

Andres Aguilera

List of Publications by Year in descending order

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214
papers

18,336
citations

13068

68
h-index

15683

125
g-index

236
all docs

236
docs citations

236
times ranked

13483
citing authors

#	ARTICLE	IF	CITATIONS
1	MutS ¹² regulates G4-associated telomeric R-loops to maintain telomere integrity in ALT cancer cells. <i>Cell Reports</i> , 2022, 39, 110602.	2.9	13
2	RNase H1 Hybrid-Binding Domain-Based Tools for Cellular Biology Studies of DNA-RNA Hybrids in Mammalian Cells. <i>Methods in Molecular Biology</i> , 2022, , 115-125.	0.4	5
3	WASp modulates RPA function on single-stranded DNA in response to replication stress and DNA damage. <i>Nature Communications</i> , 2022, 13, .	5.8	13
4	Origin matters: spontaneous DNA-RNA hybrids do not form in trans as a source of genome instability. <i>Current Genetics</i> , 2021, 67, 93-97.	0.8	5
5	BRCA2 promotes DNA-RNA hybrid resolution by DDX5 helicase at DNA breaks to facilitate their repair. <i>EMBO Journal</i> , 2021, 40, e106018.	3.5	63
6	A new interaction between BRCA2 and DDX5 promotes the repair of DNA breaks at transcribed chromatin. <i>Molecular and Cellular Oncology</i> , 2021, 8, 1910474.	0.3	4
7	R-Loop-Mediated ssDNA Breaks Accumulate Following Short-Term Exposure to the HDAC Inhibitor Romidepsin. <i>Molecular Cancer Research</i> , 2021, 19, 1361-1374.	1.5	12
8	The SWI/SNF chromatin remodeling complex helps resolve R-loop-mediated transcription-replication conflicts. <i>Nature Genetics</i> , 2021, 53, 1050-1063.	9.4	85
9	The human nucleoporin Tpr protects cells from RNA-mediated replication stress. <i>Nature Communications</i> , 2021, 12, 3937.	5.8	20
10	DNA-RNA hybrids at DSBs interfere with repair by homologous recombination. <i>ELife</i> , 2021, 10, .	2.8	26
11	Harmful R-loops are prevented via different cell cycle-specific mechanisms. <i>Nature Communications</i> , 2021, 12, 4451.	5.8	32
12	A transcription-based mechanism for oncogenic β -catenin-induced lethality in BRCA1/2-deficient cells. <i>Nature Communications</i> , 2021, 12, 4919.	5.8	6
13	The SWI/SNF complex, transcription-replication conflicts and cancer: a connection with high therapeutic potential. <i>Molecular and Cellular Oncology</i> , 2021, 8, 1976582.	0.3	2
14	A CDK-regulated chromatin segregase promoting chromosome replication. <i>Nature Communications</i> , 2021, 12, 5224.	5.8	6
15	<i>C. elegans</i> THSC/TREX-2 deficiency causes replication stress and genome instability. <i>Journal of Cell Science</i> , 2021, 134, .	1.2	1
16	ADAR-mediated RNA editing of DNA:RNA hybrids is required for DNA double strand break repair. <i>Nature Communications</i> , 2021, 12, 5512.	5.8	30
17	Heterogeneity of DNA damage incidence and repair in different chromatin contexts. <i>DNA Repair</i> , 2021, 107, 103210.	1.3	4
18	Detection of DNA Double-Strand Breaks by β -H2AX Immunodetection. <i>Methods in Molecular Biology</i> , 2021, 2153, 1-8.	0.4	9

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19	<i>VID22</i> counteracts G-quadruplex-induced genome instability. <i>Nucleic Acids Research</i> , 2021, 49, 12785-12804.	6.5	5
20	Analysis of repair of replication-born double-strand breaks by sister chromatid recombination in yeast. <i>Methods in Enzymology</i> , 2021, 661, 121-138.	0.4	0
21	The role of chromatin at transcription-replication conflicts as a genome safeguard. <i>Biochemical Society Transactions</i> , 2021, 49, 2727-2736.	1.6	8
22	Looping the (R) Loop in DSB Repair via RNA Methylation. <i>Molecular Cell</i> , 2020, 79, 361-362.	4.5	5
23	UAP56/DDX39B is a major cotranscriptional RNA-DNA helicase that unwinds harmful R loops genome-wide. <i>Genes and Development</i> , 2020, 34, 898-912.	2.7	83
24	Spontaneous DNA-RNA hybrids: differential impacts throughout the cell cycle. <i>Cell Cycle</i> , 2020, 19, 525-531.	1.3	3
25	Histone deacetylases facilitate the accurate repair of broken forks. <i>Molecular and Cellular Oncology</i> , 2020, 7, 1705731.	0.3	7
26	TDP-43 mutations link Amyotrophic Lateral Sclerosis with R-loop homeostasis and R loop-mediated DNA damage. <i>PLoS Genetics</i> , 2020, 16, e1009260.	1.5	54
27	Homologous recombination and Mus81 promote replication completion in response to replication fork blockage. <i>EMBO Reports</i> , 2020, 21, e49367.	2.0	28
28	Harmful DNA:RNA hybrids are formed in cis and in a Rad51-independent manner. <i>ELife</i> , 2020, 9, .	2.8	20
29	Histone H3E73Q and H4E53A mutations cause recombinogenic DNA damage. <i>Microbial Cell</i> , 2020, 7, 190-198.	1.4	0
30	Title is missing!. , 2020, 16, e1009260.		0
31	Title is missing!. , 2020, 16, e1009260.		0
32	Title is missing!. , 2020, 16, e1009260.		0
33	Title is missing!. , 2020, 16, e1009260.		0
34	Title is missing!. , 2020, 16, e1009260.		0
35	Title is missing!. , 2020, 16, e1009260.		0
36	Depletion of the MFAP1/SPP381 Splicing Factor Causes R-Loop-Independent Genome Instability. <i>Cell Reports</i> , 2019, 28, 1551-1563.e7.	2.9	13

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37	What causes an RNA-DNA hybrid to compromise genome integrity?. DNA Repair, 2019, 81, 102660.	1.3	14
38	R Loops: From Physiological to Pathological Roles. Cell, 2019, 179, 604-618.	13.5	395
39	Elongation Factor TFIIS Prevents Transcription Stress and R-Loop Accumulation to Maintain Genome Stability. Molecular Cell, 2019, 76, 57-69.e9.	4.5	79
40	Transcription-mediated replication hindrance: a major driver of genome instability. Genes and Development, 2019, 33, 1008-1026.	2.7	171
41	Guidelines for DNA recombination and repair studies: Cellular assays of DNA repair pathways. Microbial Cell, 2019, 6, 1-64.	1.4	47
42	The Nup84 complex coordinates the DNA damage response to warrant genome integrity. Nucleic Acids Research, 2019, 47, 4054-4067.	6.5	18
43	The THO Complex as a Paradigm for the Prevention of Cotranscriptional R-Loops. Cold Spring Harbor Symposia on Quantitative Biology, 2019, 84, 105-114.	2.0	30
44	Rpd3L and Hda1 histone deacetylases facilitate repair of broken forks by promoting sister chromatid cohesion. Nature Communications, 2019, 10, 5178.	5.8	13
45	R-Loops as Promoters of Antisense Transcription. Molecular Cell, 2019, 76, 529-530.	4.5	5
46	The DNA damage response acts as a safeguard against harmful DNA-RNA hybrids of different origins. EMBO Reports, 2019, 20, e47250.	2.0	72
47	A Meiotic Checkpoint Alters Repair Partner Bias to Permit Inter-sister Repair of Persistent DSBs. Cell Reports, 2019, 26, 775-787.e5.	2.9	24
48	The Antitumor Drugs Trabectedin and Lurbinectedin Induce Transcription-Dependent Replication Stress and Genome Instability. Molecular Cancer Research, 2019, 17, 773-782.	1.5	28
49	Multiple signaling kinases target Mrc1 to prevent genomic instability triggered by transcription-replication conflicts. Nature Communications, 2018, 9, 379.	5.8	32
50	Epigenetic features of human telomeres. Nucleic Acids Research, 2018, 46, 2347-2355.	6.5	74
51	Coordinated Activity of Y Family TLS Polymerases and EXO1 Protects Non-S Phase Cells from UV-Induced Cytotoxic Lesions. Molecular Cell, 2018, 70, 34-47.e4.	4.5	26
52	Detection of DNA-RNA Hybrids In Vivo. Methods in Molecular Biology, 2018, 1672, 347-361.	0.4	54
53	Gene gating at nuclear pores prevents the formation of R loops. Molecular and Cellular Oncology, 2018, 5, e1405140.	0.3	2
54	Guidelines and recommendations on yeast cell death nomenclature. Microbial Cell, 2018, 5, 4-31.	1.4	158

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55	Human mitochondrial degradosome prevents harmful mitochondrial R loops and mitochondrial genome instability. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 11024-11029.	3.3	67
56	Yra1-bound RNA-DNA hybrids cause orientation-independent transcription-replication collisions and telomere instability. <i>Genes and Development</i> , 2018, 32, 965-977.	2.7	58
57	DNA-RNA hybrids: the risks of DNA breakage during transcription. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 439-443.	3.6	119
58	Histone Mutants Separate R Loop Formation from Genome Instability Induction. <i>Molecular Cell</i> , 2017, 66, 597-609.e5.	4.5	87
59	Human THO-Sin3A interaction reveals new mechanisms to prevent R-loops that cause genome instability. <i>EMBO Journal</i> , 2017, 36, 3532-3547.	3.5	91
60	Physical proximity of chromatin to nuclear pores prevents harmful R loop accumulation contributing to maintain genome stability. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 10942-10947.	3.3	38
61	Differential effect of the overexpression of Rad2/XPG family endonucleases on genome integrity in yeast and human cells. <i>DNA Repair</i> , 2017, 57, 66-75.	1.3	7
62	The need to regulate replication fork speed. <i>Science</i> , 2017, 358, 722-723.	6.0	5
63	The Role of Replication-Associated Repair Factors on R-Loops. <i>Genes</i> , 2017, 8, 171.	1.0	40
64	A new role for Rrm3 in repair of replication-born DNA breakage by sister chromatid recombination. <i>PLoS Genetics</i> , 2017, 13, e1006781.	1.5	15
65	The Smc5/6 complex regulates the yeast Mph1 helicase at RNA-DNA hybrid-mediated DNA damage. <i>PLoS Genetics</i> , 2017, 13, e1007136.	1.5	47
66	International Institutions: For better or worst. <i>Reflexión Política</i> , 2017, 19, 6-15.	0.0	0
67	High-Resolution Mapping of Homologous Recombination Events in rad3 Hyper-Recombination Mutants in Yeast. <i>PLoS Genetics</i> , 2016, 12, e1005938.	1.5	8
68	Excess of Yra1 RNA-Binding Factor Causes Transcription-Dependent Genome Instability, Replication Impairment and Telomere Shortening. <i>PLoS Genetics</i> , 2016, 12, e1005966.	1.5	21
69	Roles of human POLD1 and POLD3 in genome stability. <i>Scientific Reports</i> , 2016, 6, 38873.	1.6	46
70	Transcription-replication conflicts: how they occur and how they are resolved. <i>Nature Reviews Molecular Cell Biology</i> , 2016, 17, 553-563.	16.1	292
71	FANCD2 Facilitates Replication through Common Fragile Sites. <i>Molecular Cell</i> , 2016, 64, 388-404.	4.5	151
72	Transcription as a Threat to Genome Integrity. <i>Annual Review of Biochemistry</i> , 2016, 85, 291-317.	5.0	145

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73	A unified model for the molecular basis of Xeroderma pigmentosum-Cockayne Syndrome. <i>Rare Diseases (Austin, Tex)</i> , 2015, 3, e1079362.	1.8	12
74	Polycomb RING1A/RING1B-dependent histone H2A monoubiquitylation at pericentromeric regions promotes S phase progression. <i>Journal of Cell Science</i> , 2015, 128, 3660-71.	1.2	25
75	Interdependence of the Rad50 Hook and Globular Domain Functions. <i>Molecular Cell</i> , 2015, 57, 479-491.	4.5	46
76	Replication stress and cancer. <i>Nature Reviews Cancer</i> , 2015, 15, 276-289.	12.8	755
77	Role for RNA:DNA hybrids in origin-independent replication priming in a eukaryotic system. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 5779-5784.	3.3	90
78	Methods to Study Transcription-Coupled Repair in Chromatin. <i>Methods in Molecular Biology</i> , 2015, 1288, 273-288.	0.4	4
79	R loops: new modulators of genome dynamics and function. <i>Nature Reviews Genetics</i> , 2015, 16, 583-597.	7.7	611
80	RNA polymerase II contributes to preventing transcription-mediated replication fork stalls. <i>EMBO Journal</i> , 2015, 34, 236-250.	3.5	35
81	The Fanconi Anemia Pathway Protects Genome Integrity from R-loops. <i>PLoS Genetics</i> , 2015, 11, e1005674.	1.5	244
82	Npl3, a new link between RNA-binding proteins and the maintenance of genome integrity. <i>Cell Cycle</i> , 2014, 13, 1524-1529.	1.3	8
83	Cleavage Factor I Links Transcription Termination to DNA Damage Response and Genome Integrity Maintenance in <i>Saccharomyces cerevisiae</i> . <i>PLoS Genetics</i> , 2014, 10, e1004203.	1.5	18
84	The rem Mutations in the ATP-Binding Groove of the Rad3/XPD Helicase Lead to Xeroderma pigmentosum-Cockayne Syndrome-Like Phenotypes. <i>PLoS Genetics</i> , 2014, 10, e1004859.	1.5	8
85	Transcription-Coupled Nucleotide Excision Repair Factors Promote R-Loop-Induced Genome Instability. <i>Molecular Cell</i> , 2014, 56, 777-785.	4.5	445
86	A genome-wide function of THSC/TREX-2 at active genes prevents transcription-replication collisions. <i>Nucleic Acids Research</i> , 2014, 42, 12000-12014.	6.5	17
87	The yeast and human FACT chromatin-reorganizing complexes solve R-loop-mediated transcription-replication conflicts. <i>Genes and Development</i> , 2014, 28, 735-748.	2.7	152
88	Transcription and Recombination: When RNA Meets DNA. <i>Cold Spring Harbor Perspectives in Biology</i> , 2014, 6, a016543-a016543.	2.3	65
89	BRCA2 prevents R-loop accumulation and associates with TREX-2 mRNA export factor PCID2. <i>Nature</i> , 2014, 511, 362-365.	13.7	428
90	Causes of Genome Instability. <i>Annual Review of Genetics</i> , 2013, 47, 1-32.	3.2	372

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91	Coordinated control of replication and transcription by a SAPK protects genomic integrity. <i>Nature</i> , 2013, 493, 116-119.	13.7	76
92	R Loops Are Linked to Histone H3 S10 Phosphorylation and Chromatin Condensation. <i>Molecular Cell</i> , 2013, 52, 583-590.	4.5	229
93	Transcription-Associated Genome Instability. <i>Chemical Reviews</i> , 2013, 113, 8638-8661.	23.0	53
94	Transcription coupled repair at the interface between transcription elongation and mRNA biogenesis. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2013, 1829, 141-150.	0.9	36
95	Yeast Pol4 Promotes Tel1-Regulated Chromosomal Translocations. <i>PLoS Genetics</i> , 2013, 9, e1003656.	1.5	7
96	Histone H3K56 Acetylation, Rad52, and Non-DNA Repair Factors Control Double-Strand Break Repair Choice with the Sister Chromatid. <i>PLoS Genetics</i> , 2013, 9, e1003237.	1.5	84
97	Competing roles of DNA end resection and non-homologous end joining functions in the repair of replication-born double-strand breaks by sister-chromatid recombination. <i>Nucleic Acids Research</i> , 2013, 41, 1669-1683.	6.5	14
98	The Npl3 hnRNP prevents R-loop-mediated transcription-associated replication conflicts and genome instability. <i>Genes and Development</i> , 2013, 27, 2445-2458.	2.7	72
99	R-Loop Mediated Transcription-Associated Recombination in <i>trf4^Δ</i> Mutants Reveals New Links between RNA Surveillance and Genome Integrity. <i>PLoS ONE</i> , 2013, 8, e65541.	1.1	37
100	Topological constraints impair RNA polymerase II transcription and causes instability of plasmid-borne convergent genes. <i>Nucleic Acids Research</i> , 2012, 40, 1050-1064.	6.5	23
101	Complex Chromosomal Rearrangements Mediated by Break-Induced Replication Involve Structure-Selective Endonucleases. <i>PLoS Genetics</i> , 2012, 8, e1002979.	1.5	44
102	Architecture and nucleic acids recognition mechanism of the THO complex, an mRNA assembly factor. <i>EMBO Journal</i> , 2012, 31, 1605-1616.	3.5	79
103	Distinct Roles of Mus81, Yen1, Slx1-Slx4, and Rad1 Nucleases in the Repair of Replication-Born Double-Strand Breaks by Sister Chromatid Exchange. <i>Molecular and Cellular Biology</i> , 2012, 32, 1592-1603.	1.1	58
104	R-loops cause replication impairment and genome instability during meiosis. <i>EMBO Reports</i> , 2012, 13, 923-929.	2.0	67
105	R Loops: From Transcription Byproducts to Threats to Genome Stability. <i>Molecular Cell</i> , 2012, 46, 115-124.	4.5	822
106	New clues to understand the role of THO and other functionally related factors in mRNA biogenesis. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2012, 1819, 514-520.	0.9	75
107	The <i>Caenorhabditis elegans</i> THO Complex Is Required for the Mitotic Cell Cycle and Development. <i>PLoS ONE</i> , 2012, 7, e52447.	1.1	15
108	The Replication Checkpoint Protects Fork Stability by Releasing Transcribed Genes from Nuclear Pores. <i>Cell</i> , 2011, 146, 233-246.	13.5	204

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109	Yeast Sen1 Helicase Protects the Genome from Transcription-Associated Instability. <i>Molecular Cell</i> , 2011, 41, 21-32.	4.5	301
110	A novel assay identifies transcript elongation roles for the Nup84 complex and RNA processing factors. <i>EMBO Journal</i> , 2011, 30, 1953-1964.	3.5	50
111	Differential expression of THOC1 and ALY mRNA biogenesis/export factors in human cancers. <i>BMC Cancer</i> , 2011, 11, 77.	1.1	64
112	Nab2 functions in the metabolism of RNA driven by polymerases II and III. <i>Molecular Biology of the Cell</i> , 2011, 22, 2729-2740.	0.9	33
113	Zim17/Tim15 links mitochondrial iron-sulfur cluster biosynthesis to nuclear genome stability. <i>Nucleic Acids Research</i> , 2011, 39, 6002-6015.	6.5	23
114	Control of the function of the transcription and repair factor TFIIH by the action of the cochaperone Ydj1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 15300-15305.	3.3	7
115	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
116	New Suppressors of THO Mutations Identify Thp3 (Ypr045c)-Csn12 as a Protein Complex Involved in Transcription Elongation. <i>Molecular and Cellular Biology</i> , 2011, 31, 674-685.	1.1	14
117	The Rad50 coiled-coil domain is indispensable for Mre11 complex functions. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 1124-1131.	3.6	88
118	Genome Instability and Transcription Elongation Impairment in Human Cells Depleted of THO/TREX. <i>PLoS Genetics</i> , 2011, 7, e1002386.	1.5	194
119	AID Induces Double-Strand Breaks at Immunoglobulin Switch Regions and c-MYC Causing Chromosomal Translocations in Yeast THO Mutants. <i>PLoS Genetics</i> , 2011, 7, e1002009.	1.5	39
120	Genetic and Molecular Analysis of Mitotic Recombination in <i>Saccharomyces cerevisiae</i> . <i>Methods in Molecular Biology</i> , 2011, 745, 151-172.	0.4	16
121	The THO complex as a key mRNA biogenesis factor in development and cell differentiation. <i>Journal of Biology</i> , 2010, 9, 6.	2.7	21
122	Replication fork breakage and re-start: New insights into Rad3/XPD-associated deficiencies. <i>Cell Cycle</i> , 2010, 9, 3030-3034.	1.3	18
123	A Postincision-Deficient TFIIH Causes Replication Fork Breakage and Uncovers Alternative Rad51- or Pol32-Mediated Restart Mechanisms. <i>Molecular Cell</i> , 2010, 37, 690-701.	4.5	59
124	The interface between transcription and mRNA export: From THO to THSC/TREX-2. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2010, 1799, 533-538.	0.9	78
125	R-loops do not accumulate in transcription-defective hpr1-101 mutants: implications for the functional role of THO/TREX. <i>Nucleic Acids Research</i> , 2009, 37, 4315-4321.	6.5	10
126	Chromosomal Translocations Caused by Either Pol32-Dependent or Pol32-Independent Triparental Break-Induced Replication. <i>Molecular and Cellular Biology</i> , 2009, 29, 5441-5454.	1.1	49

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127	Transcription at the proximity of the nuclear pore: A role for the THP1-SAC3-SUS1-CDC31 (THSC) complex. <i>RNA Biology</i> , 2009, 6, 145-148.	1.5	16
128	The S-Phase Checkpoint Is Required To Respond to R-Loops Accumulated in THO Mutants. <i>Molecular and Cellular Biology</i> , 2009, 29, 5203-5213.	1.1	76
129	Genome-Wide Analysis of Factors Affecting Transcription Elongation and DNA Repair: A New Role for PAF and Ccr4-Not in Transcription-Coupled Repair. <i>PLoS Genetics</i> , 2009, 5, e1000364.	1.5	81
130	Sem1 is a functional component of the nuclear pore complex-associated messenger RNA export machinery. <i>Journal of Cell Biology</i> , 2009, 184, 833-846.	2.3	96
131	The Stress-activated Protein Kinase Hog1 Mediates S Phase Delay in Response to Osmostress. <i>Molecular Biology of the Cell</i> , 2009, 20, 3572-3582.	0.9	57
132	The Dot1 Histone Methyltransferase and the Rad9 Checkpoint Adaptor Contribute to Cohesin-Dependent Double-Strand Break Repair by Sister Chromatid Recombination in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2009, 182, 437-446.	1.2	57
133	Stimulation of direct-repeat recombination by RNA polymerase III transcription. <i>DNA Repair</i> , 2009, 8, 620-626.	1.3	23
134	DNA Repair in Mammalian Cells. <i>Cellular and Molecular Life Sciences</i> , 2009, 66, 1039-1056.	2.4	266
135	Methods to Study Transcription-Coupled Repair in Chromatin. <i>Methods in Molecular Biology</i> , 2009, 523, 141-159.	0.4	12
136	Biogenesis of mRNPs: integrating different processes in the eukaryotic nucleus. <i>Chromosoma</i> , 2008, 117, 319-331.	1.0	94
137	Different physiological relevance of yeast THO/TREX subunits in gene expression and genome integrity. <i>Molecular Genetics and Genomics</i> , 2008, 279, 123-132.	1.0	32
138	A reduction in RNA polymerase II initiation rate suppresses hyper-recombination and transcription-elongation impairment of THO mutants. <i>Molecular Genetics and Genomics</i> , 2008, 280, 327-336.	1.0	11
139	CDK targets Sae2 to control DNA-end resection and homologous recombination. <i>Nature</i> , 2008, 455, 689-692.	13.7	402
140	Genome instability: a mechanistic view of its causes and consequences. <i>Nature Reviews Genetics</i> , 2008, 9, 204-217.	7.7	648
141	A Novel Class of mRNA-containing Cytoplasmic Granules Are Produced in Response to UV-Irradiation. <i>Molecular Biology of the Cell</i> , 2008, 19, 4980-4992.	0.9	31
142	The THP1-SAC3-SUS1-CDC31 Complex Works in Transcription Elongation-mRNA Export Preventing RNA-mediated Genome Instability. <i>Molecular Biology of the Cell</i> , 2008, 19, 4310-4318.	0.9	128
143	Different genetic requirements for repair of replication-born double-strand breaks by sister-chromatid recombination and break-induced replication. <i>Nucleic Acids Research</i> , 2007, 35, 6560-6570.	6.5	22
144	Nucleoporins Prevent DNA Damage Accumulation by Modulating Ulp1-dependent Sumoylation Processes. <i>Molecular Biology of the Cell</i> , 2007, 18, 2912-2923.	0.9	129

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145	SMC Proteins, New Players in the Maintenance of Genomic Stability. <i>Cell Cycle</i> , 2007, 6, 914-918.	1.3	16
146	Activation-induced cytidine deaminase action is strongly stimulated by mutations of the THO complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 8409-8414.	3.3	98
147	Impairment of transcription elongation by R-loops in vitro. <i>Biochemical and Biophysical Research Communications</i> , 2007, 360, 428-432.	1.0	70
148	A new connection of mRNP biogenesis and export with transcription-coupled repair. <i>Nucleic Acids Research</i> , 2007, 35, 3893-3906.	6.5	33
149	Sister chromatid recombination. <i>Topics in Current Genetics</i> , 2007, , 221-249.	0.7	1
150	DNA repair: From molecular mechanism to human disease. <i>DNA Repair</i> , 2006, 5, 986-996.	1.3	162
151	Smc5 and Smc6 mediate DNA double-strand-break repair by promoting sister-chromatid recombination. <i>Nature Cell Biology</i> , 2006, 8, 1032-1034.	4.6	170
152	Double-strand breaks arising by replication through a nick are repaired by cohesin-dependent sister-chromatid exchange. <i>EMBO Reports</i> , 2006, 7, 919-926.	2.0	132
153	Tho1, a Novel hnRNP, and Sub2 Provide Alternative Pathways for mRNP Biogenesis in Yeast THO Mutants. <i>Molecular and Cellular Biology</i> , 2006, 26, 4387-4398.	1.1	41
154	An hpr1 Point Mutation That Impairs Transcription and mRNP Biogenesis without Increasing Recombination. <i>Molecular and Cellular Biology</i> , 2006, 26, 7451-7465.	1.1	36
155	Replication Fork Progression Is Impaired by Transcription in Hyperrecombinant Yeast Cells Lacking a Functional THO Complex. <i>Molecular and Cellular Biology</i> , 2006, 26, 3327-3334.	1.1	143
156	Sister chromatid recombination. , 2006, , 221-249.		1
157	mRNA processing and genomic instability. <i>Nature Structural and Molecular Biology</i> , 2005, 12, 737-738.	3.6	40
158	Impairment of replication fork progression mediates RNA polII transcription-associated recombination. <i>EMBO Journal</i> , 2005, 24, 1267-1276.	3.5	251
159	Cotranscriptional mRNP assembly: from the DNA to the nuclear pore. <i>Current Opinion in Cell Biology</i> , 2005, 17, 242-250.	2.6	148
160	Partial Depletion of Histone H4 Increases Homologous Recombination-Mediated Genetic Instability. <i>Molecular and Cellular Biology</i> , 2005, 25, 1526-1536.	1.1	67
161	Interdependence between Transcription and mRNP Processing and Export, and Its Impact on Genetic Stability. <i>Molecular Cell</i> , 2005, 18, 711-722.	4.5	105
162	A Novel Yeast Mutation, rad52-L89F, Causes a Specific Defect in Rad51-Independent Recombination That Correlates With a Reduced Ability of Rad52-L89F to Interact With Rad59. <i>Genetics</i> , 2004, 168, 553-557.	1.2	21

#	ARTICLE	IF	CITATIONS
163	Molecular evidence indicating that the yeast PAF complex is required for transcription elongation. EMBO Reports, 2004, 5, 47-53.	2.0	123
164	The absence of the yeast chromatin assembly factor Asf1 increases genomic instability and sister chromatid exchange. EMBO Reports, 2004, 5, 497-502.	2.0	100
165	A Unified Nomenclature for Protein Subunits of Mediator Complexes Linking Transcriptional Regulators to RNA Polymerase II. Molecular Cell, 2004, 14, 553-557.	4.5	230
166	Molecular evidence for a positive role of Spt4 in transcription elongation. EMBO Journal, 2003, 22, 612-620.	3.5	84
167	Mitotic recombination in <i>Saccharomyces cerevisiae</i> . Current Genetics, 2003, 42, 185-198.	0.8	96
168	Control of cross-over by single-strand DNA resection. Trends in Genetics, 2003, 19, 428-431.	2.9	32
169	Relationship between G+C content, ORF-length and mRNA concentration in <i>Saccharomyces cerevisiae</i> . Yeast, 2003, 20, 703-711.	0.8	40
170	Cotranscriptionally Formed DNA:RNA Hybrids Mediate Transcription Elongation Impairment and Transcription-Associated Recombination. Molecular Cell, 2003, 12, 711-721.	4.5	630
171	Molecular Evidence That the Eukaryotic THO/TREX Complex Is Required for Efficient Transcription Elongation. Journal of Biological Chemistry, 2003, 278, 39037-39043.	1.6	92
172	Nab2p and the Thp1p-Sac3p Complex Functionally Interact at the Interface between Transcription and mRNA Metabolism. Journal of Biological Chemistry, 2003, 278, 24225-24232.	1.6	89
173	Equal Sister Chromatid Exchange Is a Major Mechanism of Double-Strand Break Repair in Yeast. Molecular Cell, 2003, 11, 1661-1671.	4.5	90
174	Defective nucleotide excision repair in yeast hpr1 and tho2 mutants. Nucleic Acids Research, 2002, 30, 2193-2201.	6.5	17
175	Characterization of two highly similar rad51 homologs of <i>Physcomitrella patens</i> . Journal of Molecular Biology, 2002, 316, 35-49.	2.0	35
176	TREX is a conserved complex coupling transcription with messenger RNA export. Nature, 2002, 417, 304-308.	13.7	736
177	The connection between transcription and genomic instability. EMBO Journal, 2002, 21, 195-201.	3.5	291
178	The yeast THO complex and mRNA export factors link RNA metabolism with transcription and genome instability. EMBO Journal, 2002, 21, 3526-3535.	3.5	232
179	Transcription and Double-Strand Breaks Induce Similar Mitotic Recombination Events in <i>Saccharomyces cerevisiae</i> . Genetics, 2002, 162, 603-614.	1.2	63
180	Double-strand break repair: are Rad51/RecA "DNA joints barriers to DNA replication?. Trends in Genetics, 2001, 17, 318-321.	2.9	37

#	ARTICLE	IF	CITATIONS
181	Hpr1 Is Preferentially Required for Transcription of Either Long or G+C-Rich DNA Sequences in <i>Saccharomyces cerevisiae</i> . <i>Molecular and Cellular Biology</i> , 2001, 21, 7054-7064.	1.1	106
182	A New Hyperrecombination Mutation Identifies a Novel Yeast Gene, <i>THP1</i> , Connecting Transcription Elongation With Mitotic Recombination. <i>Genetics</i> , 2001, 157, 79-89.	1.2	60
183	Yeast <i>spt6-140</i> Mutation, Affecting Chromatin and Transcription, Preferentially Increases Recombination in Which Rad51p-Mediated Strand Exchange Is Dispensable. <i>Genetics</i> , 2001, 158, 597-611.	1.2	40
184	Mitotic recombination in yeast: elements controlling its incidence. <i>Yeast</i> , 2000, 16, 731-754.	0.8	78
185	Susceptibility to drug-induced apoptosis correlates with differential modulation of Bad, Bcl-2 and Bcl-xL protein levels. <i>Cell Death and Differentiation</i> , 2000, 7, 574-586.	5.0	113
186	A protein complex containing Tho2, Hpr1, Mft1 and a novel protein, Thp2, connects transcription elongation with mitotic recombination in <i>Saccharomyces cerevisiae</i> . <i>EMBO Journal</i> , 2000, 19, 5824-5834.	3.5	267
187	Construction and genetic analysis of <i>S. cerevisiae</i> deletants of six novel ORFs from chromosome II, 1999, 15, 955-961.		3
188	A novel yeast gene, <i>THO2</i> , is involved in RNA pol II transcription and provides new evidence for transcriptional elongation-associated recombination. <i>EMBO Journal</i> , 1998, 17, 4859-4872.	3.5	133
189	Genetic stability and DNA rearrangements associated with a 1.1-Kb perfect palindrome in <i>Escherichia coli</i> . <i>Molecular Genetics and Genomics</i> , 1998, 259, 639-644.	2.4	12
190	Recombination between DNA repeats in yeast <i>hpr1</i> Δ cells is linked to transcription elongation. <i>EMBO Journal</i> , 1997, 16, 2826-2835.	3.5	94
191	The yeast <i>HPR1</i> gene has a functional role in transcriptional elongation that uncovers a novel source of genome instability. <i>Genes and Development</i> , 1997, 11, 3459-3470.	2.7	156
192	The Yeast <i>HRS1</i> Gene Is Involved in Positive and Negative Regulation of Transcription and Shows Genetic Characteristics Similar to <i>SIN4</i> and <i>GAL11</i> . <i>Genetics</i> , 1997, 147, 1585-1594.	1.2	52
193	Differential intrachromosomal hyper-recombination phenotype of <i>spt4</i> and <i>spt6</i> mutants of <i>S. cerevisiae</i> . <i>Current Genetics</i> , 1996, 30, 101-106.	0.8	39
194	The Yeast <i>HRS1</i> Gene Encodes a Polyglutamine-Rich Nuclear Protein Required for Spontaneous and <i>hpr1</i> -Induced Deletions Between Direct Repeats. <i>Genetics</i> , 1996, 142, 705-716.	1.2	37
195	Mutations in the Yeast <i>SRB2</i> General Transcription Factor Suppress <i>hpr1</i> -Induced Recombination and Show Defects in DNA Repair. <i>Genetics</i> , 1996, 143, 1533-1542.	1.2	29
196	Genetic evidence for different <i>RAD52</i> -dependent intrachromosomal recombination pathways in <i>Saccharomyces cerevisiae</i> . <i>Current Genetics</i> , 1995, 27, 298-305.	0.8	35
197	New in-vivo cloning methods by homologous recombination in yeast. <i>Current Genetics</i> , 1994, 25, 180-183.	0.8	17
198	Increase in incidence of chromosome instability and non-conservative recombination between repeats in <i>Saccharomyces cerevisiae hpr1</i> ^Δ strains. <i>Molecular Genetics and Genomics</i> , 1994, 245, 224-236.	2.4	40

#	ARTICLE	IF	CITATIONS
199	High levels of chromosome instability in polyploids of <i>Saccharomyces cerevisiae</i> . <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 1990, 231, 177-186.	0.4	140
200	Molecular analysis of RGP1, a new yeast gene required for proper mitotic growth. <i>Nucleic Acids Research</i> , 1990, 18, 1064-1064.	6.5	4
201	Nucleotide sequence and characterization of temperature-sensitive pol1 mutants of <i>Saccharomyces cerevisiae</i> . <i>Gene</i> , 1990, 90, 99-104.	1.0	54
202	Synergistic effects of ethanol and temperature on yeast mitochondria. <i>Current Microbiology</i> , 1989, 18, 179-188.	1.0	14
203	The phosphofructokinase genes of yeast evolved from two duplication events. <i>Gene</i> , 1989, 78, 309-321.	1.0	94
204	Relationship between growth, fermentation, and respiration rates in <i>Saccharomyces cerevisiae</i> : A study based on the analysis of the yield Y _{px} . <i>Biotechnology and Bioengineering</i> , 1988, 32, 240-244.	1.7	13
205	Mitotic gene conversion of large DNA heterologies in <i>Saccharomyces cerevisiae</i> . <i>Molecular Genetics and Genomics</i> , 1988, 211, 455-458.	2.4	3
206	Mutations suppressing the effects of a deletion of the Phosphoglucose isomerase gene PGI1 in <i>Saccharomyces cerevisiae</i> . <i>Current Genetics</i> , 1987, 11, 429-434.	0.8	19
207	Ethanol-sensitive mutants of <i>Saccharomyces cerevisiae</i> . <i>Archives of Microbiology</i> , 1986, 143, 337-344.	1.0	39
208	Deletion of the phosphoglucose isomerase structural gene makes growth and sporulation glucose dependent in <i>Saccharomyces cerevisiae</i> . <i>Molecular Genetics and Genomics</i> , 1986, 204, 310-316.	2.4	56
209	Isolation and molecular analysis of the phosphoglucose isomerase structural gene of <i>Saccharomyces cerevisiae</i> . <i>Molecular Genetics and Genomics</i> , 1986, 202, 83-89.	2.4	55
210	Role of mitochondria in ethanol tolerance of <i>Saccharomyces cerevisiae</i> . <i>Archives of Microbiology</i> , 1985, 142, 389-392.	1.0	56
211	Specific gene probes as tools in yeast taxonomy. <i>Current Genetics</i> , 1985, 10, 103-110.	0.8	35
212	Instability of <i>Saccharomyces cerevisiae</i> heterokaryons. <i>Current Genetics</i> , 1984, 8, 345-352.	0.8	2
213	Selection of Wine Yeasts for Growth and Fermentation in the Presence of Ethanol and Sucrose. <i>Applied and Environmental Microbiology</i> , 1983, 45, 1429-1436.	1.4	68
214	Elongation Factor TFIIS Prevents Transcription Stress and R-Loop Accumulation to Maintain Genome Stability. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0