearrangements arise synergistically from Mec1 kinase and RecQ helicase mutations. Genes and Development, 2005, 19, 3055-3069.	5.9	171
50	Perinuclear Anchoring of H3K9-Methylated Chromatin Stabilizes Induced Cell Fate in C.Âelegans Embryos. Cell, 2015, 163, 1333-1347.	28.9	169
51	Sir-Mediated Repression Can Occur Independently of Chromosomal and Subnuclear Contexts. Cell, 2004, 119, 955-967.	28.9	168
52	Yeast telomerase and the SUN domain protein Mps3 anchor telomeres and repress subtelomeric recombination. Genes and Development, 2009, 23, 928-938.	5.9	164
53	SWR1 and INO80 Chromatin Remodelers Contribute to DNA Double-Strand Break Perinuclear Anchorage Site Choice. Molecular Cell, 2014, 55, 626-639.	9.7	164
54	Ino80 Chromatin Remodeling Complex Promotes Recovery of Stalled Replication Forks. Current Biology, 2008, 18, 566-575.	3.9	162

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55	Targeted INO80 enhances subnuclear chromatin movement and ectopic homologous recombination. Genes and Development, 2012, 26, 369-383.	5.9	156
56	On TADs and LADs: Spatial Control Over Gene Expression. Trends in Genetics, 2016, 32, 485-495.	6.7	151
57	A cytosolic NAD-dependent deacetylase, Hst2p, can modulate nucleolar and telomeric silencing in yeast. EMBO Journal, 2001, 20, 197-209.	7.8	147
58	Establishment of H3K9-methylated heterochromatin and its functions in tissue differentiation and maintenance. Nature Reviews Molecular Cell Biology, 2022, 23, 623-640.	37.0	145
59	Scaffold attachment of DNA loops in metaphase chromosomes. Journal of Molecular Biology, 1988, 200, 101-109.	4.2	142
60	Telomeres and the functional architecture of the nucleus. Trends in Cell Biology, 1993, 3, 128-134.	7.9	140
61	ATR/Mec1: coordinating fork stability and repair. Current Opinion in Cell Biology, 2009, 21, 237-244.	5.4	136
62	Heterochromatin protein 1: donâ€™t judge the book by its cover!. Current Opinion in Genetics and Development, 2006, 16, 143-150.	3.3	134
63	Mechanistically distinct roles for Sgs1p in checkpoint activation and replication fork maintenance. EMBO Journal, 2005, 24, 405-417.	7.8	132
64	Positions of Potential:Nuclear Organization and Gene Expression. Cell, 2001, 104, 639-642.	28.9	130
65	The nuclear envelopeâ€"a scaffold for silencing?. Current Opinion in Genetics and Development, 2009, 19, 180-186.	3.3	130
66	Histones and histone modifications in perinuclear chromatin anchoring: from yeast to man. EMBO Reports, 2016, 17, 139-155.	4.5	128
67	An EDMD Mutation in C.Âelegans Lamin Blocks Muscle-Specific Gene Relocation and Compromises Muscle Integrity. Current Biology, 2011, 21, 1603-1614.	3.9	125
68	Checkpoint kinases and the INO80 nucleosome remodeling complex enhance global chromatin mobility in response to DNA damage. Genes and Development, 2013, 27, 1999-2008.	5.9	114
69	A role for the Cdc7 kinase regulatory subunit Dbf4p in the formation of initiation-competent origins of replication. Genes and Development, 1999, 13, 2159-2176.	5.9	114
70	The functional importance of telomere clustering: Global changes in gene expression result from SIR factor dispersion. Genome Research, 2009, 19, 611-625.	5.5	110
71	SIR Proteins and the Assembly of Silent Chromatin in Budding Yeast. Annual Review of Genetics, 2013, 47, 275-306.	7.6	109
72	Regulation of recombination at yeast nuclear pores controls repair and triplet repeat stability. Genes and Development, 2015, 29, 1006-1017.	5.9	109

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73	RecQ helicases: multiple roles in genome maintenance. Trends in Cell Biology, 2003, 13, 493-501.	7.9	108
74	LifeTime and improving European healthcare through cell-based interceptive medicine. Nature, 2020, 587, 377-386.	27.8	108
75	PolySUMOylation by Siz2 and Mms21 triggers relocation of DNA breaks to nuclear pores through the Slx5/Slx8 STUbL. Genes and Development, 2016, 30, 931-945.	5.9	107
76	Repeat DNA in genome organization and stability. Current Opinion in Genetics and Development, 2015, 31, 12-19.	3.3	106
77	The Budding Yeast Nucleus. Cold Spring Harbor Perspectives in Biology, 2010, 2, a000612-a000612.	5.5	105
78	INO80 and SWR complexes: relating structure to function in chromatin remodeling. Trends in Cell Biology, 2014, 24, 619-631.	7.9	105
79	The Origin Recognition Complex Functions in Sister-Chromatid Cohesion in Saccharomyces cerevisiae. Cell, 2007, 128, 85-99.	28.9	104
80	Reconstitution of Yeast Silent Chromatin: Multiple Contact Sites and O-AADPR Binding Load SIR Complexes onto Nucleosomes In Vitro. Molecular Cell, 2009, 33, 323-334.	9.7	103
81	Mec1, INO80, and the PAF1 complex cooperate to limit transcription replication conflicts through RNAPII removal during replication stress. Genes and Development, 2016, 30, 337-354.	5.9	103
82	Nuclear Actin and Actin-Binding Proteins in DNA Repair. Trends in Cell Biology, 2019, 29, 462-476.	7.9	101
83	ATP-Dependent Chromatin Remodeling and DNA Double-Strand Break Repair. Cell Cycle, 2005, 4, 1011-1014.	2.6	99
84	Active chromatin marks drive spatial sequestration of heterochromatin in C. elegans nuclei. Nature, 2019, 569, 734-739.	27.8	97
85	Visualization of Chromatin Decompaction and Break Site Extrusion as Predicted by Statistical Polymer Modeling of Single-Locus Trajectories. Cell Reports, 2017, 18, 1200-1214.	6.4	96
86	Identification and purification of a protein that binds the yeast ARS consensus sequence. Cell, 1991, 64, 951-960.	28.9	94
87	Structural Maintenance of Chromosomes Protein C-terminal Domains Bind Preferentially to DNA with Secondary Structure. Journal of Biological Chemistry, 1998, 273, 24088-24094.	3.4	93
88	The Dynamics of Yeast Telomeres and Silencing Proteins through the Cell Cycle. Journal of Structural Biology, 2000, 129, 159-174.	2.8	91
89	The INO80 remodeller in transcription, replication and repair. Philosophical Transactions of the Royal Society B: Biological Sciences, 2017, 372, 20160290.	4.0	91
90	An N-terminal domain of Dbf4p mediates interaction with both origin recognition complex (ORC) and Rad53p and can deregulate late origin firing. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 16087-16092.	7.1	88

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91	The PIAS homologue Siz2 regulates perinuclear telomere position and telomerase activity in buddingÂyeast. Nature Cell Biology, 2011, 13, 867-874.	10.3	88
92	Cohesin and the nucleolus constrain the mobility of spontaneous repair foci. EMBO Reports, 2013, 14, 984-991.	4.5	87
93	Nuclear organization in genome stability: SUMO connections. Cell Research, 2011, 21, 474-485.	12.0	86
94	Nucleosome remodelers in double-strand break repair. Current Opinion in Genetics and Development, 2013, 23, 174-184.	3.3	85
95	A dual role of H4K16 acetylation in the establishment of yeast silent chromatin. EMBO Journal, 2011, 30, 2610-2621.	7.8	84
96	Epigenetics in Saccharomyces cerevisiae. Cold Spring Harbor Perspectives in Biology, 2013, 5, a017491-a017491.	5.5	84
97	Repressive Chromatin in <i>Caenorhabditis elegans</i>: Establishment, Composition, and Function. Genetics, 2018, 208, 491-511.	2.9	82
98	Chromosome dynamics: the SMC protein family. Current Opinion in Genetics and Development, 1998, 8, 254-259.	3.3	80
99	Mechanisms of heterochromatin subnuclear localization. Trends in Biochemical Sciences, 2013, 38, 356-363.	7.5	80
100	Visualizing Yeast Chromosomes and Nuclear Architecture. Methods in Enzymology, 2010, 470, 535-567.	1.0	78
101	Nuclear Geometry and Rapid Mitosis Ensure Asymmetric Episome Segregation in Yeast. Current Biology, 2011, 21, 25-33.	3.9	78
102	Myosin-like proteins 1 and 2 are not required for silencing or telomere anchoring, but act in the Tel1 pathway of telomere length control. Journal of Structural Biology, 2002, 140, 79-91.	2.8	76
103	Controlled exchange of chromosomal arms reveals principles driving telomere interactions in yeast. Genome Research, 2008, 18, 261-271.	5.5	76
104	Improved methods for the isolation of individual and clustered mitotic chromosomes. Experimental Cell Research, 1987, 173, 85-98.	2.6	74
105	An N-terminal acidic region of Sgs1 interacts with Rpa70 and recruits Rad53 kinase to stalled forks. EMBO Journal, 2012, 31, 3768-3783.	7.8	74
106	Replication foci dynamics: replication patterns are modulated by S-phase checkpoint kinases in fission yeast. EMBO Journal, 2007, 26, 1315-1326.	7.8	73
107	DNA loops: structural and functional properties of scaffold-attached regions. Molecular Microbiology, 1992, 6, 419-423.	2.5	72
108	Temporal separation of replication and recombination requires the intra-S checkpoint. Journal of Cell Biology, 2005, 168, 537-544.	5.2	72

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109	Meiotic behaviours of chromosomes and microtubules in budding yeast: relocalization of centromeres and telomeres during meiotic prophase. Genes To Cells, 1998, 3, 587-601.	1.2	71
110	Regulation of Nuclear Positioning and Dynamics of the Silent Mating Type Loci by the Yeast Ku70/Ku80 Complex. Molecular and Cellular Biology, 2009, 29, 835-848.	2.3	71
111	TORC2 Signaling Pathway Guarantees Genome Stability in the Face of DNA Strand Breaks. Molecular Cell, 2013, 51, 829-839.	9.7	71
112	DNA topoisomerase II mutations and resistance to anti-tumor drugs. BioEssays, 1995, 17, 767-774.	2.5	70
113	Regulation of topoisomerase II by phosphorylation: a role for casein kinase II. Journal of Cell Science, 1993, 104, 219-225.	2.0	70
114	A Sense of the End. Science, 2000, 288, 1377-1379.	12.6	68
115	Locking the genome: nuclear organization and cell fate. Current Opinion in Genetics and Development, 2011, 21, 167-174.	3.3	68
116	Chromatin states and nuclear organization in development â€" a view from the nuclear lamina. Genome Biology, 2015, 16, 174.	8.8	67
117	Intracellular trafficking of yeast telomerase components. EMBO Reports, 2002, 3, 652-659.	4.5	66
118	Silent chromatin at the middle and ends: lessons from yeasts. EMBO Journal, 2009, 28, 2149-2161.	7.8	64
119	Multiple pathways for telomere tethering: functional implications of subnuclear position for heterochromatin formation. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 2004, 1677, 120-128.	2.4	63
120	Modules for cloningâ€free chromatin tagging in <i>Saccharomyces cerevisae</i>. Yeast, 2008, 25, 235-239.	1.7	63
121	Yeast PP4 Interacts with ATR Homolog Ddc2-Mec1 and Regulates Checkpoint Signaling. Molecular Cell, 2015, 57, 273-289.	9.7	63
122	Turning telomeres off and on. Current Opinion in Cell Biology, 2001, 13, 281-289.	5.4	61
123	Actin-related proteins in the nucleus: life beyond chromatin remodelers. Current Opinion in Cell Biology, 2010, 22, 383-391.	5.4	61
124	Chromosome Dynamics in Response to DNA Damage. Annual Review of Genetics, 2018, 52, 295-319.	7.6	61
125	Promoter- and RNA polymerase IIâ€"dependent <i>hsp-16</i> gene association with nuclear pores in <i>Caenorhabditis elegans</i>. Journal of Cell Biology, 2013, 200, 589-604.	5.2	60
126	Chromatin organization and dynamics in double-strand break repair. Current Opinion in Genetics and Development, 2017, 43, 9-16.	3.3	59

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127	Nuclear organization and transcriptional silencing in yeast. Experientia, 1996, 52, 1136-1147.	1.2	58
128	RPA Mediates Recruitment of MRX to Forks and Double-Strand Breaks to Hold Sister Chromatids Together. Molecular Cell, 2016, 64, 951-966.	9.7	57
129	ORC-dependent and origin-specific initiation of DNA replication at defined foci in isolated yeast nuclei.. Genes and Development, 1997, 11, 1504-1518.	5.9	56
130	Heterochromatin Protein 1Î² (HP1Î²) has distinct functions and distinct nuclear distribution in pluripotent versus differentiated cells. Genome Biology, 2015, 16, 213.	8.8	55
131	Structural Basis of Mec1-Ddc2-RPA Assembly and Activation on Single-Stranded DNA at Sites of Damage. Molecular Cell, 2017, 68, 431-445.e5.	9.7	55
132	Nuclear organization and silencing: putting things in their place. Nature Cell Biology, 2002, 4, E53-E55.	10.3	54
133	Kuâ€deficient yeast strains exhibit alternative states of silencing competence. EMBO Reports, 2001, 2, 203-210.	4.5	53
134	The processing of double-strand breaks and binding of single-strand-binding proteins RPA and Rad51 modulate the formation of ATR-kinase foci in yeast. Journal of Cell Science, 2007, 120, 4209-4220.	2.0	53
135	Analysis of Sir2p Domains Required for rDNA and Telomeric Silencing in Saccharomyces cerevisiae. Genetics, 2000, 154, 1069-1083.	2.9	53
136	Analysis of Etoposide Binding to Subdomains of Human DNA Topoisomerase IIÎ±in the Absence of DNAâ€. Biochemistry, 2001, 40, 1624-1634.	2.5	52
137	Actin-Related Protein Arp6 Influences H2A.Z-Dependent and -Independent Gene Expression and Links Ribosomal Protein Genes to Nuclear Pores. PLoS Genetics, 2010, 6, e1000910.	3.5	52
138	Caenorhabditis elegans Heterochromatin protein 1 (HPL-2) links developmental plasticity, longevity and lipid metabolism. Genome Biology, 2011, 12, R123.	9.6	52
139	Replication Checkpoint: Tuning and Coordination of Replication Forks in S Phase. Genes, 2013, 4, 388-434.	2.4	52
140	INO80-C and SWR-C: Guardians of the Genome. Journal of Molecular Biology, 2015, 427, 637-651.	4.2	52
141	RecQ helicases: at the heart of genetic stability. FEBS Letters, 2002, 529, 43-48.	2.8	49
142	Imaging the Asymmetrical DNA Bend Induced by Repressor Activator Protein 1 with Scanning Tunneling Microscopy. Journal of Structural Biology, 1994, 113, 1-12.	2.8	48
143	Synergistic lethality between BRCA1 and H3K9me2 loss reflects satellite derepression. Genes and Development, 2019, 33, 436-451.	5.9	48
144	Methods for Visualizing Chromatin Dynamics in Living Yeast. Methods in Enzymology, 2003, 375, 345-365.	1.0	47

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145	Challenges and guidelines toward 4D nucleome data and model standards. Nature Genetics, 2018, 50, 1352-1358.	21.4	47
146	Guidelines for DNA recombination and repair studies: Cellular assays of DNA repair pathways. Microbial Cell, 2019, 6, 1-64.	3.2	47
147	The composition and morphology of yeast nuclear scaffolds. Journal of Cell Science, 1990, 96, 439-450.	2.0	46
148	Telomere maintenance and gene repression: a common end?. Current Opinion in Cell Biology, 1994, 6, 373-379.	5.4	45
149	The nucleolus: Nucleolar space for RENT. Current Biology, 1999, 9, R575-R576.	3.9	45
150	The shelterin protein POT-1 anchors <i>Caenorhabditis elegans</i> telomeres through SUN-1 at the nuclear periphery. Journal of Cell Biology, 2013, 203, 727-735.	5.2	44
151	Ribosome biogenesis factors bind a nuclear envelope SUN domain protein to cluster yeast telomeres. EMBO Journal, 2011, 30, 3799-3811.	7.8	43
152	MAP kinase signaling induces nuclear reorganization in budding yeast. Current Biology, 2000, 10, 373-382.	3.9	42
153	A Homotrimerâ€"Heterotrimer Switch in Sir2 Structure Differentiates rDNA and Telomeric Silencing. Molecular Cell, 2006, 21, 825-836.	9.7	42
154	Functional Characterization of the N Terminus of Sir3p. Molecular and Cellular Biology, 1998, 18, 6110-6120.	2.3	41
155	Subtelomeric factors antagonize telomere anchoring and Tel1-independent telomere length regulation. EMBO Journal, 2006, 25, 857-867.	7.8	41
156	DNA Damage-Induced Nucleosome Depletion Enhances Homology Search Independently of Local Break Movement. Molecular Cell, 2020, 80, 311-326.e4.	9.7	41
157	Loss of an H3K9me anchor rescues laminopathy-linked changes in nuclear organization and muscle function in an Emery-Dreifuss muscular dystrophy model. Genes and Development, 2020, 34, 560-579.	5.9	41
158	The Function of Telomere Clustering in Yeast: The Circe Effect. Cold Spring Harbor Symposia on Quantitative Biology, 2004, 69, 327-338.	1.1	40
159	Structural basis for the role of the Sir3 AAA⁺ domain in silencing: interaction with Sir4 and unmethylated histone H3K79. Genes and Development, 2011, 25, 1835-1846.	5.9	40
160	RAP1 stimulates single- to double-strand association of yeast telomeric DNA: implications for telomere - telomere interactions. Nucleic Acids Research, 1994, 22, 5310-5320.	14.5	39
161	Chromosome Structure: Coiling up chromosomes. Current Biology, 1995, 5, 357-360.	3.9	39
162	Heterochromatin: a meiotic matchmaker?. Trends in Cell Biology, 1997, 7, 201-205.	7.9	39

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163	Sif2p interacts with the Sir4p amino-terminal domain and antagonizes telomeric silencing in yeast. Current Biology, 1998, 8, 787-S2.	3.9	38
164	H3K9me selectively blocks transcription factor activity and ensures differentiated tissue integrity. Nature Cell Biology, 2021, 23, 1163-1175.	10.3	37
165	From snapshots to moving pictures: new perspectives on nuclear organization. Trends in Cell Biology, 2001, 11, 519-525.	7.9	36
166	Targeting Sir Proteins to Sites of Action: A General Mechanism for Regulated Repression. Cold Spring Harbor Symposia on Quantitative Biology, 1998, 63, 401-412.	1.1	36
167	Preparation and characterization of yeast nuclear extracts for efficient RNA polymerase B (II)-dependent transcriptionin vitro. Nucleic Acids Research, 1990, 18, 7033-7039.	14.5	35
168	SIRâ€"nucleosome interactions: Structureâ€"function relationships in yeast silent chromatin. Gene, 2013, 527, 10-25.	2.2	35
169	<scp>TORC</scp>2â€"a new player in genome stability. EMBO Molecular Medicine, 2014, 6, 995-1002.	6.9	35
170	Taz1p and Teb1p, two telobox proteins in Schizosaccharomyces pombe, recognize different telomere-related DNA sequences. Nucleic Acids Research, 1999, 27, 4687-4694.	14.5	34
171	Phosphorylation of the C-terminal Domain of Yeast Topoisomerase II by Casein Kinase II Affects DNA-Protein Interaction. Journal of Molecular Biology, 1994, 243, 10-24.	4.2	32
172	Cell cycle-dependent phosphorylation of Rad53 kinase by Cdc5 and Cdc28 modulates checkpoint adaptation. Cell Cycle, 2010, 9, 350-363.	2.6	32
173	Meiosis-specific prophase-like pathway controls cleavage-independent release of cohesin by Wapl phosphorylation. PLoS Genetics, 2019, 15, e1007851.	3.5	32
174	Damage-induced chromatome dynamics link Ubiquitin ligase and proteasome recruitment to histone loss and efficient DNA repair. Molecular Cell, 2021, 81, 811-829.e6.	9.7	32
175	Analysis of nuclear organization in Saccharomyces cerevisiae. Methods in Enzymology, 1999, 304, 663-672.	1.0	30
176	Redundancy, insult-specific sensors and thresholds: unlocking the S-phase checkpoint response. Current Opinion in Genetics and Development, 2004, 14, 292-300.	3.3	30
177	Biosynthesis of the ubiquinol-cytochrome c reductase complex in yeast. Characterization of precursor forms of the 44-kDa, 40-kDa and 17-kDa subunits and identification of individual messenger RNAs for these and other imported subunits of the complex. FEBS Journal, 1983, 135, 457-463.	0.2	29
178	Early initiation of a replication origin tethered at the nuclear periphery. Journal of Cell Science, 2010, 123, 1015-1019.	2.0	29
179	Dimerization of Sir3 via its C-terminal winged helix domain is essential for yeast heterochromatin formation. EMBO Journal, 2013, 32, 437-449.	7.8	29
180	Semi-conservative replication in yeast nuclear extracts requires Dna2 helicase and supercoiled template 1 1Edited by M. Yaniv. Journal of Molecular Biology, 1998, 281, 631-649.	4.2	28

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181	Dot1 binding induces chromatin rearrangements by histone methylation-dependent and -independent mechanisms. Epigenetics and Chromatin, 2011, 4, 2.	3.9	28
182	[32] Import of polypeptides into isolated yeast mitochondria. Methods in Enzymology, 1983, 97, 329-336.	1.0	27
183	Chromatin: A sticky silence. Current Biology, 1996, 6, 1222-1225.	3.9	26
184	Ectopic expression of inactive forms of yeast DNA topoisomerase II confers resistance to the anti-tumour drug, etoposide. British Journal of Cancer, 1996, 73, 1201-1209.	6.4	25
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