

Andres Aguilera

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9470752/publications.pdf>

Version: 2024-02-01

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	R Loops: From Transcription Byproducts to Threats to Genome Stability. <i>Molecular Cell</i> , 2012, 46, 115-124.	4.5	822
2	Replication stress and cancer. <i>Nature Reviews Cancer</i> , 2015, 15, 276-289.	12.8	755
3	TREX is a conserved complex coupling transcription with messenger RNA export. <i>Nature</i> , 2002, 417, 304-308.	13.7	736
4	Genome instability: a mechanistic view of its causes and consequences. <i>Nature Reviews Genetics</i> , 2008, 9, 204-217.	7.7	648
5	Cotranscriptionally Formed DNA:RNA Hybrids Mediate Transcription Elongation Impairment and Transcription-Associated Recombination. <i>Molecular Cell</i> , 2003, 12, 711-721.	4.5	630
6	R loops: new modulators of genome dynamics and function. <i>Nature Reviews Genetics</i> , 2015, 16, 583-597.	7.7	611
7	Transcription-Coupled Nucleotide Excision Repair Factors Promote R-Loop-Induced Genome Instability. <i>Molecular Cell</i> , 2014, 56, 777-785.	4.5	445
8	BRCA2 prevents R-loop accumulation and associates with TREX-2 mRNA export factor PCID2. <i>Nature</i> , 2014, 511, 362-365.	13.7	428
9	CDK targets Sae2 to control DNA-end resection and homologous recombination. <i>Nature</i> , 2008, 455, 689-692.	13.7	402
10	R Loops: From Physiological to Pathological Roles. <i>Cell</i> , 2019, 179, 604-618.	13.5	395
11	Causes of Genome Instability. <i>Annual Review of Genetics</i> , 2013, 47, 1-32.	3.2	372
12	Yeast Sen1 Helicase Protects the Genome from Transcription-Associated Instability. <i>Molecular Cell</i> , 2011, 41, 21-32.	4.5	301
13	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
14	The connection between transcription and genomic instability. <i>EMBO Journal</i> , 2002, 21, 195-201.	3.5	291
15	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
16	DNA Repair in Mammalian Cells. <i>Cellular and Molecular Life Sciences</i> , 2009, 66, 1039-1056.	2.4	266
17	Impairment of replication fork progression mediates RNA polII transcription-associated recombination. <i>EMBO Journal</i> , 2005, 24, 1267-1276.	3.5	251
18	The Fanconi Anemia Pathway Protects Genome Integrity from R-loops. <i>PLoS Genetics</i> , 2015, 11, e1005674.	1.5	244

#	ARTICLE	IF	CITATIONS
19	The yeast THO complex and mRNA export factors link RNA metabolism with transcription and genome instability. <i>EMBO Journal</i> , 2002, 21, 3526-3535.	3.5	232
20	A Unified Nomenclature for Protein Subunits of Mediator Complexes Linking Transcriptional Regulators to RNA Polymerase II. <i>Molecular Cell</i> , 2004, 14, 553-557.	4.5	230
21	R Loops Are Linked to Histone H3 S10 Phosphorylation and Chromatin Condensation. <i>Molecular Cell</i> , 2013, 52, 583-590.	4.5	229
22	The Replication Checkpoint Protects Fork Stability by Releasing Transcribed Genes from Nuclear Pores. <i>Cell</i> , 2011, 146, 233-246.	13.5	204
23	Genome Instability and Transcription Elongation Impairment in Human Cells Depleted of THO/TREX. <i>PLoS Genetics</i> , 2011, 7, e1002386.	1.5	194
24	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
25	Transcription-mediated replication hindrance: a major driver of genome instability. <i>Genes and Development</i> , 2019, 33, 1008-1026.	2.7	171
26	Smc5â€“Smc6 mediate DNA double-strand-break repair by promoting sister-chromatid recombination. <i>Nature Cell Biology</i> , 2006, 8, 1032-1034.	4.6	170
27	DNA repair: From molecular mechanism to human disease. <i>DNA Repair</i> , 2006, 5, 986-996.	1.3	162
28	Guidelines and recommendations on yeast cell death nomenclature. <i>Microbial Cell</i> , 2018, 5, 4-31.	1.4	158
29	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
30	The yeast and human FACT chromatin-reorganizing complexes solve R-loop-mediated transcriptionâ€“replication conflicts. <i>Genes and Development</i> , 2014, 28, 735-748.	2.7	152
31	FANCD2 Facilitates Replication through Common Fragile Sites. <i>Molecular Cell</i> , 2016, 64, 388-404.	4.5	151
32	Cotranscriptional mRNP assembly: from the DNA to the nuclear pore. <i>Current Opinion in Cell Biology</i> , 2005, 17, 242-250.	2.6	148
33	Transcription as a Threat to Genome Integrity. <i>Annual Review of Biochemistry</i> , 2016, 85, 291-317.	5.0	145
34	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
35	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
36	A novel yeast gene, THO2, 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

#	ARTICLE	IF	CITATIONS
37	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
38	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
39	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
40	Molecular evidence indicating that the yeast PAF complex is required for transcription elongation. <i>EMBO Reports</i> , 2004, 5, 47-53.	2.0	123
41	DNA-RNA hybrids: the risks of DNA breakage during transcription. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 439-443.	3.6	119
42	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
43	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
44	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
45	The absence of the yeast chromatin assembly factor Asf1 increases genomic instability and sister chromatid exchange. <i>EMBO Reports</i> , 2004, 5, 497-502.	2.0	100
46	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
47	Mitotic recombination in <i>Saccharomyces cerevisiae</i> . <i>Current Genetics</i> , 2003, 42, 185-198.	0.8	96
48	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
49	The phosphofructokinase genes of yeast evolved from two duplication events. <i>Gene</i> , 1989, 78, 309-321.	1.0	94
50	Recombination between DNA repeats in yeast hpr1Delta cells is linked to transcription elongation. <i>EMBO Journal</i> , 1997, 16, 2826-2835.	3.5	94
51	Biogenesis of mRNPs: integrating different processes in the eukaryotic nucleus. <i>Chromosoma</i> , 2008, 117, 319-331.	1.0	94
52	Molecular Evidence That the Eukaryotic THO/TREX Complex Is Required for Efficient Transcription Elongation. <i>Journal of Biological Chemistry</i> , 2003, 278, 39037-39043.	1.6	92
53	Human THO-Sin3A interaction reveals new mechanisms to prevent loops that cause genome instability. <i>EMBO Journal</i> , 2017, 36, 3532-3547.	3.5	91
54	Equal Sister Chromatid Exchange Is a Major Mechanism of Double-Strand Break Repair in Yeast. <i>Molecular Cell</i> , 2003, 11, 1661-1671.	4.5	90

#	ARTICLE	IF	CITATIONS
55	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
56	Nab2p and the Thp1p-Sac3p Complex Functionally Interact at the Interface between Transcription and mRNA Metabolism. <i>Journal of Biological Chemistry</i> , 2003, 278, 24225-24232.	1.6	89
57	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
58	Histone Mutants Separate R Loop Formation from Genome Instability Induction. <i>Molecular Cell</i> , 2017, 66, 597-609.e5.	4.5	87
59	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
60	Molecular evidence for a positive role of Spt4 in transcription elongation. <i>EMBO Journal</i> , 2003, 22, 612-620.	3.5	84
61	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
62	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
63	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
64	Architecture and nucleic acids recognition mechanism of the THO complex, an mRNP assembly factor. <i>EMBO Journal</i> , 2012, 31, 1605-1616.	3.5	79
65	Elongation Factor TFIIIS Prevents Transcription Stress and R-Loop Accumulation to Maintain Genome Stability. <i>Molecular Cell</i> , 2019, 76, 57-69.e9.	4.5	79
66	Mitotic recombination in yeast: elements controlling its incidence. <i>Yeast</i> , 2000, 16, 731-754.	0.8	78
67	The interface between transcription and mRNP export: From THO to THSC/TREX-2. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2010, 1799, 533-538.	0.9	78
68	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
69	Coordinated control of replication and transcription by a SAPK protects genomic integrity. <i>Nature</i> , 2013, 493, 116-119.	13.7	76
70	New clues to understand the role of THO and other functionally related factors in mRNP biogenesis. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2012, 1819, 514-520.	0.9	75
71	Epigenetic features of human telomeres. <i>Nucleic Acids Research</i> , 2018, 46, 2347-2355.	6.5	74
72	The Npl3 hnRNP prevents R-loop-mediated transcription–replication conflicts and genome instability. <i>Genes and Development</i> , 2013, 27, 2445-2458.	2.7	72

#	ARTICLE	IF	CITATIONS
73	The DNA damage response acts as a safeguard against harmful DNA-RNA hybrids of different origins. <i>EMBO Reports</i> , 2019, 20, e47250.	2.0	72
74	Impairment of transcription elongation by R-loops in vitro. <i>Biochemical and Biophysical Research Communications</i> , 2007, 360, 428-432.	1.0	70
75	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
76	Partial Depletion of Histone H4 Increases Homologous Recombination-Mediated Genetic Instability. <i>Molecular and Cellular Biology</i> , 2005, 25, 1526-1536.	1.1	67
77	R-loops cause replication impairment and genome instability during meiosis. <i>EMBO Reports</i> , 2012, 13, 923-929.	2.0	67
78	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
79	Transcription and Recombination: When RNA Meets DNA. <i>Cold Spring Harbor Perspectives in Biology</i> , 2014, 6, a016543-a016543.	2.3	65
80	Differential expression of THOC1 and ALY mRNP biogenesis/export factors in human cancers. <i>BMC Cancer</i> , 2011, 11, 77.	1.1	64
81	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
82	Transcription and Double-Strand Breaks Induce Similar Mitotic Recombination Events in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2002, 162, 603-614.	1.2	63
83	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
84	A Postincision-Deficient TFIH Causes Replication Fork Breakage and Uncovers Alternative Rad51- or Pol32-Mediated Restart Mechanisms. <i>Molecular Cell</i> , 2010, 37, 690-701.	4.5	59
85	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
86	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
87	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
88	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
89	Role of mitochondria in ethanol tolerance of <i>Saccharomyces cerevisiae</i> . <i>Archives of Microbiology</i> , 1985, 142, 389-392.	1.0	56
90	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

#	ARTICLE	IF	CITATIONS
91	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
92	Nucleotide sequence and characterization of temperature-sensitive <i>pol1</i> mutants of <i>Saccharomyces cerevisiae</i> . <i>Gene</i> , 1990, 90, 99-104.	1.0	54
93	Detection of DNA-RNA Hybrids In Vivo. <i>Methods in Molecular Biology</i> , 2018, 1672, 347-361.	0.4	54
94	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
95	Transcription-Associated Genome Instability. <i>Chemical Reviews</i> , 2013, 113, 8638-8661.	23.0	53
96	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
97	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
98	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
99	Guidelines for DNA recombination and repair studies: Cellular assays of DNA repair pathways. <i>Microbial Cell</i> , 2019, 6, 1-64.	1.4	47
100	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
101	Interdependence of the Rad50 Hook and Globular Domain Functions. <i>Molecular Cell</i> , 2015, 57, 479-491.	4.5	46
102	Roles of human POLD1 and POLD3 in genome stability. <i>Scientific Reports</i> , 2016, 6, 38873.	1.6	46
103	Complex Chromosomal Rearrangements Mediated by Break-Induced Replication Involve Structure-Selective Endonucleases. <i>PLoS Genetics</i> , 2012, 8, e1002979.	1.5	44
104	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
105	Increase in incidence of chromosome instability and non-conservative recombination between repeats in <i>Saccharomyces cerevisiae</i> <i>hpr1^Δ</i> strains. <i>Molecular Genetics and Genomics</i> , 1994, 245, 224-236.	2.4	40
106	Relationship between G+C content, ORF-length and mRNA concentration in <i>Saccharomyces cerevisiae</i> . <i>Yeast</i> , 2003, 20, 703-711.	0.8	40
107	mRNA processing and genomic instability. <i>Nature Structural and Molecular Biology</i> , 2005, 12, 737-738.	3.6	40
108	The Role of Replication-Associated Repair Factors on R-Loops. <i>Genes</i> , 2017, 8, 171.	1.0	40

#	ARTICLE	IF	CITATIONS
109	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
110	Ethanol-sensitive mutants of <i>Saccharomyces cerevisiae</i> . <i>Archives of Microbiology</i> , 1986, 143, 337-344.	1.0	39
111	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
112	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
113	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
114	Double-strand break repair: are Rad51/RecA "DNA joints barriers to DNA replication?. <i>Trends in Genetics</i> , 2001, 17, 318-321.	2.9	37
115	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
116	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
117	An <i>hpr1</i> Point Mutation That Impairs Transcription and mRNP Biogenesis without Increasing Recombination. <i>Molecular and Cellular Biology</i> , 2006, 26, 7451-7465.	1.1	36
118	Transcription coupled repair at the interface between transcription elongation and mRNP biogenesis. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2013, 1829, 141-150.	0.9	36
119	Specific gene probes as tools in yeast taxonomy. <i>Current Genetics</i> , 1985, 10, 103-110.	0.8	35
120	Genetic evidence for different RAD52-dependent intrachromosomal recombination pathways in <i>Saccharomyces cerevisiae</i> . <i>Current Genetics</i> , 1995, 27, 298-305.	0.8	35
121	Characterization of two highly similar <i>rad51</i> homologs of <i>Physcomitrella patens</i> . <i>Journal of Molecular Biology</i> , 2002, 316, 35-49.	2.0	35
122	RNA polymerase II contributes to preventing transcription-mediated replication fork stalls. <i>EMBO Journal</i> , 2015, 34, 236-250.	3.5	35
123	A new connection of mRNP biogenesis and export with transcription-coupled repair. <i>Nucleic Acids Research</i> , 2007, 35, 3893-3906.	6.5	33
124	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
125	Control of cross-over by single-strand DNA resection. <i>Trends in Genetics</i> , 2003, 19, 428-431.	2.9	32
126	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

#	ARTICLE	IF	CITATIONS
127	Multiple signaling kinases target Mrc1 to prevent genomic instability triggered by transcription-replication conflicts. <i>Nature Communications</i> , 2018, 9, 379.	5.8	32
128	Harmful R-loops are prevented via different cell cycle-specific mechanisms. <i>Nature Communications</i> , 2021, 12, 4451.	5.8	32
129	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
130	The THO Complex as a Paradigm for the Prevention of Cotranscriptional R-Loops. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2019, 84, 105-114.	2.0	30
131	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
132	Mutations in the Yeast SRB2 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
133	The Antitumor Drugs Trabectedin and Lurbinectedin Induce Transcription-Dependent Replication Stress and Genome Instability. <i>Molecular Cancer Research</i> , 2019, 17, 773-782.	1.5	28
134	Homologous recombination and Mus81 promote replication completion in response to replication fork blockage. <i>EMBO Reports</i> , 2020, 21, e49367.	2.0	28
135	Coordinated Activity of Y Family TLS Polymerases and EXO1 Protects Non-S Phase Cells from UV-Induced Cytotoxic Lesions. <i>Molecular Cell</i> , 2018, 70, 34-47.e4.	4.5	26
136	DNA-RNA hybrids at DSBs interfere with repair by homologous recombination. <i>ELife</i> , 2021, 10, .	2.8	26
137	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
138	A Meiotic Checkpoint Alters Repair Partner Bias to Permit Inter-sister Repair of Persistent DSBs. <i>Cell Reports</i> , 2019, 26, 775-787.e5.	2.9	24
139	Stimulation of direct-repeat recombination by RNA polymerase III transcription. <i>DNA Repair</i> , 2009, 8, 620-626.	1.3	23
140	Zim17/Tim15 links mitochondrial iron-sulfur cluster biosynthesis to nuclear genome stability. <i>Nucleic Acids Research</i> , 2011, 39, 6002-6015.	6.5	23
141	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
142	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
143	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
144	The THO complex as a key mRNP biogenesis factor in development and cell differentiation. <i>Journal of Biology</i> , 2010, 9, 6.	2.7	21

#	ARTICLE	IF	CITATIONS
145	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
146	The human nucleoporin Tpr protects cells from RNA-mediated replication stress. <i>Nature Communications</i> , 2021, 12, 3937.	5.8	20
147	Harmful DNA:RNA hybrids are formed in cis and in a Rad51-independent manner. <i>ELife</i> , 2020, 9, .	2.8	20
148	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
149	Replication fork breakage and re-start: New insights into Rad3/XPD-associated deficiencies. <i>Cell Cycle</i> , 2010, 9, 3030-3034.	1.3	18
150	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
151	The Nup84 complex coordinates the DNA damage response to warrant genome integrity. <i>Nucleic Acids Research</i> , 2019, 47, 4054-4067.	6.5	18
152	New in-vivo cloning methods by homologous recombination in yeast. <i>Current Genetics</i> , 1994, 25, 180-183.	0.8	17
153	Defective nucleotide excision repair in yeast hpr1 and tho2 mutants. <i>Nucleic Acids Research</i> , 2002, 30, 2193-2201.	6.5	17
154	A genome-wide function of THSC/TREX-2 at active genes prevents transcriptionâ€“replication collisions. <i>Nucleic Acids Research</i> , 2014, 42, 12000-12014.	6.5	17
155	SMC Proteins, New Players in the Maintenance of Genomic Stability. <i>Cell Cycle</i> , 2007, 6, 914-918.	1.3	16
156	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
157	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
158	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
159	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
160	Synergistic effects of ethanol and temperature on yeast mitochondria. <i>Current Microbiology</i> , 1989, 18, 179-188.	1.0	14
161	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
162	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

#	ARTICLE	IF	CITATIONS
163	What causes an RNA-DNA hybrid to compromise genome integrity?. DNA Repair, 2019, 81, 102660.	1.3	14
164	Relationship between growth, fermentation, and respiration rates in <i>Saccharomyces cerevisiae</i> : A study based on the analysis of the yield Y _{px} . Biotechnology and Bioengineering, 1988, 32, 240-244.	1.7	13
165	Depletion of the MFAP1/SPP381 Splicing Factor Causes R-Loop-Independent Genome Instability. Cell Reports, 2019, 28, 1551-1563.e7.	2.9	13
166	Rpd3L and Hda1 histone deacetylases facilitate repair of broken forks by promoting sister chromatid cohesion. Nature Communications, 2019, 10, 5178.	5.8	13
167	MutS ^{Δ2} regulates G4-associated telomeric R-loops to maintain telomere integrity in ALT cancer cells. Cell Reports, 2022, 39, 110602.	2.9	13
168	WASp modulates RPA function on single-stranded DNA in response to replication stress and DNA damage. Nature Communications, 2022, 13, .	5.8	13
169	Genetic stability and DNA rearrangements associated with a 2.1-Kb perfect palindrome in <i>Escherichia coli</i> . Molecular Genetics and Genomics, 1998, 259, 639-644.	2.4	12
170	Methods to Study Transcription-Coupled Repair in Chromatin. Methods in Molecular Biology, 2009, 523, 141-159.	0.4	12
171	A unified model for the molecular basis of Xeroderma pigmentosum-Cockayne Syndrome. Rare Diseases (Austin, Tex), 2015, 3, e1079362.	1.8	12
172	R-Loop-Mediated ssDNA Breaks Accumulate Following Short-Term Exposure to the HDAC Inhibitor Romidepsin. Molecular Cancer Research, 2021, 19, 1361-1374.	1.5	12
173	A reduction in RNA polymerase II initiation rate suppresses hyper-recombination and transcription-elongation impairment of THO mutants. Molecular Genetics and Genomics, 2008, 280, 327-336.	1.0	11
174	R-loops do not accumulate in transcription-defective hpr1-101 mutants: implications for the functional role of THO/TREX. Nucleic Acids Research, 2009, 37, 4315-4321.	6.5	10
175	Detection of DNA Double-Strand Breaks by ³ H2AX Immunodetection. Methods in Molecular Biology, 2021, 2153, 1-8.	0.4	9
176	Npl3, a new link between RNA-binding proteins and the maintenance of genome integrity. Cell Cycle, 2014, 13, 1524-1529.	1.3	8
177	The rem Mutations in the ATP-Binding Groove of the Rad3/XPD Helicase Lead to Xeroderma pigmentosum-Cockayne Syndrome-Like Phenotypes. PLoS Genetics, 2014, 10, e1004859.	1.5	8
178	High-Resolution Mapping of Homologous Recombination Events in rad3 Hyper-Recombination Mutants in Yeast. PLoS Genetics, 2016, 12, e1005938.	1.5	8
179	The role of chromatin at transcription-replication conflicts as a genome safeguard. Biochemical Society Transactions, 2021, 49, 2727-2736.	1.6	8
180	Control of the function of the transcription and repair factor TFIIH by the action of the cochaperone Ydj1. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 15300-15305.	3.3	7

#	ARTICLE	IF	CITATIONS
181	Yeast Pol4 Promotes Tel1-Regulated Chromosomal Translocations. <i>PLoS Genetics</i> , 2013, 9, e1003656.	1.5	7
182	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
183	Histone deacetylases facilitate the accurate repair of broken forks. <i>Molecular and Cellular Oncology</i> , 2020, 7, 1705731.	0.3	7
184	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
185	A CDK-regulated chromatin segregase promoting chromosome replication. <i>Nature Communications</i> , 2021, 12, 5224.	5.8	6
186	The need to regulate replication fork speed. <i>Science</i> , 2017, 358, 722-723.	6.0	5
187	R-Loops as Promoters of Antisense Transcription. <i>Molecular Cell</i> , 2019, 76, 529-530.	4.5	5
188	Looping the (R) Loop in DSB Repair via RNA Methylation. <i>Molecular Cell</i> , 2020, 79, 361-362.	4.5	5
189	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
190	<i>VID22</i> counteracts G-quadruplex-induced genome instability. <i>Nucleic Acids Research</i> , 2021, 49, 12785-12804.	6.5	5
191	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
192	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
193	Methods to Study Transcription-Coupled Repair in Chromatin. <i>Methods in Molecular Biology</i> , 2015, 1288, 273-288.	0.4	4
194	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
195	Heterogeneity of DNA damage incidence and repair in different chromatin contexts. <i>DNA Repair</i> , 2021, 107, 103210.	1.3	4
196	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
197	Construction and genetic analysis of <i>S. cerevisiae</i> deletants of six novel ORFs from chromosome II. , 1999, 15, 955-961.		3
198	Spontaneous DNA-RNA hybrids: differential impacts throughout the cell cycle. <i>Cell Cycle</i> , 2020, 19, 525-531.	1.3	3

#	ARTICLE	IF	CITATIONS
199	Instability of <i>Saccharomyces cerevisiae</i> heterokaryons. <i>Current Genetics</i> , 1984, 8, 345-352.	0.8	2
200	Gene gating at nuclear pores prevents the formation of R loops. <i>Molecular and Cellular Oncology</i> , 2018, 5, e1405140.	0.3	2
201	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
202	Sister chromatid recombination. , 2006, , 221-249.		1
203	<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
204	Sister chromatid recombination. <i>Topics in Current Genetics</i> , 2007, , 221-249.	0.7	1
205	International Institutions: For better or worst. <i>Reflexi3n Pol3tica</i> , 2017, 19, 6-15.	0.0	0
206	Elongation Factor TFIIIS Prevents Transcription Stress and R-Loop Accumulation to Maintain Genome Stability. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
207	Histone H3E73Q and H4E53A mutations cause recombinogenic DNA damage. <i>Microbial Cell</i> , 2020, 7, 190-198.	1.4	0
208	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
209	Title is missing!. , 2020, 16, e1009260.		0
210	Title is missing!. , 2020, 16, e1009260.		0
211	Title is missing!. , 2020, 16, e1009260.		0
212	Title is missing!. , 2020, 16, e1009260.		0
213	Title is missing!. , 2020, 16, e1009260.		0
214	Title is missing!. , 2020, 16, e1009260.		0