

Xu-Dong Zhu

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

24
papers

1,449
citations

14
h-index

27
g-index

27
ext. papers

1,617
ext. citations

11.3
avg, IF

4.24
L-index

#	Paper	IF	Citations
24	The Winged Helix Domain of CSB Regulates RNAPII Occupancy at Promoter Proximal Pause Sites. <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	1
23	CSB cooperates with SMARCAL1 to maintain telomere stability in ALT cells. <i>Journal of Cell Science</i> , 2020 , 133,	5.3	9
22	CSB interacts with BRCA1 in late S/G2 to promote MRN- and CtIP-mediated DNA end resection. <i>Nucleic Acids Research</i> , 2019 , 47, 10678-10692	20.1	10
21	Biphasic recruitment of TRF2 to DNA damage sites promotes non-sister chromatid homologous recombination repair. <i>Journal of Cell Science</i> , 2018 , 131,	5.3	10
20	Efficient UV repair requires disengagement of the CSB winged helix domain from the CSB ATPase domain. <i>DNA Repair</i> , 2018 , 68, 58-67	4.3	7
19	ATM and CDK2 control chromatin remodeler CSB to inhibit RIF1 in DSB repair pathway choice. <i>Nature Communications</i> , 2017 , 8, 1921	17.4	33
18	TRF1 phosphorylation on T271 modulates telomerase-dependent telomere length maintenance as well as the formation of ALT-associated PML bodies. <i>Scientific Reports</i> , 2016 , 6, 36913	4.9	8
17	Cdk-dependent phosphorylation regulates TRF1 recruitment to PML bodies and promotes C-circle production in ALT cells. <i>Journal of Cell Science</i> , 2016 , 129, 2559-72	5.3	10
16	Cockayne syndrome group B protein regulates DNA double-strand break repair and checkpoint activation. <i>EMBO Journal</i> , 2015 , 34, 1399-416	13	41
15	ATM and ATR Signaling Regulate the Recruitment of Human Telomerase to Telomeres. <i>Cell Reports</i> , 2015 , 13, 1633-46	10.6	84
14	Methylated TRF2 associates with the nuclear matrix and serves as a potential biomarker for cellular senescence. <i>Aging</i> , 2014 , 6, 248-63	5.6	11
13	Phosphorylated (pT371)TRF1 is recruited to sites of DNA damage to facilitate homologous recombination and checkpoint activation. <i>Nucleic Acids Research</i> , 2013 , 41, 10268-82	20.1	14
12	Post-translational modifications of TRF1 and TRF2 and their roles in telomere maintenance. <i>Mechanisms of Ageing and Development</i> , 2012 , 133, 421-34	5.6	41
11	ATM regulates proteasome-dependent subnuclear localization of TRF1, which is important for telomere maintenance. <i>Nucleic Acids Research</i> , 2012 , 40, 3975-89	20.1	30
10	Cockayne Syndrome group B protein interacts with TRF2 and regulates telomere length and stability. <i>Nucleic Acids Research</i> , 2012 , 40, 9661-74	20.1	35
9	Cyclin B-dependent kinase 1 regulates human TRF1 to modulate the resolution of sister telomeres. <i>Nature Communications</i> , 2011 , 2, 371	17.4	29
8	Arginine methylation regulates telomere length and stability. <i>Molecular and Cellular Biology</i> , 2009 , 29, 4918-34	4.8	51

7	Human XPF controls TRF2 and telomere length maintenance through distinctive mechanisms. <i>Mechanisms of Ageing and Development</i> , 2008 , 129, 602-10	5.6	44
6	MRE11-RAD50-NBS1 and ATM function as co-mediators of TRF1 in telomere length control. <i>Nature Structural and Molecular Biology</i> , 2007 , 14, 832-40	17.6	92
5	XPF with mutations in its conserved nuclease domain is defective in DNA repair but functions in TRF2-mediated telomere shortening. <i>DNA Repair</i> , 2007 , 6, 157-66	4.3	34
4	ERCC1/XPF removes the 3' overhang from uncapped telomeres and represses formation of telomeric DNA-containing double minute chromosomes. <i>Molecular Cell</i> , 2003 , 12, 1489-98	17.6	319
3	Cell-cycle-regulated association of RAD50/MRE11/NBS1 with TRF2 and human telomeres. <i>Nature Genetics</i> , 2000 , 25, 347-52	36.3	509
2	The role of single-stranded DNA in Flp-mediated strand exchange. <i>Journal of Biological Chemistry</i> , 1998 , 273, 4921-7	5.4	1
1	Cleavage-dependent ligation by the FLP recombinase. Characterization of a mutant FLP protein with an alteration in a catalytic amino acid. <i>Journal of Biological Chemistry</i> , 1995 , 270, 23044-54	5.4	26