

Tanya T Paull

List of Publications by Citations

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114
papers

13,378
citations

55
h-index

115
g-index

122
ext. papers

14,921
ext. citations

12.8
avg, IF

6.78
L-index

#	Paper	IF	Citations
114	A critical role for histone H2AX in recruitment of repair factors to nuclear foci after DNA damage. <i>Current Biology</i> , 2000 , 10, 886-95	6.3	1695
113	ATM activation by DNA double-strand breaks through the Mre11-Rad50-Nbs1 complex. <i>Science</i> , 2005 , 308, 551-4	33.3	1072
112	ATM activation by oxidative stress. <i>Science</i> , 2010 , 330, 517-21	33.3	797
111	The 3' to 5' exonuclease activity of Mre 11 facilitates repair of DNA double-strand breaks. <i>Molecular Cell</i> , 1998 , 1, 969-79	17.6	696
110	Direct activation of the ATM protein kinase by the Mre11/Rad50/Nbs1 complex. <i>Science</i> , 2004 , 304, 93-6	33.3	587
109	MDC1 maintains genomic stability by participating in the amplification of ATM-dependent DNA damage signals. <i>Molecular Cell</i> , 2006 , 21, 187-200	17.6	490
108	Nbs1 potentiates ATP-driven DNA unwinding and endonuclease cleavage by the Mre11/Rad50 complex. <i>Genes and Development</i> , 1999 , 13, 1276-88	12.6	411
107	Activation and regulation of ATM kinase activity in response to DNA double-strand breaks. <i>Oncogene</i> , 2007 , 26, 7741-8	9.2	408
106	Mechanisms of ATM Activation. <i>Annual Review of Biochemistry</i> , 2015 , 84, 711-38	29.1	287
105	The nonspecific DNA-binding and -bending proteins HMG1 and HMG2 promote the assembly of complex nucleoprotein structures. <i>Genes and Development</i> , 1993 , 7, 1521-34	12.6	287
104	A forward chemical genetic screen reveals an inhibitor of the Mre11-Rad50-Nbs1 complex. <i>Nature Chemical Biology</i> , 2008 , 4, 119-25	11.7	285
103	ATM functions at the peroxisome to induce pexophagy in response to ROS. <i>Nature Cell Biology</i> , 2015 , 17, 1259-1269	23.4	266
102	The ATM protein kinase and cellular redox signaling: beyond the DNA damage response. <i>Trends in Biochemical Sciences</i> , 2012 , 37, 15-22	10.3	241
101	Sae2 is an endonuclease that processes hairpin DNA cooperatively with the Mre11/Rad50/Xrs2 complex. <i>Molecular Cell</i> , 2007 , 28, 638-51	17.6	225
100	Direct DNA binding by Brca1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001 , 98, 6086-91	11.5	213
99	Stimulation of V(D)J cleavage by high mobility group proteins. <i>EMBO Journal</i> , 1997 , 16, 2665-70	13	205
98	Involvement of human MOF in ATM function. <i>Molecular and Cellular Biology</i> , 2005 , 25, 5292-305	4.8	196

97	Single-stranded DNA-binding protein hSSB1 is critical for genomic stability. <i>Nature</i> , 2008 , 453, 677-81	50.4	187
96	<i>Saccharomyces cerevisiae</i> Mre11/Rad50/Xrs2 and Ku proteins regulate association of Exo1 and Dna2 with DNA breaks. <i>EMBO Journal</i> , 2010 , 29, 3370-80	13	175
95	Mre11-Rad50-Xrs2 and Sae2 promote 5Tstrand resection of DNA double-strand breaks. <i>Nature Structural and Molecular Biology</i> , 2010 , 17, 1478-85	17.6	171
94	A mechanistic basis for Mre11-directed DNA joining at microhomologies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000 , 97, 6409-14	11.5	167
93	Quantitation of DNA double-strand break resection intermediates in human cells. <i>Nucleic Acids Research</i> , 2014 , 42, e19	20.1	144
92	ATM activation in the presence of oxidative stress. <i>Cell Cycle</i> , 2010 , 9, 4805-11	4.7	140
91	The Mre11/Rad50/Nbs1 complex and its role as a DNA double-strand break sensor for ATM. <i>Cell Cycle</i> , 2005 , 4, 737-40	4.7	139
90	Catalytic and noncatalytic roles of the CtIP endonuclease in double-strand break end resection. <i>Molecular Cell</i> , 2014 , 54, 1022-33	17.6	132
89	Hyperthermia activates a subset of ataxia-telangiectasia mutated effectors independent of DNA strand breaks and heat shock protein 70 status. <i>Cancer Research</i> , 2007 , 67, 3010-7	10.1	132
88	DNA replication initiates at multiple sites on plasmid DNA in <i>Xenopus</i> egg extracts. <i>Nucleic Acids Research</i> , 1992 , 20, 1457-62	20.1	129
87	Cell-free V(D)J recombination. <i>Nature</i> , 1997 , 388, 488-91	50.4	127
86	The <i>P. furiosus</i> mre11/rad50 complex promotes 5Tstrand resection at a DNA double-strand break. <i>Cell</i> , 2008 , 135, 250-60	56.2	124
85	Single-Molecule Imaging Reveals How Mre11-Rad50-Nbs1 Initiates DNA Break Repair. <i>Molecular Cell</i> , 2017 , 67, 891-898.e4	17.6	114
84	ATP-driven Rad50 conformations regulate DNA tethering, end resection, and ATM checkpoint signaling. <i>EMBO Journal</i> , 2014 , 33, 482-500	13	111
83	Ctp1/CtIP and the MRN complex collaborate in the initial steps of homologous recombination. <i>Molecular Cell</i> , 2007 , 28, 351-2	17.6	104
82	Mre11 Is Essential for the Removal of Lethal Topoisomerase 2 Covalent Cleavage Complexes. <i>Molecular Cell</i> , 2016 , 64, 580-592	17.6	101
81	Human Mre11/human Rad50/Nbs1 and DNA ligase IIIalpha/XRCC1 protein complexes act together in an alternative nonhomologous end joining pathway. <i>Journal of Biological Chemistry</i> , 2011 , 286, 33845-54	5.4	101
80	Nbs1 Converts the Human Mre11/Rad50 Nuclease Complex into an Endo/Exonuclease Machine Specific for Protein-DNA Adducts. <i>Molecular Cell</i> , 2016 , 64, 593-606	17.6	98

79	53BP1 promotes ATM activity through direct interactions with the MRN complex. <i>EMBO Journal</i> , 2010 , 29, 574-85	13	94
78	Yeast HMG proteins NHP6A/B potentiate promoter-specific transcriptional activation in vivo and assembly of preinitiation complexes in vitro. <i>Genes and Development</i> , 1996 , 10, 2769-81	12.6	94
77	DNA looping by <i>Saccharomyces cerevisiae</i> high mobility group proteins NHP6A/B. Consequences for nucleoprotein complex assembly and chromatin condensation. <i>Journal of Biological Chemistry</i> , 1995 , 270, 8744-54	5.4	89
76	Rad50 adenylate kinase activity regulates DNA tethering by Mre11/Rad50 complexes. <i>Molecular Cell</i> , 2007 , 25, 647-61	17.6	85
75	Multiple autophosphorylation sites are dispensable for murine ATM activation in vivo. <i>Journal of Cell Biology</i> , 2008 , 183, 777-83	7.3	83
74	Loss of ATM kinase activity leads to embryonic lethality in mice. <i>Journal of Cell Biology</i> , 2012 , 198, 295-304	7.3	80
73	Correction for Fu et al., Phosphorylation-Regulated Transitions in an Oligomeric State Control the Activity of the Sae2 DNA Repair Enzyme. <i>Molecular and Cellular Biology</i> , 2014 , 34, 4213-4213	4.8	78
72	Regulation of Mre11/Rad50 by Nbs1: effects on nucleotide-dependent DNA binding and association with ataxia-telangiectasia-like disorder mutant complexes. <i>Journal of Biological Chemistry</i> , 2003 , 278, 45171-81	5.4	77
71	The rad50 signature motif: essential to ATP binding and biological function. <i>Journal of Molecular Biology</i> , 2004 , 335, 937-51	6.5	75
70	Polo-like kinase 3 regulates CtIP during DNA double-strand break repair in G1. <i>Journal of Cell Biology</i> , 2014 , 206, 877-94	7.3	74
69	Regulation of the DNA Damage Response by DNA-PKcs Inhibitory Phosphorylation of ATM. <i>Molecular Cell</i> , 2017 , 65, 91-104	17.6	73
68	Collaboration of Werner syndrome protein and BRCA1 in cellular responses to DNA interstrand cross-links. <i>Nucleic Acids Research</i> , 2006 , 34, 2751-60	20.1	73
67	20 Years of Mre11 Biology: No End in Sight. <i>Molecular Cell</i> , 2018 , 71, 419-427	17.6	71
66	CtIP: A DNA damage response protein at the intersection of DNA metabolism. <i>DNA Repair</i> , 2015 , 32, 75-81	4.3	65
65	Single-molecule imaging reveals the mechanism of Exo1 regulation by single-stranded DNA binding proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, E1170-5	11.5	65
64	The SOSS1 single-stranded DNA binding complex promotes DNA end resection in concert with Exo1. <i>EMBO Journal</i> , 2013 , 32, 126-39	13	65
63	Ataxia telangiectasia-mutated (ATM) kinase activity is regulated by ATP-driven conformational changes in the Mre11/Rad50/Nbs1 (MRN) complex. <i>Journal of Biological Chemistry</i> , 2013 , 288, 12840-51	5.4	65
62	Making the best of the loose ends: Mre11/Rad50 complexes and Sae2 promote DNA double-strand break resection. <i>DNA Repair</i> , 2010 , 9, 1283-91	4.3	63

61	ATM protein-dependent phosphorylation of Rad50 protein regulates DNA repair and cell cycle control. <i>Journal of Biological Chemistry</i> , 2011 , 286, 31542-56	5.4	56
60	ATM directs DNA damage responses and proteostasis via genetically separable pathways. <i>Science Signaling</i> , 2018 , 11,	8.8	55
59	MRI Is a DNA Damage Response Adaptor during Classical Non-homologous End Joining. <i>Molecular Cell</i> , 2018 , 71, 332-342.e8	17.6	55
58	DNA-dependent protein kinase promotes DNA end processing by MRN and CtIP. <i>Science Advances</i> , 2020 , 6, eaay0922	14.3	51
57	Targeting p38 β Increases DNA Damage, Chromosome Instability, and the Anti-tumoral Response to Taxanes in Breast Cancer Cells. <i>Cancer Cell</i> , 2018 , 33, 1094-1110.e8	24.3	49
56	ZMYM3 regulates BRCA1 localization at damaged chromatin to promote DNA repair. <i>Genes and Development</i> , 2017 , 31, 260-274	12.6	47
55	Systematic bromodomain protein screens identify homologous recombination and R-loop suppression pathways involved in genome integrity. <i>Genes and Development</i> , 2019 , 33, 1751-1774	12.6	47
54	EXD2 promotes homologous recombination by facilitating DNA end resection. <i>Nature Cell Biology</i> , 2016 , 18, 271-280	23.4	46
53	Mitochondrial redox sensing by the kinase ATM maintains cellular antioxidant capacity. <i>Science Signaling</i> , 2018 , 11,	8.8	45
52	Visualization of local DNA unwinding by Mre11/Rad50/Nbs1 using single-molecule FRET. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 18868-73	11.5	44
51	The Mre11/Rad50/Xrs2 complex and non-homologous end-joining of incompatible ends in <i>S. cerevisiae</i> . <i>DNA Repair</i> , 2005 , 4, 1281-94	4.3	44
50	DNA-dependent protein kinase regulates DNA end resection in concert with Mre11-Rad50-Nbs1 (MRN) and ataxia telangiectasia-mutated (ATM). <i>Journal of Biological Chemistry</i> , 2013 , 288, 37112-25	5.4	42
49	The Mre11/Rad50/Nbs1 complex: recent insights into catalytic activities and ATP-driven conformational changes. <i>Experimental Cell Research</i> , 2014 , 329, 139-47	4.2	40
48	ATM and PRDM9 regulate SPO11-bound recombination intermediates during meiosis. <i>Nature Communications</i> , 2020 , 11, 857	17.4	38
47	Sae2/CtIP prevents R-loop accumulation in eukaryotic cells. <i>ELife</i> , 2018 , 7,	8.9	37
46	Phosphorylation-regulated transitions in an oligomeric state control the activity of the Sae2 DNA repair enzyme. <i>Molecular and Cellular Biology</i> , 2014 , 34, 778-93	4.8	36
45	Purification and biochemical characterization of ataxia-telangiectasia mutated and Mre11/Rad50/Nbs1. <i>Methods in Enzymology</i> , 2006 , 408, 529-39	1.7	34
44	RPA Phosphorylation Inhibits DNA Resection. <i>Molecular Cell</i> , 2019 , 75, 145-153.e5	17.6	33

43	Functional activation of ATM by the prostate cancer suppressor NKX3.1. <i>Cell Reports</i> , 2013 , 4, 516-29	10.6	29
42	Sumoylation influences DNA break repair partly by increasing the solubility of a conserved end resection protein. <i>PLoS Genetics</i> , 2015 , 11, e1004899	6	26
41	Damage-induced BRCA1 phosphorylation by Chk2 contributes to the timing of end resection. <i>Cell Cycle</i> , 2015 , 14, 437-48	4.7	26
40	BRCA1 and CtIP Are Both Required to Recruit Dna2 at Double-Strand Breaks in Homologous Recombination. <i>PLoS ONE</i> , 2015 , 10, e0124495	3.7	23
39	Ancient and recent adaptive evolution of primate non-homologous end joining genes. <i>PLoS Genetics</i> , 2010 , 6, e1001169	6	23
38	Saving the ends for last: the role of pol mu in DNA end joining. <i>Molecular Cell</i> , 2005 , 19, 294-6	17.6	23
37	Cellular functions of the protein kinase ATM and their relevance to human disease. <i>Nature Reviews Molecular Cell Biology</i> , 2021 , 22, 796-814	48.7	23
36	Rad50 ATPase activity is regulated by DNA ends and requires coordination of both active sites. <i>Nucleic Acids Research</i> , 2017 , 45, 5255-5268	20.1	22
35	Mitochondria at the crossroads of ATM-mediated stress signaling and regulation of reactive oxygen species. <i>Redox Biology</i> , 2020 , 32, 101511	11.3	22
34	Direct activation of ATM by resveratrol under oxidizing conditions. <i>PLoS ONE</i> , 2014 , 9, e97969	3.7	22
33	HU and functional analogs in eukaryotes promote Hin invertasome assembly. <i>Biochimie</i> , 1994 , 76, 992-1004	10.4	20
32	Proteome-wide detection and quantitative analysis of irreversible cysteine oxidation using long column UPLC-pSRM. <i>Journal of Proteome Research</i> , 2013 , 12, 4302-15	5.6	19
31	V(D)J recombination: links to transposition and double-strand break repair. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 1999 , 64, 161-7	3.9	19
30	New glimpses of an old machine. <i>Cell</i> , 2001 , 107, 563-5	56.2	16
29	Proteome-wide identification of HSP70/HSC70 chaperone clients in human cells. <i>PLoS Biology</i> , 2020 , 18, e3000606	9.7	14
28	Poly-ADP-ribosylation drives loss of protein homeostasis in ATM and Mre11 deficiency. <i>Molecular Cell</i> , 2021 , 81, 1515-1533.e5	17.6	14
27	RNA-DNA hybrids and the convergence with DNA repair. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2019 , 54, 371-384	8.7	12
26	Homology-directed repair protects the replicating genome from metabolic assaults. <i>Developmental Cell</i> , 2021 , 56, 461-477.e7	10.2	12

25	Direct measurement of single-stranded DNA intermediates in mammalian cells by quantitative polymerase chain reaction. <i>Analytical Biochemistry</i> , 2015 , 479, 48-50	3.1	11
24	Redox activation of ATM enhances GSNOR translation to sustain mitophagy and tolerance to oxidative stress. <i>EMBO Reports</i> , 2021 , 22, e50500	6.5	11
23	Genetic Separation of Sae2 Nuclease Activity from Mre11 Nuclease Functions in Budding Yeast. <i>Molecular and Cellular Biology</i> , 2017 , 37,	4.8	8
22	The ARK Assay Is a Sensitive and Versatile Method for the Global Detection of DNA-Protein Crosslinks. <i>Cell Reports</i> , 2020 , 30, 1235-1245.e4	10.6	7
21	Homeodomain Proteins Directly Regulate ATM Kinase Activity. <i>Cell Reports</i> , 2018 , 24, 1471-1483	10.6	6
20	The Conserved ATM Kinase RAG2-S365 Phosphorylation Site Limits Cleavage Events in Individual Cells Independent of Any Repair Defect. <i>Cell Reports</i> , 2017 , 21, 979-993	10.6	4
19	Quantifying DNA End Resection in Human Cells. <i>Methods in Molecular Biology</i> , 2021 , 2153, 59-69	1.4	4
18	Purification and Biophysical Characterization of the Mre11-Rad50-Nbs1 Complex. <i>Methods in Molecular Biology</i> , 2019 , 2004, 269-287	1.4	3
17	The Cancer-Associated ATM R3008H Mutation Reveals the Link between ATM Activation and Its Exchange. <i>Cancer Research</i> , 2021 , 81, 426-437	10.1	3
16	Reconsidering pathway choice: a sequential model of mammalian DNA double-strand break pathway decisions. <i>Current Opinion in Genetics and Development</i> , 2021 , 71, 55-62	4.9	3
15	Rad17, the clamp loader that loads more than clamps. <i>EMBO Journal</i> , 2014 , 33, 783-5	13	2
14	Upregulation of E. coli 38kDa proteins induced by glutaraldehyde and formaldehyde. <i>Current Microbiology</i> , 1990 , 21, 117-121	2.4	2
13	ATM and PRDM9 Regulate SPO11-bound Recombination Intermediates During Meiosis		2
12	DNA-dependent protein kinase promotes DNA end processing by MRN and CtIP		2
11	Growth-Regulated Hsp70 Phosphorylation Regulates Stress Responses and Prion Maintenance. <i>Molecular and Cellular Biology</i> , 2020 , 40,	4.8	1
10	DNA damage and regulation of protein homeostasis. <i>DNA Repair</i> , 2021 , 105, 103155	4.3	1
9	Characterization of DNA-PK-Bound End Fragments Using GLASS-ChIP.. <i>Methods in Molecular Biology</i> , 2022 , 2444, 171-182	1.4	0
8	Characterization of DNA-PK-bound end fragments using GLASS-ChIP. <i>Methods in Enzymology</i> , 2021 , 661, 205-217	1.7	

- 7 The Mre11/Rad50 complex and its roles in processing of DNA double-strand breaks. *FASEB Journal*, **2008**, 22, 405.2 0.9
- 6 Proteome-wide identification of HSP70/HSC70 chaperone clients in human cells **2020**, 18, e3000606
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