

MarÃ-a L GarcÃ-a-Rubio

List of Publications by Year in descending order

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38
papers

3,276
citations

218677

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docs citations

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times ranked

3415
citing authors

#	ARTICLE	IF	CITATIONS
1	WASp modulates RPA function on single-stranded DNA in response to replication stress and DNA damage. <i>Nature Communications</i> , 2022, 13, .	12.8	13
2	Harmful R-loops are prevented via different cell cycle-specific mechanisms. <i>Nature Communications</i> , 2021, 12, 4451.	12.8	32
3	<i>C. elegans</i> THSC/TREX-2 deficiency causes replication stress and genome instability. <i>Journal of Cell Science</i> , 2021, 134, .	2.0	1
4	<i>VID22</i> counteracts G-quadruplex-induced genome instability. <i>Nucleic Acids Research</i> , 2021, 49, 12785-12804.	14.5	5
5	Harmful DNA:RNA hybrids are formed in cis and in a Rad51-independent manner. <i>ELife</i> , 2020, 9, .	6.0	20
6	The DNA damage response acts as a safeguard against harmful DNAâ€“RNA hybrids of different origins. <i>EMBO Reports</i> , 2019, 20, e47250.	4.5	72
7	Multiple signaling kinases target Mrc1 to prevent genomic instability triggered by transcription-replication conflicts. <i>Nature Communications</i> , 2018, 9, 379.	12.8	32
8	Detection of DNA-RNA Hybrids In Vivo. <i>Methods in Molecular Biology</i> , 2018, 1672, 347-361.	0.9	54
9	Yra1-bound RNAâ€“DNA hybrids cause orientation-independent transcriptionâ€“replication collisions and telomere instability. <i>Genes and Development</i> , 2018, 32, 965-977.	5.9	58
10	Histone Mutants Separate R Loop Formation from Genome Instability Induction. <i>Molecular Cell</i> , 2017, 66, 597-609.e5.	9.7	87
11	Excess of Yra1 RNA-Binding Factor Causes Transcription-Dependent Genome Instability, Replication Impairment and Telomere Shortening. <i>PLoS Genetics</i> , 2016, 12, e1005966.	3.5	21
12	FANCD2 Facilitates Replication through Common Fragile Sites. <i>Molecular Cell</i> , 2016, 64, 388-404.	9.7	151
13	RNA polymerase II contributes to preventing transcriptionâ€“mediated replication fork stalls. <i>EMBO Journal</i> , 2015, 34, 236-250.	7.8	35
14	The Fanconi Anemia Pathway Protects Genome Integrity from R-loops. <i>PLoS Genetics</i> , 2015, 11, e1005674.	3.5	244
15	Transcription-Coupled Nucleotide Excision Repair Factors Promote R-Loop-Induced Genome Instability. <i>Molecular Cell</i> , 2014, 56, 777-785.	9.7	445
16	A genome-wide function of THSC/TREX-2 at active genes prevents transcriptionâ€“replication collisions. <i>Nucleic Acids Research</i> , 2014, 42, 12000-12014.	14.5	17
17	The yeast and human FACT chromatin-reorganizing complexes solve R-loop-mediated transcriptionâ€“replication conflicts. <i>Genes and Development</i> , 2014, 28, 735-748.	5.9	152
18	BRCA2 prevents R-loop accumulation and associates with TREX-2 mRNA export factor PCID2. <i>Nature</i> , 2014, 511, 362-365.	27.8	428

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19	Coordinated control of replication and transcription by a SAPK protects genomic integrity. <i>Nature</i> , 2013, 493, 116-119.	27.8	76
20	The Npl3 hnRNP prevents R-loop-mediated transcription—replication conflicts and genome instability. <i>Genes and Development</i> , 2013, 27, 2445-2458.	5.9	72
21	Topological constraints impair RNA polymerase II transcription and causes instability of plasmid-borne convergent genes. <i>Nucleic Acids Research</i> , 2012, 40, 1050-1064.	14.5	23
22	A novel assay identifies transcript elongation roles for the Nup84 complex and RNA processing factors. <i>EMBO Journal</i> , 2011, 30, 1953-1964.	7.8	50
23	Zim17/Tim15 links mitochondrial iron—sulfur cluster biosynthesis to nuclear genome stability. <i>Nucleic Acids Research</i> , 2011, 39, 6002-6015.	14.5	23
24	Genome-wide function of THO/TREX in active genes prevents R-loop-dependent replication obstacles. <i>EMBO Journal</i> , 2011, 30, 3106-3119.	7.8	191
25	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.	2.3	14
26	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.	3.5	81
27	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.	2.1	57
28	Different physiological relevance of yeast THO/TREX subunits in gene expression and genome integrity. <i>Molecular Genetics and Genomics</i> , 2008, 279, 123-132.	2.1	32
29	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.	2.1	11
30	Nucleoporins Prevent DNA Damage Accumulation by Modulating Ulp1-dependent Sumoylation Processes. <i>Molecular Biology of the Cell</i> , 2007, 18, 2912-2923.	2.1	129
31	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.	2.3	41
32	An hpr1 Point Mutation That Impairs Transcription and mRNP Biogenesis without Increasing Recombination. <i>Molecular and Cellular Biology</i> , 2006, 26, 7451-7465.	2.3	36
33	Interdependence between Transcription and mRNP Processing and Export, and Its Impact on Genetic Stability. <i>Molecular Cell</i> , 2005, 18, 711-722.	9.7	105
34	Molecular evidence indicating that the yeast PAF complex is required for transcription elongation. <i>EMBO Reports</i> , 2004, 5, 47-53.	4.5	123
35	Molecular evidence for a positive role of Spt4 in transcription elongation. <i>EMBO Journal</i> , 2003, 22, 612-620.	7.8	84
36	Molecular Evidence That the Eukaryotic THO/TREX Complex Is Required for Efficient Transcription Elongation. <i>Journal of Biological Chemistry</i> , 2003, 278, 39037-39043.	3.4	92

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37	Transcription and Double-Strand Breaks Induce Similar Mitotic Recombination Events in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2002, 162, 603-614.	2.9	63
38	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.	2.3	106