

Tanya T Paull

List of Publications by Year in descending order

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108
papers

15,909
citations

20759

60
h-index

28224

105
g-index

122
all docs

122
docs citations

122
times ranked

15689
citing authors

#	ARTICLE	IF	CITATIONS
1	A critical role for histone H2AX in recruitment of repair factors to nuclear foci after DNA damage. <i>Current Biology</i> , 2000, 10, 886-895.	1.8	1,867
2	ATM Activation by DNA Double-Strand Breaks Through the Mre11-Rad50-Nbs1 Complex. <i>Science</i> , 2005, 308, 551-554.	6.0	1,218
3	ATM Activation by Oxidative Stress. <i>Science</i> , 2010, 330, 517-521.	6.0	931
4	The 3' to 5' Exonuclease Activity of Mre11 Facilitates Repair of DNA Double-Strand Breaks. <i>Molecular Cell</i> , 1998, 1, 969-979.	4.5	793
5	Direct Activation of the ATM Protein Kinase by the Mre11/Rad50/Nbs1 Complex. <i>Science</i> , 2004, 304, 93-96.	6.0	653
6	MDC1 Maintains Genomic Stability by Participating in the Amplification of ATM-Dependent DNA Damage Signals. <i>Molecular Cell</i> , 2006, 21, 187-200.	4.5	553
7	Nbs1 potentiates ATP-driven DNA unwinding and endonuclease cleavage by the Mre11/Rad50 complex. <i>Genes and Development</i> , 1999, 13, 1276-1288.	2.7	471
8	Activation and regulation of ATM kinase activity in response to DNA double-strand breaks. <i>Oncogene</i> , 2007, 26, 7741-7748.	2.6	456
9	Mechanisms of ATM Activation. <i>Annual Review of Biochemistry</i> , 2015, 84, 711-738.	5.0	374
10	ATM functions at the peroxisome to induce pexophagy in response to ROS. <i>Nature Cell Biology</i> , 2015, 17, 1259-1269.	4.6	361
11	A forward chemical genetic screen reveals an inhibitor of the Mre11-Rad50-Nbs1 complex. <i>Nature Chemical Biology</i> , 2008, 4, 119-125.	3.9	340
12	The nonspecific DNA-binding and -bending proteins HMG1 and HMG2 promote the assembly of complex nucleoprotein structures. <i>Genes and Development</i> , 1993, 7, 1521-1534.	2.7	320
13	The ATM protein kinase and cellular redox signaling: beyond the DNA damage response. <i>Trends in Biochemical Sciences</i> , 2012, 37, 15-22.	3.7	289
14	Sae2 Is an Endonuclease that Processes Hairpin DNA Cooperatively with the Mre11/Rad50/Xrs2 Complex. <i>Molecular Cell</i> , 2007, 28, 638-651.	4.5	253
15	Direct DNA binding by Brca1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 6086-6091.	3.3	239
16	Stimulation of V(D)J cleavage by high mobility group proteins. <i>EMBO Journal</i> , 1997, 16, 2665-2670.	3.5	234
17	Single-stranded DNA-binding protein hSSB1 is critical for genomic stability. <i>Nature</i> , 2008, 453, 677-681.	13.7	220
18	Involvement of Human MOF in ATM Function. <i>Molecular and Cellular Biology</i> , 2005, 25, 5292-5305.	1.1	215

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19	Saccharomyces cerevisiae Mre11/Rad50/Xrs2 and Ku proteins regulate association of Exo1 and Dna2 with DNA breaks. EMBO Journal, 2010, 29, 3370-3380.	3.5	197
20	Quantitation of DNA double-strand break resection intermediates in human cells. Nucleic Acids Research, 2014, 42, e19-e19.	6.5	197
21	Mre11/Rad50/Xrs2 and Sae2 promote 5' strand resection of DNA double-strand breaks. Nature Structural and Molecular Biology, 2010, 17, 1478-1485.	3.6	195
22	A mechanistic basis for Mre11-directed DNA joining at microhomologies. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 6409-6414.	3.3	181
23	The Mre11/Rad50/Nbs1 Complex and Its Role as a DNA Double-Strand Break Sensor for ATM. Cell Cycle, 2005, 4, 737-740.	1.3	163
24	ATM activation in the presence of oxidative stress. Cell Cycle, 2010, 9, 4805-4811.	1.3	159
25	Catalytic and Noncatalytic Roles of the CtIP Endonuclease in Double-Strand Break End Resection. Molecular Cell, 2014, 54, 1022-1033.	4.5	158
26	Single-Molecule Imaging Reveals How Mre11-Rad50-Nbs1 Initiates DNA Break Repair. Molecular Cell, 2017, 67, 891-898.e4.	4.5	156
27	Hyperthermia Activates a Subset of Ataxia-Telangiectasia Mutated Effectors Independent of DNA Strand Breaks and Heat Shock Protein 70 Status. Cancer Research, 2007, 67, 3010-3017.	0.4	153
28	The P. furiosus Mre11/Rad50 Complex Promotes 5' Strand Resection at a DNA Double-Strand Break. Cell, 2008, 135, 250-260.	13.5	146
29	DNA replication initiates at multiple sites on plasmid DNA in Xenopus egg extracts. Nucleic Acids Research, 1992, 20, 1457-1462.	6.5	145
30	Mre11 Is Essential for the Removal of Lethal Topoisomerase 2 Covalent Cleavage Complexes. Molecular Cell, 2016, 64, 580-592.	4.5	144
31	Cell-free V(D)J recombination. Nature, 1997, 388, 488-491.	13.7	136
32	Nbs1 Converts the Human Mre11/Rad50 Nuclease Complex into an Endo/Exonuclease Machine Specific for Protein-DNA Adducts. Molecular Cell, 2016, 64, 593-606.	4.5	131
33	ATP-driven Rad50 conformations regulate DNA tethering, end resection, and ATM checkpoint signaling. EMBO Journal, 2014, 33, 482-500.	3.5	129
34	Ctp1/CtIP and the MRN Complex Collaborate in the Initial Steps of Homologous Recombination. Molecular Cell, 2007, 28, 351-352.	4.5	115
35	Human Mre11/Human Rad50/Nbs1 and DNA Ligase III \pm /XRCC1 Protein Complexes Act Together in an Alternative Nonhomologous End Joining Pathway. Journal of Biological Chemistry, 2011, 286, 33845-33853.	1.6	113
36	20 Years of Mre11 Biology: No End in Sight. Molecular Cell, 2018, 71, 419-427.	4.5	108

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37	53BP1 promotes ATM activity through direct interactions with the MRN complex. <i>EMBO Journal</i> , 2010, 29, 574-585.	3.5	105
38	Regulation of the DNA Damage Response by DNA-PKcs Inhibitory Phosphorylation of ATM. <i>Molecular Cell</i> , 2017, 65, 91-104.	4.5	105
39	Cellular functions of the protein kinase ATM and their relevance to human disease. <i>Nature Reviews Molecular Cell Biology</i> , 2021, 22, 796-814.	16.1	105
40	DNA Looping by <i>Saccharomyces cerevisiae</i> High Mobility Group Proteins NHP6A/B. <i>Journal of Biological Chemistry</i> , 1995, 270, 8744-8754.	1.6	102
41	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, 2769-2781.	2.7	102
42	Multiple autophosphorylation sites are dispensable for murine ATM activation in vivo. <i>Journal of Cell Biology</i> , 2008, 183, 777-783.	2.3	100
43	Rad50 Adenylate Kinase Activity Regulates DNA Tethering by Mre11/Rad50 Complexes. <i>Molecular Cell</i> , 2007, 25, 647-661.	4.5	94
44	Loss of ATM kinase activity leads to embryonic lethality in mice. <i>Journal of Cell Biology</i> , 2012, 198, 295-304.	2.3	94
45	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, 12840-12851.	1.6	92
46	Polo-like kinase 3 regulates CtIP during DNA double-strand break repair in G1. <i>Journal of Cell Biology</i> , 2014, 206, 877-894.	2.3	92
47	DNA-dependent protein kinase promotes DNA end processing by MRN and CtIP. <i>Science Advances</i> , 2020, 6, eaay0922.	4.7	92
48	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.	2.7	89
49	ATM directs DNA damage responses and proteostasis via genetically separable pathways. <i>Science Signaling</i> , 2018, 11, .	1.6	87
50	The Rad50 Signature Motif: Essential to ATP Binding and Biological Function. <i>Journal of Molecular Biology</i> , 2004, 335, 937-951.	2.0	85
51	CtIP: A DNA damage response protein at the intersection of DNA metabolism. <i>DNA Repair</i> , 2015, 32, 75-81.	1.3	83
52	Collaboration of Werner syndrome protein and BRCA1 in cellular responses to DNA interstrand cross-links. <i>Nucleic Acids Research</i> , 2006, 34, 2751-2760.	6.5	82
53	Regulation of Mre11/Rad50 by Nbs1. <i>Journal of Biological Chemistry</i> , 2003, 278, 45171-45181.	1.6	81
54	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, E1170-9.	3.3	81

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55	ATM and PRDM9 regulate SPO11-bound recombination intermediates during meiosis. <i>Nature Communications</i> , 2020, 11, 857.	5.8	81
56	MRI Is a DNA Damage Response Adaptor during Classical Non-homologous End Joining. <i>Molecular Cell</i> , 2018, 71, 332-342.e8.	4.5	76
57	ATM Protein-dependent Phosphorylation of Rad50 Protein Regulates DNA Repair and Cell Cycle Control. <i>Journal of Biological Chemistry</i> , 2011, 286, 31542-31556.	1.6	74
58	The SOSS1 single-stranded DNA binding complex promotes DNA end resection in concert with Exo1. <i>EMBO Journal</i> , 2012, 32, 126-139.	3.5	74
59	RPA Phosphorylation Inhibits DNA Resection. <i>Molecular Cell</i> , 2019, 75, 145-153.e5.	4.5	73
60	Mitochondrial redox sensing by the kinase ATM maintains cellular antioxidant capacity. <i>Science Signaling</i> , 2018, 11, .	1.6	71
61	Making the best of the loose ends: Mre11/Rad50 complexes and Sae2 promote DNA double-strand break resection. <i>DNA Repair</i> , 2010, 9, 1283-1291.	1.3	70
62	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.	7.7	70
63	ZMYM3 regulates BRCA1 localization at damaged chromatin to promote DNA repair. <i>Genes and Development</i> , 2017, 31, 260-274.	2.7	65
64	EXD2 promotes homologous recombination by facilitating DNA end resection. <i>Nature Cell Biology</i> , 2016, 18, 271-280.	4.6	61
65	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, 37112-37125.	1.6	58
66	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, 18868-18873.	3.3	55
67	Sae2/CtIP prevents R-loop accumulation in eukaryotic cells. <i>ELife</i> , 2018, 7, .	2.8	55
68	The Mre11/Rad50/Xrs2 complex and non-homologous end-joining of incompatible ends in <i>S. cerevisiae</i> . <i>DNA Repair</i> , 2005, 4, 1281-1294.	1.3	53
69	Mitochondria at the crossroads of ATM-mediated stress signaling and regulation of reactive oxygen species. <i>Redox Biology</i> , 2020, 32, 101511.	3.9	50
70	The Mre11/Rad50/Nbs1 complex: Recent insights into catalytic activities and ATP-driven conformational changes. <i>Experimental Cell Research</i> , 2014, 329, 139-147.	1.2	44
71	Proteome-wide identification of HSP70/HSC70 chaperone clients in human cells. <i>PLoS Biology</i> , 2020, 18, e3000606.	2.6	43
72	Phosphorylation-Regulated Transitions in an Oligomeric State Control the Activity of the Sae2 DNA Repair Enzyme. <i>Molecular and Cellular Biology</i> , 2014, 34, 778-793.	1.1	41

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73	Homology-directed repair protects the replicating genome from metabolic assaults. <i>Developmental Cell</i> , 2021, 56, 461-477.e7.	3.1	38
74	Purification and Biochemical Characterization of Ataxia-telangiectasia Mutated and Mre11/Rad50/Nbs1. <i>Methods in Enzymology</i> , 2006, 408, 529-539.	0.4	36
75	Functional Activation of ATM by the Prostate Cancer Suppressor NKX3.1. <i>Cell Reports</i> , 2013, 4, 516-529.	2.9	33
76	BRCA1 and CtIP Are Both Required to Recruit Dna2 at Double-Strand Breaks in Homologous Recombination. <i>PLoS ONE</i> , 2015, 10, e0124495.	1.1	33
77	Damage-induced BRCA1 phosphorylation by Chk2 contributes to the timing of end resection. <i>Cell Cycle</i> , 2015, 14, 437-448.	1.3	33
78	Poly-ADP-ribosylation drives loss of protein homeostasis in ATM and Mre11 deficiency. <i>Molecular Cell</i> , 2021, 81, 1515-1533.e5.	4.5	33
79	Redox activation of ATM enhances GSNOR translation to sustain mitophagy and tolerance to oxidative stress. <i>EMBO Reports</i> , 2021, 22, e50500.	2.0	30
80	Ancient and Recent Adaptive Evolution of Primate Non-Homologous End Joining Genes. <i>PLoS Genetics</i> , 2010, 6, e1001169.	1.5	28
81	Sumoylation Influences DNA Break Repair Partly by Increasing the Solubility of a Conserved End Resection Protein. <i>PLoS Genetics</i> , 2015, 11, e1004899.	1.5	27
82	Rad50 ATPase activity is regulated by DNA ends and requires coordination of both active sites. <i>Nucleic Acids Research</i> , 2017, 45, 5255-5268.	6.5	27
83	Saving the Ends for Last: The Role of Pol η in DNA End Joining. <i>Molecular Cell</i> , 2005, 19, 294-296.	4.5	26
84	Direct Activation of ATM by Resveratrol under Oxidizing Conditions. <i>PLoS ONE</i> , 2014, 9, e97969.	1.1	26
85	HU and functional analogs in eukaryotes promote Hin invertasome assembly. <i>Biochimie</i> , 1994, 76, 992-1004.	1.3	22
86	V(D)J Recombination: Links to Transposition and Double-strand Break Repair. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 1999, 64, 161-168.	2.0	22
87	Proteome-wide Detection and Quantitative Analysis of Irreversible Cysteine Oxidation Using Long Column UPLC-pSRM. <i>Journal of Proteome Research</i> , 2013, 12, 4302-4315.	1.8	22
88	New Glimpses of an Old Machine. <i>Cell</i> , 2001, 107, 563-565.	13.5	19
89	Direct measurement of single-stranded DNA intermediates in mammalian cells by quantitative polymerase chain reaction. <i>Analytical Biochemistry</i> , 2015, 479, 48-50.	1.1	19
90	RNA-DNA hybrids and the convergence with DNA repair. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2019, 54, 371-384.	2.3	19

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91	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.	2.9	18
92	Tails of histones lost. <i>Nature</i> , 2006, 439, 406-407.	13.7	17
93	Genetic Separation of Sae2 Nuclease Activity from Mre11 Nuclease Functions in Budding Yeast. <i>Molecular and Cellular Biology</i> , 2017, 37, .	1.1	13
94	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.	1.5	12
95	Homeodomain Proteins Directly Regulate ATM Kinase Activity. <i>Cell Reports</i> , 2018, 24, 1471-1483.	2.9	7
96	The Cancer-Associated ATM R3008H Mutation Reveals the Link between ATM Activation and Its Exchange. <i>Cancer Research</i> , 2021, 81, 426-437.	0.4	7
97	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.	2.9	6
98	Purification and Biophysical Characterization of the Mre11-Rad50-Nbs1 Complex. <i>Methods in Molecular Biology</i> , 2019, 2004, 269-287.	0.4	6
99	DNA damage and regulation of protein homeostasis. <i>DNA Repair</i> , 2021, 105, 103155.	1.3	6
100	Quantifying DNA End Resection in Human Cells. <i>Methods in Molecular Biology</i> , 2021, 2153, 59-69.	0.4	5
101	Growth-Regulated Hsp70 Phosphorylation Regulates Stress Responses and Prion Maintenance. <i>Molecular and Cellular Biology</i> , 2020, 40, .	1.1	4
102	Rad17, the clamp loader that loads more than clamps. <i>EMBO Journal</i> , 2014, 33, 783-785.	3.5	3
103	Upregulation of E. coli 38kDa proteins induced by glutaraldehyde and formaldehyde. <i>Current Microbiology</i> , 1990, 21, 117-121.	1.0	2
104	Characterization of DNA-PK-Bound End Fragments Using GLASS-ChIP. <i>Methods in Molecular Biology</i> , 2022, 2444, 171-182.	0.4	2
105	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.	1.1	0
106	Visualizing the First Steps of Human Double-Strand Break Repair on a Crowded DNA Track. <i>Biophysical Journal</i> , 2016, 110, 65a.	0.2	0
107	The Mre11/Rad50 complex and its roles in processing of DNA double-strand breaks. <i>FASEB Journal</i> , 2008, 22, 405.2.	0.2	0
108	Characterization of DNA-PK-bound end fragments using GLASS-ChIP. <i>Methods in Enzymology</i> , 2021, 661, 205-217.	0.4	0