

Susan M Gasser

List of Publications by Year in descending order

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Version: 2024-02-01

253
papers

26,149
citations

5430

85
h-index

8878

150
g-index

267
all docs

267
docs citations

267
times ranked

16909
citing authors

#	ARTICLE	IF	CITATIONS
1	SETDB1-like MET-2 promotes transcriptional silencing and development independently of its H3K9me-associated catalytic activity. <i>Nature Structural and Molecular Biology</i> , 2022, 29, 85-96.	3.6	11
2	Lessons in chromatin organization and gender equity in research: an interview with Susan Gasser. <i>Epigenomics</i> , 2022, 14, 331-337.	1.0	1
3	Establishment of H3K9-methylated heterochromatin and its functions in tissue differentiation and maintenance. <i>Nature Reviews Molecular Cell Biology</i> , 2022, 23, 623-640.	16.1	145
4	A Role for the Mre11-Rad50-Xrs2 Complex in Gene Expression and Chromosome Organization. <i>Molecular Cell</i> , 2021, 81, 183-197.e6.	4.5	15
5	Argonaute NRDE-3 and MBT domain protein LIN-61 redundantly recruit an H3K9me3 HMT to prevent embryonic lethality and transposon expression. <i>Genes and Development</i> , 2021, 35, 82-101.	2.7	16
6	Damage-induced chromatome dynamics link Ubiquitin ligase and proteasome recruitment to histone loss and efficient DNA repair. <i>Molecular Cell</i> , 2021, 81, 811-829.e6.	4.5	32
7	Nadeshiko revisited. <i>EMBO Reports</i> , 2021, 22, e52528.	2.0	2
8	Editorial overview: Breaking open the mysteries of nuclear and chromatin organization. <i>Current Opinion in Genetics and Development</i> , 2021, 67, iii-vii.	1.5	1
9	In Vitro-Evolved Peptides Bind Monomeric Actin and Mimic Actin-Binding Protein Thymosin- β 4. <i>ACS Chemical Biology</i> , 2021, 16, 820-828.	1.6	2
10	Underappreciated Roles of DNA Polymerase ϵ in Replication Stress Survival. <i>Trends in Genetics</i> , 2021, 37, 476-487.	2.9	22
11	The stabilized Pol31-Pol3 interface counteracts Pol32 ablation with differential effects on repair. <i>Life Science Alliance</i> , 2021, 4, e202101138.	1.3	1
12	A regulatory phosphorylation site on Mec1 controls chromatin occupancy of RNA polymerases during replication stress. <i>EMBO Journal</i> , 2021, 40, e108439.	3.5	14
13	Cytoskeleton integrity influences XRCC1 and PCNA dynamics at DNA damage. <i>Molecular Biology of the Cell</i> , 2021, 32, br6.	0.9	8
14	Sucrose gradient chromatin enrichment for quantitative proteomics analysis in budding yeast. <i>STAR Protocols</i> , 2021, 2, 100825.	0.5	0
15	H3K9me selectively blocks transcription factor activity and ensures differentiated tissue integrity. <i>Nature Cell Biology</i> , 2021, 23, 1163-1175.	4.6	37
16	DNA Damage-Induced Nucleosome Depletion Enhances Homology Search Independently of Local Break Movement. <i>Molecular Cell</i> , 2020, 80, 311-326.e4.	4.5	41
17	LifeTime and improving European healthcare through cell-based interceptive medicine. <i>Nature</i> , 2020, 587, 377-386.	13.7	108
18	Disease-associated DNA2 nuclease-helicase protects cells from lethal chromosome under-replication. <i>Nucleic Acids Research</i> , 2020, 48, 7265-7278.	6.5	11

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19	Loss of an H3K9me anchor rescues laminopathy-linked changes in nuclear organization and muscle function in an Emery-Dreifuss muscular dystrophy model. <i>Genes and Development</i> , 2020, 34, 560-579.	2.7	41
20	LSM2-8 and XRN-2 contribute to the silencing of H3K27me3-marked genes through targeted RNA decay. <i>Nature Cell Biology</i> , 2020, 22, 579-590.	4.6	17
21	The Sir4 H ϵ -BRCT domain interacts with phospho ϵ proteins to sequester and repress yeast heterochromatin. <i>EMBO Journal</i> , 2019, 38, e101744.	3.5	6
22	Srs2 helicase prevents the formation of toxic DNA damage during late prophase I of yeast meiosis. <i>Chromosoma</i> , 2019, 128, 453-471.	1.0	10
23	Active chromatin marks drive spatial sequestration of heterochromatin in <i>C. elegans</i> nuclei. <i>Nature</i> , 2019, 569, 734-739.	13.7	97
24	Guidelines for DNA recombination and repair studies: Cellular assays of DNA repair pathways. <i>Microbial Cell</i> , 2019, 6, 1-64.	1.4	47
25	Once and Only Once. <i>Cell</i> , 2019, 177, 495-498.	13.5	4
26	Nuclear Actin and Actin-Binding Proteins in DNA Repair. <i>Trends in Cell Biology</i> , 2019, 29, 462-476.	3.6	101
27	Heterochromatic foci and transcriptional repression by an unstructured MET-2/SETDB1 co-factor LIN-65. <i>Journal of Cell Biology</i> , 2019, 218, 820-838.	2.3	21
28	Synergistic lethality between BRCA1 and H3K9me2 loss reflects satellite derepression. <i>Genes and Development</i> , 2019, 33, 436-451.	2.7	48
29	Meiosis-specific prophase-like pathway controls cleavage-independent release of cohesin by Wapl phosphorylation. <i>PLoS Genetics</i> , 2019, 15, e1007851.	1.5	32
30	A Nuclear RNA Degradation Pathway Helps Silence Polycomb/H3K27me3-Marked Loci in <i>Caenorhabditis elegans</i> . <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2019, 84, 141-153.	2.0	0
31	Repressive Chromatin in <i>Caenorhabditis elegans</i> : Establishment, Composition, and Function. <i>Genetics</i> , 2018, 208, 491-511.	1.2	82
32	Challenges and guidelines toward 4D nucleome data and model standards. <i>Nature Genetics</i> , 2018, 50, 1352-1358.	9.4	47
33	Chromosome Dynamics in Response to DNA Damage. <i>Annual Review of Genetics</i> , 2018, 52, 295-319.	3.2	61
34	Asymmetric Processing of DNA Ends at a Double-Strand Break Leads to Unconstrained Dynamics and Ectopic Translocation. <i>Cell Reports</i> , 2018, 24, 2614-2628.e4.	2.9	23
35	Histone degradation in response to DNA damage enhances chromatin dynamics and recombination rates. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 99-107.	3.6	220
36	A game of musical chairs: Pro- and anti-resection factors compete for TOPBP1 binding after DNA damage. <i>Journal of Cell Biology</i> , 2017, 216, 535-537.	2.3	1

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37	Visualization of Chromatin Decompaction and Break Site Extrusion as Predicted by Statistical Polymer Modeling of Single-Locus Trajectories. <i>Cell Reports</i> , 2017, 18, 1200-1214.	2.9	96
38	Structural Basis of Mec1-Ddc2-RPA Assembly and Activation on Single-Stranded DNA at Sites of Damage. <i>Molecular Cell</i> , 2017, 68, 431-445.e5.	4.5	55
39	Chromatin modifiers and remodellers in DNA repair and signalling. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2017, 372, 20160279.	1.8	18
40	The INO80 remodeller in transcription, replication and repair. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2017, 372, 20160290.	1.8	91
41	The Importance of Satellite Sequence Repression for Genome Stability. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2017, 82, 15-24.	2.0	23
42	Chromatin organization and dynamics in double-strand break repair. <i>Current Opinion in Genetics and Development</i> , 2017, 43, 9-16.	1.5	59
43	Chromatin and nucleosome dynamics in DNA damage and repair. <i>Genes and Development</i> , 2017, 31, 2204-2221.	2.7	254
44	The MRX Complex Ensures NHEJ Fidelity through Multiple Pathways Including Xrs2-FHA-Dependent Tel1 Activation. <i>PLoS Genetics</i> , 2016, 12, e1005942.	1.5	25
45	Histones and histone modifications in perinuclear chromatin anchoring: from yeast to man. <i>EMBO Reports</i> , 2016, 17, 139-155.	2.0	128
46	Spatial segregation of heterochromatin: Uncovering functionality in a multicellular organism. <i>Nucleus</i> , 2016, 7, 301-307.	0.6	20
47	PolySUMOylation by Siz2 and Mms21 triggers relocation of DNA breaks to nuclear pores through the Slx5/Slx8 STUbL. <i>Genes and Development</i> , 2016, 30, 931-945.	2.7	107
48	Nuclear Architecture: Past and Future Tense. <i>Trends in Cell Biology</i> , 2016, 26, 473-475.	3.6	13
49	Histone H3K9 methylation is dispensable for <i>Caenorhabditis elegans</i> development but suppresses RNA:DNA hybrid-associated repeat instability. <i>Nature Genetics</i> , 2016, 48, 1385-1395.	9.4	173
50	SUMO wrestles breaks to the nuclear ring's edge. <i>Cell Cycle</i> , 2016, 15, 3011-3013.	1.3	9
51	RPA Mediates Recruitment of MRX to Forks and Double-Strand Breaks to Hold Sister Chromatids Together. <i>Molecular Cell</i> , 2016, 64, 951-966.	4.5	57
52	Selfish DNA and Epigenetic Repression Revisited. <i>Genetics</i> , 2016, 204, 837-839.	1.2	6
53	Mechanism of chromatin segregation to the nuclear periphery in <i>C. elegans</i> embryos. <i>Worm</i> , 2016, 5, e1190900.	1.0	7
54	On TADs and LADs: Spatial Control Over Gene Expression. <i>Trends in Genetics</i> , 2016, 32, 485-495.	2.9	151

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55	Mec1, INO80, and the PAF1 complex cooperate to limit transcription replication conflicts through RNAPII removal during replication stress. <i>Genes and Development</i> , 2016, 30, 337-354.	2.7	103
56	Heterochromatin Protein 1 ² (HP1 ²) has distinct functions and distinct nuclear distribution in pluripotent versus differentiated cells. <i>Genome Biology</i> , 2015, 16, 213.	3.8	55
57	Repeat DNA in genome organization and stability. <i>Current Opinion in Genetics and Development</i> , 2015, 31, 12-19.	1.5	106
58	Nuclear organization in DNA end processing: Telomeres vs double-strand breaks. <i>DNA Repair</i> , 2015, 32, 134-140.	1.3	17
59	Regulation of recombination at yeast nuclear pores controls repair and triplet repeat stability. <i>Genes and Development</i> , 2015, 29, 1006-1017.	2.7	109
60	Chromatin states and nuclear organization in development – a view from the nuclear lamina. <i>Genome Biology</i> , 2015, 16, 174.	3.8	67
61	Perinuclear Anchoring of H3K9-Methylated Chromatin Stabilizes Induced Cell Fate in <i>C.Âlegans</i> Embryos. <i>Cell</i> , 2015, 163, 1333-1347.	13.5	169
62	Yeast PP4 Interacts with ATR Homolog Ddc2-Mec1 and Regulates Checkpoint Signaling. <i>Molecular Cell</i> , 2015, 57, 273-289.	4.5	63
63	INO80-C and SWR-C: Guardians of the Genome. <i>Journal of Molecular Biology</i> , 2015, 427, 637-651.	2.0	52
64	Visualizing the Spatiotemporal Dynamics of DNA Damage in Budding Yeast. <i>Methods in Molecular Biology</i> , 2015, 1292, 77-96.	0.4	9
65	Remodelers move chromatin in response to DNA damage. <i>Cell Cycle</i> , 2014, 13, 877-878.	1.3	14
66	<sc>TORC</sc>2 – a new player in genome stability. <i>EMBO Molecular Medicine</i> , 2014, 6, 995-1002.	3.3	35
67	INO80 and SWR complexes: relating structure to function in chromatin remodeling. <i>Trends in Cell Biology</i> , 2014, 24, 619-631.	3.6	105
68	SWR1 and INO80 Chromatin Remodelers Contribute to DNA Double-Strand Break Perinuclear Anchorage Site Choice. <i>Molecular Cell</i> , 2014, 55, 626-639.	4.5	164
69	Open questions: Epigenetics and the role of heterochromatin in development. <i>BMC Biology</i> , 2013, 11, 21.	1.7	2
70	Nucleosome remodelers in double-strand break repair. <i>Current Opinion in Genetics and Development</i> , 2013, 23, 174-184.	1.5	85
71	Epigenetics in <i>Saccharomyces cerevisiae</i> . <i>Cold Spring Harbor Perspectives in Biology</i> , 2013, 5, a017491-a017491.	2.3	84
72	SIR Proteins and the Assembly of Silent Chromatin in Budding Yeast. <i>Annual Review of Genetics</i> , 2013, 47, 275-306.	3.2	109

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73	Cohesin and the nucleolus constrain the mobility of spontaneous repair foci. <i>EMBO Reports</i> , 2013, 14, 984-991.	2.0	87
74	TORC2 Signaling Pathway Guarantees Genome Stability in the Face of DNA Strand Breaks. <i>Molecular Cell</i> , 2013, 51, 829-839.	4.5	71
75	SIR nucleosome interactions: Structure-function relationships in yeast silent chromatin. <i>Gene</i> , 2013, 527, 10-25.	1.0	35
76	Chromatin Movement in the Maintenance of Genome Stability. <i>Cell</i> , 2013, 152, 1355-1364.	13.5	202
77	Promoter- and RNA polymerase II-dependent <i>hsp-16</i> gene association with nuclear pores in <i>Caenorhabditis elegans</i> . <i>Journal of Cell Biology</i> , 2013, 200, 589-604.	2.3	60
78	Mechanisms of heterochromatin subnuclear localization. <i>Trends in Biochemical Sciences</i> , 2013, 38, 356-363.	3.7	80
79	Dimerization of Sir3 via its C-terminal winged helix domain is essential for yeast heterochromatin formation. <i>EMBO Journal</i> , 2013, 32, 437-449.	3.5	29
80	Checkpoint kinases and the INO80 nucleosome remodeling complex enhance global chromatin mobility in response to DNA damage. <i>Genes and Development</i> , 2013, 27, 1999-2008.	2.7	114
81	The shelterin protein POT-1 anchors <i>Caenorhabditis elegans</i> telomeres through SUN-1 at the nuclear periphery. <i>Journal of Cell Biology</i> , 2013, 203, 727-735.	2.3	44
82	The formation and sequestration of heterochromatin during development. <i>FEBS Journal</i> , 2013, 280, 3212-3219.	2.2	8
83	Replication Checkpoint: Tuning and Coordination of Replication Forks in S Phase. <i>Genes</i> , 2013, 4, 388-434.	1.0	52
84	A Rad53 Independent Function of Rad9 Becomes Crucial for Genome Maintenance in the Absence of the RecQ Helicase Sgs1. <i>PLoS ONE</i> , 2013, 8, e81015.	1.1	13
85	Regulating Repression: Roles for the Sir4 N-Terminus in Linker DNA Protection and Stabilization of Epigenetic States. <i>PLoS Genetics</i> , 2012, 8, e1002727.	1.5	15
86	Rare day to highlight rare diseases. <i>Nature</i> , 2012, 481, 265-265.	13.7	4
87	Targeted INO80 enhances subnuclear chromatin movement and ectopic homologous recombination. <i>Genes and Development</i> , 2012, 26, 369-383.	2.7	156
88	Step-Wise Methylation of Histone H3K9 Positions Heterochromatin at the Nuclear Periphery. <i>Cell</i> , 2012, 150, 934-947.	13.5	524
89	Structure and Function in the Budding Yeast Nucleus. <i>Genetics</i> , 2012, 192, 107-129.	1.2	183
90	An N-terminal acidic region of Sgs1 interacts with Rpa70 and recruits Rad53 kinase to stalled forks. <i>EMBO Journal</i> , 2012, 31, 3768-3783.	3.5	74

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91	Increased mobility of double-strand breaks requires Mec1, Rad9 and the homologous recombination machinery. <i>Nature Cell Biology</i> , 2012, 14, 502-509.	4.6	286
92	DNA Replication: Pif1 Pulls the Plug on Stalled Replication Forks. <i>Current Biology</i> , 2012, 22, R404-R405.	1.8	4
93	Nuclear organization in genome stability: SUMO connections. <i>Cell Research</i> , 2011, 21, 474-485.	5.7	86
94	A dual role of H4K16 acetylation in the establishment of yeast silent chromatin. <i>EMBO Journal</i> , 2011, 30, 2610-2621.	3.5	84
95	<i>Caenorhabditis elegans</i> Heterochromatin protein 1 (HPL-2) links developmental plasticity, longevity and lipid metabolism. <i>Genome Biology</i> , 2011, 12, R123.	13.9	52
96	Locking the genome: nuclear organization and cell fate. <i>Current Opinion in Genetics and Development</i> , 2011, 21, 167-174.	1.5	68
97	Nuclear Geometry and Rapid Mitosis Ensure Asymmetric Episome Segregation in Yeast. <i>Current Biology</i> , 2011, 21, 25-33.	1.8	78
98	An EDMD Mutation in <i>C. elegans</i> Lamin Blocks Muscle-Specific Gene Relocation and Compromises Muscle Integrity. <i>Current Biology</i> , 2011, 21, 1603-1614.	1.8	125
99	The PIAS homologue Siz2 regulates perinuclear telomere position and telomerase activity in budding yeast. <i>Nature Cell Biology</i> , 2011, 13, 867-874.	4.6	88
100	Ribosome biogenesis factors bind a nuclear envelope SUN domain protein to cluster yeast telomeres. <i>EMBO Journal</i> , 2011, 30, 3799-3811.	3.5	43
101	Dot1 binding induces chromatin rearrangements by histone methylation-dependent and -independent mechanisms. <i>Epigenetics and Chromatin</i> , 2011, 4, 2.	1.8	28
102	$\hat{1}^3$ H2A is a component of yeast heterochromatin required for telomere elongation. <i>Cell Cycle</i> , 2011, 10, 293-300.	1.3	24
103	Structural basis for the role of the Sir3 AAA domain in silencing: interaction with Sir4 and unmethylated histone H3K79. <i>Genes and Development</i> , 2011, 25, 1835-1846.	2.7	40
104	How Broken DNA Finds Its Template for Repair: A Computational Approach. <i>Progress of Theoretical Physics Supplement</i> , 2011, 191, 20-29.	0.2	23
105	Actin-related proteins in the nucleus: life beyond chromatin remodelers. <i>Current Opinion in Cell Biology</i> , 2010, 22, 383-391.	2.6	61
106	The spatial dynamics of tissue-specific promoters during <i>C. elegans</i> development. <i>Genes and Development</i> , 2010, 24, 766-782.	2.7	180
107	Roles for nuclear organization in the maintenance of genome stability. <i>Epigenomics</i> , 2010, 2, 289-305.	1.0	24
108	Mitotic Expression of Spo13 Alters M-Phase Progression and Nucleolar Localization of Cdc14 in Budding Yeast. <i>Genetics</i> , 2010, 185, 841-854.	1.2	7

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109	Early initiation of a replication origin tethered at the nuclear periphery. <i>Journal of Cell Science</i> , 2010, 123, 1015-1019.	1.2	29
110	Actin-Related Protein Arp6 Influences H2A.Z-Dependent and -Independent Gene Expression and Links Ribosomal Protein Genes to Nuclear Pores. <i>PLoS Genetics</i> , 2010, 6, e1000910.	1.5	52
111	The Budding Yeast Nucleus. <i>Cold Spring Harbor Perspectives in Biology</i> , 2010, 2, a000612-a000612.	2.3	105
112	Cell cycle-dependent phosphorylation of Rad53 kinase by Cdc5 and Cdc28 modulates checkpoint adaptation. <i>Cell Cycle</i> , 2010, 9, 350-363.	1.3	32
113	Visualizing Yeast Chromosomes and Nuclear Architecture. <i>Methods in Enzymology</i> , 2010, 470, 535-567.	0.4	78
114	Yeast telomerase and the SUN domain protein Mps3 anchor telomeres and repress subtelomeric recombination. <i>Genes and Development</i> , 2009, 23, 928-938.	2.7	164
115	The functional importance of telomere clustering: Global changes in gene expression result from SIR factor dispersion. <i>Genome Research</i> , 2009, 19, 611-625.	2.4	110
116	Regulation of Nuclear Positioning and Dynamics of the Silent Mating Type Loci by the Yeast Ku70/Ku80 Complex. <i>Molecular and Cellular Biology</i> , 2009, 29, 835-848.	1.1	71
117	Crosstalk between histone modifications during the DNA damage response. <i>Trends in Cell Biology</i> , 2009, 19, 207-217.	3.6	457
118	Posttranslational modifications of repair factors and histones in the cellular response to stalled replication forks. <i>DNA Repair</i> , 2009, 8, 1089-1100.	1.3	16
119	ATR/Mec1: coordinating fork stability and repair. <i>Current Opinion in Cell Biology</i> , 2009, 21, 237-244.	2.6	136
120	Lte1, Cdc14 and MEN-controlled Cdk inactivation in yeast coordinate rDNA decompaction with late telophase progression. <i>EMBO Journal</i> , 2009, 28, 1562-1575.	3.5	19
121	Silent chromatin at the middle and ends: lessons from yeasts. <i>EMBO Journal</i> , 2009, 28, 2149-2161.	3.5	64
122	The nuclear envelopeâ€”a scaffold for silencing?. <i>Current Opinion in Genetics and Development</i> , 2009, 19, 180-186.	1.5	130
123	Reconstitution of Yeast Silent Chromatin: Multiple Contact Sites and O-AADPR Binding Load SIR Complexes onto Nucleosomes In Vitro. <i>Molecular Cell</i> , 2009, 33, 323-334.	4.5	103
124	Modules for cloningâ€”free chromatin tagging in <i>Saccharomyces cerevisiae</i> . <i>Yeast</i> , 2008, 25, 235-239.	0.8	63
125	Ino80 Chromatin Remodeling Complex Promotes Recovery of Stalled Replication Forks. <i>Current Biology</i> , 2008, 18, 566-575.	1.8	162
126	Controlled exchange of chromosomal arms reveals principles driving telomere interactions in yeast. <i>Genome Research</i> , 2008, 18, 261-271.	2.4	76

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127	Functional Targeting of DNA Damage to a Nuclear Pore-Associated SUMO-Dependent Ubiquitin Ligase. <i>Science</i> , 2008, 322, 597-602.	6.0	401
128	Multiple Pathways Tether Telomeres and Silent Chromatin at the Nuclear Periphery: Functional Implications for Sir-Mediated Repression. <i>Novartis Foundation Symposium</i> , 2008, , 140-165.	1.2	20
129	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. <i>Journal of Cell Science</i> , 2007, 120, 4209-4220.	1.2	53
130	The Origin Recognition Complex Functions in Sister-Chromatid Cohesion in <i>Saccharomyces cerevisiae</i> . <i>Cell</i> , 2007, 128, 85-99.	13.5	104
131	The nuclear envelope and transcriptional control. <i>Nature Reviews Genetics</i> , 2007, 8, 507-517.	7.7	396
132	Replication foci dynamics: replication patterns are modulated by S-phase checkpoint kinases in fission yeast. <i>EMBO Journal</i> , 2007, 26, 1315-1326.	3.5	73
133	Distinct roles for SWR1 and INO80 chromatin remodeling complexes at chromosomal double-strand breaks. <i>EMBO Journal</i> , 2007, 26, 4113-4125.	3.5	292
134	Gene regulation through nuclear organization. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 1049-1055.	3.6	215
135	Nucleus and gene expression. <i>Current Opinion in Cell Biology</i> , 2007, 19, 247-249.	2.6	1
136	Measuring Limits of Telomere Movement on Nuclear Envelope. <i>Biophysical Journal</i> , 2006, 90, L24-L26.	0.2	14
137	In and out of the Replication Factory. <i>Cell</i> , 2006, 125, 1233-1235.	13.5	22
138	Heterochromatin protein 1: don't judge the book by its cover!. <i>Current Opinion in Genetics and Development</i> , 2006, 16, 143-150.	1.5	134
139	A Homotrimer-Heterotrimer Switch in Sir2 Structure Differentiates rDNA and Telomeric Silencing. <i>Molecular Cell</i> , 2006, 21, 825-836.	4.5	42
140	Nuclear pore association confers optimal expression levels for an inducible yeast gene. <i>Nature</i> , 2006, 441, 774-778.	13.7	357
141	Subtelomeric factors antagonize telomere anchoring and Tel1-independent telomere length regulation. <i>EMBO Journal</i> , 2006, 25, 857-867.	3.5	41
142	Repairing subtelomeric DSBs at the nuclear periphery. <i>Trends in Cell Biology</i> , 2006, 16, 225-228.	3.6	5
143	Tracking Individual Chromosomes with Intergrated Arrays of lacop Sites and GFP-laci Repressor Analyzing Position and Dynamics of Chromosomal Loci in <i>Saccharomyces cerevisiae</i> . , 2006, , 359-367.		2
144	The histone code at DNA breaks: a guide to repair?. <i>Nature Reviews Molecular Cell Biology</i> , 2005, 6, 757-765.	16.1	270

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145	Mechanistically distinct roles for Sgs1p in checkpoint activation and replication fork maintenance. <i>EMBO Journal</i> , 2005, 24, 405-417.	3.5	132
146	Temporal separation of replication and recombination requires the intra-S checkpoint. <i>Journal of Cell Biology</i> , 2005, 168, 537-544.	2.3	72
147	ATP-Dependent Chromatin Remodeling and DNA Double-Strand Break Repair. <i>Cell Cycle</i> , 2005, 4, 1011-1014.	1.3	99
148	Replisome instability, fork collapse, and gross chromosomal rearrangements arise synergistically from Mec1 kinase and RecQ helicase mutations. <i>Genes and Development</i> , 2005, 19, 3055-3069.	2.7	171
149	Automatic tracking of individual fluorescence particles: application to the study of chromosome dynamics. <i>IEEE Transactions on Image Processing</i> , 2005, 14, 1372-1383.	6.0	391
150	Chromosome looping in yeast. <i>Journal of Cell Biology</i> , 2005, 168, 375-387.	2.3	186
151	Separation of silencing from perinuclear anchoring functions in yeast Ku80, Sir4 and Esc1 proteins. <i>EMBO Journal</i> , 2004, 23, 1301-1312.	3.5	237
152	Multiple pathways for telomere tethering: functional implications of subnuclear position for heterochromatin formation. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 2004, 1677, 120-128.	2.4	63
153	Long-range compaction and flexibility of interphase chromatin in budding yeast analyzed by high-resolution imaging techniques. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 16495-16500.	3.3	274
154	The Function of Nuclear Architecture: A Genetic Approach. <i>Annual Review of Genetics</i> , 2004, 38, 305-345.	3.2	200
155	Sir-Mediated Repression Can Occur Independently of Chromosomal and Subnuclear Contexts. <i>Cell</i> , 2004, 119, 955-967.	13.5	168
156	Recruitment of the INO80 Complex by H2A Phosphorylation Links ATP-Dependent Chromatin Remodeling with DNA Double-Strand Break Repair. <i>Cell</i> , 2004, 119, 777-788.	13.5	538
157	Redundancy, insult-specific sensors and thresholds: unlocking the S-phase checkpoint response. <i>Current Opinion in Genetics and Development</i> , 2004, 14, 292-300.	1.5	30
158	The Function of Telomere Clustering in Yeast: The Circe Effect. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2004, 69, 327-338.	2.0	40
159	DNA polymerase stabilization at stalled replication forks requires Mec1 and the RecQ helicase Sgs1. <i>EMBO Journal</i> , 2003, 22, 4325-4336.	3.5	301
160	RecQ helicases: multiple roles in genome maintenance. <i>Trends in Cell Biology</i> , 2003, 13, 493-501.	3.6	108
161	Methods for Visualizing Chromatin Dynamics in Living Yeast. <i>Methods in Enzymology</i> , 2003, 375, 345-365.	0.4	47
162	Modulation of drug sensitivity in yeast cells by the ATP-binding domain of human DNA topoisomerase II α . <i>Nucleic Acids Research</i> , 2003, 31, 5714-5722.	6.5	17

#	ARTICLE	IF	CITATIONS
163	An N-terminal domain of Dbf4p mediates interaction with both origin recognition complex (ORC) and Rad53p and can deregulate late origin firing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 16087-16092.	3.3	88
164	ORC and the intra-S-phase checkpoint: a threshold regulates Rad53p activation in S phase. <i>Genes and Development</i> , 2002, 16, 3236-3252.	2.7	188
165	In vitro DNA replication assays in yeast extracts. <i>Methods in Enzymology</i> , 2002, 351, 184-199.	0.4	2
166	Visualizing Chromatin Dynamics in Interphase Nuclei. <i>Science</i> , 2002, 296, 1412-1416.	6.0	300
167	RecQ helicases: at the heart of genetic stability. <i>FEBS Letters</i> , 2002, 529, 43-48.	1.3	49
168	Myosin-like proteins 1 and 2 are not required for silencing or telomere anchoring, but act in the Tel1 pathway of telomere length control. <i>Journal of Structural Biology</i> , 2002, 140, 79-91.	1.3	76
169	Live Imaging of Telomeres. <i>Current Biology</i> , 2002, 12, 2076-2089.	1.8	276
170	Nuclear organization and silencing: putting things in their place. <i>Nature Cell Biology</i> , 2002, 4, E53-E55.	4.6	54
171	Intracellular trafficking of yeast telomerase components. <i>EMBO Reports</i> , 2002, 3, 652-659.	2.0	66
172	RecQ helicases and genome stability: lessons from model organisms and human disease. <i>Swiss Medical Weekly</i> , 2002, 132, 433-42.	0.8	19
173	Analysis of Etoposide Binding to Subdomains of Human DNA Topoisomerase II α in the Absence of DNA. <i>Biochemistry</i> , 2001, 40, 1624-1634.	1.2	52
174	Chromosome Dynamics in the Yeast Interphase Nucleus. <i>Science</i> , 2001, 294, 2181-2186.	6.0	431
175	The molecular biology of the SIR proteins. <i>Gene</i> , 2001, 279, 1-16.	1.0	257
176	Positions of Potential: Nuclear Organization and Gene Expression. <i>Cell</i> , 2001, 104, 639-642.	13.5	130
177	Ku α -deficient yeast strains exhibit alternative states of silencing competence. <i>EMBO Reports</i> , 2001, 2, 203-210.	2.0	53
178	A cytosolic NAD-dependent deacetylase, Hst2p, can modulate nucleolar and telomeric silencing in yeast. <i>EMBO Journal</i> , 2001, 20, 197-209.	3.5	147
179	From snapshots to moving pictures: new perspectives on nuclear organization. <i>Trends in Cell Biology</i> , 2001, 11, 519-525.	3.6	36
180	Turning telomeres off and on. <i>Current Opinion in Cell Biology</i> , 2001, 13, 281-289.	2.6	61

#	ARTICLE	IF	CITATIONS
181	The Positioning and Dynamics of Origins of Replication in the Budding Yeast Nucleus. <i>Journal of Cell Biology</i> , 2001, 152, 385-400.	2.3	178
182	Ectopic expression of human topoisomerase II \pm fragments and etoposide resistance in mammalian cells. <i>International Journal of Cancer</i> , 2000, 88, 99-107.	2.3	9
183	MAP kinase signaling induces nuclear reorganization in budding yeast. <i>Current Biology</i> , 2000, 10, 373-382.	1.8	42
184	The Dynamics of Yeast Telomeres and Silencing Proteins through the Cell Cycle. <i>Journal of Structural Biology</i> , 2000, 129, 159-174.	1.3	91
185	A Sense of the End. <i>Science</i> , 2000, 288, 1377-1379.	6.0	68
186	Analysis of Sir2p Domains Required for rDNA and Telomeric Silencing in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2000, 154, 1069-1083.	1.2	53
187	The yeast Sgs1p helicase acts upstream of Rad53p in the DNA replication checkpoint and colocalizes with Rad53p in S-phase-specific foci. <i>Genes and Development</i> , 2000, 14, 81-96.	2.7	229
188	Analysis of nuclear organization in <i>Saccharomyces cerevisiae</i> . <i>Methods in Enzymology</i> , 1999, 304, 663-672.	0.4	30
189	Taz1p and Teb1p, two telobox proteins in <i>Schizosaccharomyces pombe</i> , recognize different telomere-related DNA sequences. <i>Nucleic Acids Research</i> , 1999, 27, 4687-4694.	6.5	34
190	The nucleolus: Nucleolar space for RENT. <i>Current Biology</i> , 1999, 9, R575-R576.	1.8	45
191	Nuclear compartments and gene regulation. <i>Current Opinion in Genetics and Development</i> , 1999, 9, 199-205.	1.5	238
192	Relocalization of Telomeric Ku and SIR Proteins in Response to DNA Strand Breaks in Yeast. <i>Cell</i> , 1999, 97, 621-633.	13.5	438
193	The Cytochrome b5 Tail Anchors and Stabilizes Subdomains of Human DNA Topoisomerase II \pm in the Cytoplasm of Retrovirally Infected Mammalian Cells. <i>Experimental Cell Research</i> , 1999, 249, 308-319.	1.2	5
194	In Vitro DNA Replication in Yeast Nuclear Extracts. <i>Methods</i> , 1999, 18, 368-376.	1.9	7
195	Cyclin B-Cdk1 Kinase Stimulates ORC- and Cdc6-Independent Steps of Semiconservative Plasmid Replication in Yeast Nuclear Extracts. <i>Molecular and Cellular Biology</i> , 1999, 19, 1226-1241.	1.1	24
196	A role for the Cdc7 kinase regulatory subunit Dbf4p in the formation of initiation-competent origins of replication. <i>Genes and Development</i> , 1999, 13, 2159-2176.	2.7	114
197	Mutation of yeast Ku genes disrupts the subnuclear organization of telomeres. <i>Current Biology</i> , 1998, 8, 653-657.	1.8	330
198	Sif2p interacts with the Sir4p amino-terminal domain and antagonizes telomeric silencing in yeast. <i>Current Biology</i> , 1998, 8, 787-S2.	1.8	38

#	ARTICLE	IF	CITATIONS
199	Meiotic behaviours of chromosomes and microtubules in budding yeast: relocalization of centromeres and telomeres during meiotic prophase. <i>Genes To Cells</i> , 1998, 3, 587-601.	0.5	71
200	New systems for replicating DNA in vitro. <i>Current Opinion in Cell Biology</i> , 1998, 10, 304-310.	2.6	20
201	Chromosomes and expression mechanisms New excitement over an old word: "chromatin". <i>Current Opinion in Genetics and Development</i> , 1998, 8, 137-139.	1.5	3
202	Chromosome dynamics: the SMC protein family. <i>Current Opinion in Genetics and Development</i> , 1998, 8, 254-259.	1.5	80
203	Structural Maintenance of Chromosomes Protein C-terminal Domains Bind Preferentially to DNA with Secondary Structure. <i>Journal of Biological Chemistry</i> , 1998, 273, 24088-24094.	1.6	93
204	Semi-conservative replication in yeast nuclear extracts requires Dna2 helicase and supercoiled template 1 Edited by M. Yaniv. <i>Journal of Molecular Biology</i> , 1998, 281, 631-649.	2.0	28
205	Functional Interaction between the Estrogen Receptor and CTF1: Analysis of the Vitellogenin Gene B1 Promoter in Yeast. <i>Molecular Endocrinology</i> , 1998, 12, 1525-1541.	3.7	7
206	Functional Characterization of the N Terminus of Sir3p. <i>Molecular and Cellular Biology</i> , 1998, 18, 6110-6120.	1.1	41
207	Targeting Sir Proteins to Sites of Action: A General Mechanism for Regulated Repression. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 1998, 63, 401-412.	2.0	36
208	Nuclear Organization and Silencing: Trafficking of Sir Proteins. <i>Novartis Foundation Symposium</i> , 1998, 214, 114-132.	1.2	8
209	ORC-dependent and origin-specific initiation of DNA replication at defined foci in isolated yeast nuclei. <i>Genes and Development</i> , 1997, 11, 1504-1518.	2.7	56
210	Redistribution of Silencing Proteins from Telomeres to the Nucleolus Is Associated with Extension of Life Span in <i>S. cerevisiae</i> . <i>Cell</i> , 1997, 89, 381-391.	13.5	368
211	Heterochromatin: a meiotic matchmaker?. <i>Trends in Cell Biology</i> , 1997, 7, 201-205.	3.6	39
212	Localization of Sir2p: the nucleolus as a compartment for silent information regulators. <i>EMBO Journal</i> , 1997, 16, 3243-3255.	3.5	229
213	Ectopic expression of inactive forms of yeast DNA topoisomerase II confers resistance to the anti-tumour drug, etoposide. <i>British Journal of Cancer</i> , 1996, 73, 1201-1209.	2.9	25
214	Nuclear organization and transcriptional silencing in yeast. <i>Experientia</i> , 1996, 52, 1136-1147.	1.2	58
215	Chromatin: A sticky silence. <i>Current Biology</i> , 1996, 6, 1222-1225.	1.8	26
216	Evidence for silencing compartments within the yeast nucleus: a role for telomere proximity and Sir protein concentration in silencer-mediated repression. <i>Genes and Development</i> , 1996, 10, 1796-1811.	2.7	256

#	ARTICLE	IF	CITATIONS
217	The Telobox, a Myb-Related Telomeric DNA Binding Motif Found in Proteins from Yeast, Plants and Human. <i>Nucleic Acids Research</i> , 1996, 24, 1294-1303.	6.5	218
218	The clustering of telomeres and colocalization with Rap1, Sir3, and Sir4 proteins in wild-type <i>Saccharomyces cerevisiae</i> .. <i>Journal of Cell Biology</i> , 1996, 134, 1349-1363.	2.3	440
219	Chromosome Structure: Coiling up chromosomes. <i>Current Biology</i> , 1995, 5, 357-360.	1.8	39
220	DNA topoisomerase II mutations and resistance to anti-tumor drugs. <i>BioEssays</i> , 1995, 17, 767-774.	1.2	70
221	The carboxy termini of Sir4 and Rap1 affect Sir3 localization: evidence for a multicomponent complex required for yeast telomeric silencing.. <i>Journal of Cell Biology</i> , 1995, 129, 909-924.	2.3	181
222	Histone H3 and H4 N-termini interact with SIR3 and SIR4 proteins: A molecular model for the formation of heterochromatin in yeast. <i>Cell</i> , 1995, 80, 583-592.	13.5	799
223	RAP1 stimulates single- to double-strand association of yeast telomeric DNA: implications for telomere - telomere interactions. <i>Nucleic Acids Research</i> , 1994, 22, 5310-5320.	6.5	39
224	The yeast protein encoded by PUB1 binds T-rich single stranded DNA. <i>Nucleic Acids Research</i> , 1994, 22, 32-40.	6.5	17
225	Phosphorylation of the C-terminal Domain of Yeast Topoisomerase II by Casein Kinase II Affects DNA-Protein Interaction. <i>Journal of Molecular Biology</i> , 1994, 243, 10-24.	2.0	32
226	Imaging the Asymmetrical DNA Bend Induced by Repressor Activator Protein 1 with Scanning Tunneling Microscopy. <i>Journal of Structural Biology</i> , 1994, 113, 1-12.	1.3	48
227	Telomere maintenance and gene repression: a common end?. <i>Current Opinion in Cell Biology</i> , 1994, 6, 373-379.	2.6	45
228	Telomeres and the functional architecture of the nucleus. <i>Trends in Cell Biology</i> , 1993, 3, 128-134.	3.6	140
229	Distortion of the DNA Double Helix by RAP1 at Silencers and Multiple Telomeric Binding Sites. <i>Journal of Molecular Biology</i> , 1993, 231, 293-310.	2.0	201
230	SIR3 and SIR4 proteins are required for the positioning and integrity of yeast telomeres. <i>Cell</i> , 1993, 75, 543-555.	13.5	397
231	The Positioning of Yeast Telomeres Depends on SIR3, SIR4, and the Integrity of the Nuclear Membrane. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 1993, 58, 733-746.	2.0	23
232	Regulation of topoisomerase II by phosphorylation: a role for casein kinase II. <i>Journal of Cell Science</i> , 1993, 104, 219-225.	1.2	70
233	Localization of RAP1 and topoisomerase II in nuclei and meiotic chromosomes of yeast. <i>Journal of Cell Biology</i> , 1992, 117, 935-948.	2.3	301
234	Functional Aspects of Chromosome Organization: Scaffold Attachment Regions and their Ligands. <i>Advances in Molecular and Cell Biology</i> , 1992, 4, 75-101.	0.1	3

#	ARTICLE	IF	CITATIONS
235	Topoisomerase II: its functions and phosphorylation. <i>Antonie Van Leeuwenhoek</i> , 1992, 62, 15-24.	0.7	22
236	DNA loops: structural and functional properties of scaffold-attached regions. <i>Molecular Microbiology</i> , 1992, 6, 419-423.	1.2	72
237	Topoisomerase II: its functions and phosphorylation. , 1992, , 15-24.		0
238	Replication origins, factors and attachment sites. <i>Current Opinion in Cell Biology</i> , 1991, 3, 407-413.	2.6	24
239	Identification and purification of a protein that binds the yeast ARS consensus sequence. <i>Cell</i> , 1991, 64, 951-960.	13.5	94
240	Ultrastructural cryoimmunocytochemistry is a convenient tool for the study of DNA replication in cultured cells. <i>Journal of Electron Microscopy Technique</i> , 1991, 18, 91-105.	1.1	22
241	Preparation and characterization of yeast nuclear extracts for efficient RNA polymerase B (II)-dependent transcription <i>in vitro</i> . <i>Nucleic Acids Research</i> , 1990, 18, 7033-7039.	6.5	35
242	The composition and morphology of yeast nuclear scaffolds. <i>Journal of Cell Science</i> , 1990, 96, 439-450.	1.2	46
243	RAP-1 factor is necessary for DNA loop formation <i>in vitro</i> at the silent mating type locus HML. <i>Cell</i> , 1989, 57, 725-737.	13.5	208
244	Chromosomal ARS and CEN elements bind specifically to the yeast nuclear scaffold. <i>Cell</i> , 1988, 54, 967-978.	13.5	282
245	Scaffold attachment of DNA loops in metaphase chromosomes. <i>Journal of Molecular Biology</i> , 1988, 200, 101-109.	2.0	142
246	Improved methods for the isolation of individual and clustered mitotic chromosomes. <i>Experimental Cell Research</i> , 1987, 173, 85-98.	1.2	74
247	Cohabitation of scaffold binding regions with upstream/enhancer elements of three developmentally regulated genes of <i>D. melanogaster</i> . <i>Cell</i> , 1986, 46, 521-530.	13.5	621
248	Metaphase chromosome structure. <i>Journal of Molecular Biology</i> , 1986, 188, 613-629.	2.0	543
249	How mitochondria import proteins. <i>BBA - Biomembranes</i> , 1984, 779, 65-87.	7.9	415
250	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. <i>FEBS Journal</i> , 1983, 135, 457-463.	0.2	29
251	[23] Assessing import of proteins into mitochondria: An overview. <i>Methods in Enzymology</i> , 1983, 97, 245-254.	0.4	6
252	[32] Import of polypeptides into isolated yeast mitochondria. <i>Methods in Enzymology</i> , 1983, 97, 329-336.	0.4	27

#	ARTICLE	IF	CITATIONS
253	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.	3.3	200