

GaÃ«lle Legube

List of Publications by Year in descending order

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Version: 2024-02-01

36
papers

4,992
citations

218677

26
h-index

345221

36
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39
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39
docs citations

39
times ranked

5889
citing authors

#	ARTICLE	IF	CITATIONS
1	Nuclear HMGB1 protects from nonalcoholic fatty liver disease through negative regulation of liver X receptor. <i>Science Advances</i> , 2022, 8, eabg9055.	10.3	7
2	A POLD3/BLM dependent pathway handles DSBs in transcribed chromatin upon excessive RNA:DNA hybrid accumulation. <i>Nature Communications</i> , 2022, 13, 1012.	12.8	20
3	Loop extrusion as a mechanism for formation of DNA damage repair foci. <i>Nature</i> , 2021, 590, 660-665.	27.8	175
4	R-loops as Janus-faced modulators of DNA repair. <i>Nature Cell Biology</i> , 2021, 23, 305-313.	10.3	94
5	Repair of DNA double-strand breaks in RNAPI- and RNAPII-transcribed loci. <i>DNA Repair</i> , 2021, 104, 103139.	2.8	6
6	Analyzing Homologous Recombination at a Genome-Wide Level. <i>Methods in Molecular Biology</i> , 2021, 2153, 427-438.	0.9	1
7	The Secret Life of Chromosome Loops upon DNA Double-Strand Break. <i>Journal of Molecular Biology</i> , 2020, 432, 724-736.	4.2	28
8	m6A RNA modification as a new player in R-loop regulation. <i>Nature Genetics</i> , 2020, 52, 27-28.	21.4	18
9	Studying DNA Double-Strand Break Repair: An Ever-Growing Toolbox. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 24.	3.5	99
10	A cohesin/HUSH- and LINC-dependent pathway controls ribosomal DNA double-strand break repair. <i>Genes and Development</i> , 2019, 33, 1175-1190.	5.9	78
11	Non-canonical DNA/RNA structures during Transcription-Coupled Double-Strand Break Repair: Roadblocks or Bona fide repair intermediates?. <i>DNA Repair</i> , 2019, 81, 102661.	2.8	73
12	A Snapshot on the Cis Chromatin Response to DNA Double-Strand Breaks. <i>Trends in Genetics</i> , 2019, 35, 330-345.	6.7	83
13	Genome editing in primary cells and in vivo using viral-derived Nanoblades loaded with Cas9-sgRNA ribonucleoproteins. <i>Nature Communications</i> , 2019, 10, 45.	12.8	195
14	Senataxin resolves RNA:DNA hybrids forming at DNA double-strand breaks to prevent translocations. <i>Nature Communications</i> , 2018, 9, 533.	12.8	252
15	Comprehensive Mapping of Histone Modifications at DNA Double-Strand Breaks Deciphers Repair Pathway Chromatin Signatures. <i>Molecular Cell</i> , 2018, 72, 250-262.e6.	9.7	232
16	Organizing DNA repair in the nucleus: DSBs hit the road. <i>Current Opinion in Cell Biology</i> , 2017, 46, 1-8.	5.4	57
17	Genome-wide mapping of long-range contacts unveils clustering of DNA double-strand breaks at damaged active genes. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 353-361.	8.2	221
18	Histone demethylase KDM5A regulates the ZMYND8 NuRD chromatin remodeler to promote DNA repair. <i>Journal of Cell Biology</i> , 2017, 216, 1959-1974.	5.2	132

#	ARTICLE	IF	CITATIONS
19	Taming Tricky DSBs: ATM on duty. <i>DNA Repair</i> , 2017, 56, 84-91.	2.8	30
20	Transcription-Coupled DNA Double-Strand Break Repair: Active Genes Need Special Care. <i>Journal of Molecular Biology</i> , 2017, 429, 1277-1288.	4.2	119
21	A meeting at risk: Unrepaired DSBs go for broke. <i>Nucleus</i> , 2017, 8, 589-599.	2.2	8
22	The TIP60 Complex Regulates Bivalent Chromatin Recognition by 53BP1 through Direct H4K20me Binding and H2AK15 Acetylation. <i>Molecular Cell</i> , 2016, 62, 409-421.	9.7	198
23	DNA-PK triggers histone ubiquitination and signaling in response to DNA double-strand breaks produced during the repair of transcription-blocking topoisomerase I lesions. <i>Nucleic Acids Research</i> , 2016, 44, 1161-1178.	14.5	75
24	A TAD closer to ATM. <i>Molecular and Cellular Oncology</i> , 2016, 3, e1134411.	0.7	12
25	DNA double strand break repair pathway choice: a chromatin based decision?. <i>Nucleus</i> , 2015, 6, 107-113.	2.2	87
26	Screen identifies bromodomain protein ZMYND8 in chromatin recognition of transcription-associated DNA damage that promotes homologous recombination. <i>Genes and Development</i> , 2015, 29, 197-211.	5.9	204
27	Non-redundant Functions of ATM and DNA-PKcs in Response to DNA Double-Strand Breaks. <i>Cell Reports</i> , 2015, 13, 1598-1609.	6.4	104
28	SETD2-Dependent Histone H3K36 Trimethylation Is Required for Homologous Recombination Repair and Genome Stability. <i>Cell Reports</i> , 2014, 7, 2006-2018.	6.4	370
29	Quantitation of DNA double-strand break resection intermediates in human cells. <i>Nucleic Acids Research</i> , 2014, 42, e19-e19.	14.5	197
30	Transcriptionally active chromatin recruits homologous recombination at DNA double-strand breaks. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 366-374.	8.2	536
31	Dynamics of yeast histone H2A and H2B phosphorylation in response to a double-strand break. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 103-109.	8.2	85
32	Quantifying DNA double-strand breaks induced by site-specific endonucleases in living cells by ligation-mediated purification. <i>Nature Protocols</i> , 2014, 9, 517-528.	12.0	32
33	Cohesin Protects Genes against γ H2AX Induced by DNA Double-Strand Breaks. <i>PLoS Genetics</i> , 2012, 8, e1002460.	3.5	111
34	Human HDAC1 and HDAC2 function in the DNA-damage response to promote DNA nonhomologous end-joining. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 1144-1151.	8.2	542
35	High-resolution profiling of γ H2AX around DNA double strand breaks in the mammalian genome. <i>EMBO Journal</i> , 2010, 29, 1446-1457.	7.8	442
36	Deciphering the chromatin landscape induced around DNA double strand breaks. <i>Cell Cycle</i> , 2010, 9, 3035-3044.	2.6	53