John H J Petrini

List of Publications by Year
in descending order

96 papers	9,994 citations	41344 49 h-index	48315 88 g-index
102 all docs	102 docs citations	102 times ranked	10601 citing authors

#	Article	IF	Citations
1	RTEL1 influences the abundance and localization of TERRA RNA. Nature Communications, 2021, 12, 3016.	12.8	30
2	RTEL1 suppresses G-quadruplex-associated R-loops at difficult-to-replicate loci in the human genome. Nature Structural and Molecular Biology, 2020, 27, 424-437.	8.2	60
3	Tumour predisposition and cancer syndromes as models to study geneâ€“environment interactions. Nature Reviews Cancer, 2020, 20, 533-549.	28.4	93
4	Modeling cancer genomic data in yeast reveals selection against ATM function during tumorigenesis. PLoS Genetics, 2020, 16, e1008422.	3.5	17
5	A P53-Independent DNA Damage Response Suppresses Oncogenic Proliferation and Genome Instability. Cell Reports, 2020, 30, 1385-1399.e7.	6.4	29
6	A Disease-Causing Single Amino Acid Deletion in the Coiled-Coil Domain of RAD50 Impairs MRE11 Complex Functions in Yeast and Humans. Cell Reports, 2020, 33, 108559.	6.4	7
7	Oncogene-induced DNA damage: cyclic AMP steps into the ring. Journal of Clinical Investigation, 2020, 130, 5668-5670.	8.2	4
8	Modeling cancer genomic data in yeast reveals selection against ATM function during tumorigenesis. , 2020, 16, e1008422.		0
9	Modeling cancer genomic data in yeast reveals selection against ATM function during tumorigenesis. , 2020, 16, e1008422.		0
10	Modeling cancer genomic data in yeast reveals selection against ATM function during tumorigenesis. , 2020, 16, e1008422.		0
11	Modeling cancer genomic data in yeast reveals selection against ATM function during tumorigenesis. , 2020, 16, e1008422.		0
12	Modeling cancer genomic data in yeast reveals selection against ATM function during tumorigenesis. , 2020, 16, e1008422.		0
13	Modeling cancer genomic data in yeast reveals selection against ATM function during tumorigenesis. , 2020, 16, e1008422.		0
14	Nej1 Interacts with Mre11 to Regulate Tethering and Dna2 Binding at DNA Double-Strand Breaks. Cell Reports, 2019, 28, 1564-1573.e3.	6.4	27
15	Nbnâ^'Mre11 interaction is required for tumor suppression and genomic integrity. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 15178-15183.	7.1	8
16	The telomere-binding protein Rif2 and ATP-bound Rad50 have opposing roles in the activation of yeast Tel1ATM kinase. Journal of Biological Chemistry, 2019, 294, 18846-18852.	3.4	19
17	Mouse DCUN1D1 (SCCRO) is required for spermatogenetic individualization. PLoS ONE, 2019, 14, e0209995.	2.5	8
18	Eukaryotic Rad50 functions as a rod-shaped dimer. Nature Structural and Molecular Biology, 2017, 24, 248-257.	8.2	63

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19	The Mre11-Nbs1 Interface Is Essential for Viability and Tumor Suppression. Cell Reports, 2017, 18, 496-507.	6.4	39
20	Therapeutic targeting of PGBD5-induced DNA repair dependency in pediatric solid tumors. Science Translational Medicine, 2017, 9, .	12.4	48
21	Massively parallel sequencing of phyllodes tumours of the breast reveals actionable mutations, and <i><scp>TERT</scp></i> promoter hotspot mutations and <i>TERT</i> gene amplification as likely drivers of progression. Journal of Pathology, 2016, 238, 508-518.	4.5	102
22	Generation of a novel, multi-stage, progressive, and transplantable model of plasma cell neoplasms. Scientific Reports, 2016, 6, 22760.	3.3	4
23	A Damage-Independent Role for 53BP1 that Impacts Break Order and Igh Architecture during Class Switch Recombination. Cell Reports, 2016, 16, 48-55.	6.4	29
24	Defining ATM-Independent Functions of the Mre11 Complex with a Novel Mouse Model. Molecular Cancer Research, 2016, 14, 185-195.	3.4	9
25	Functions of the MRE11 complex in the development and maintenance of oocytes. Chromosoma, 2016, 125, 151-162.	2.2	17
26	TRF2 Recruits RTEL1 to Telomeres in S Phase to Promote T-Loop Unwinding. Molecular Cell, 2015, 57, 622-635.	9.7	143
27	Interdependence of the Rad50 Hook and Globular Domain Functions. Molecular Cell, 2015, 57, 479-491.	9.7	46
28	The Rad50 hook domain regulates DNA damage signaling and tumorigenesis. Genes and Development, 2014, 28, 451-462.	5.9	43
29	Synthetic Lethality in ATM-Deficient <i>RAD50</i>-Mutant Tumors Underlies Outlier Response to Cancer Therapy. Cancer Discovery, 2014, 4, 1014-1021.	9.4	114
30	Aberrant topoisomerase-1 DNA lesions are pathogenic in neurodegenerative genome instability syndromes. Nature Neuroscience, 2014, 17, 813-821.	14.8	128
31	Rad50-CARD9 interactions link cytosolic DNA sensing to IL-1Î² production. Nature Immunology, 2014, 15, 538-545.	14.5	132
32	The Mre11 Complex Suppresses Oncogene-Driven Breast Tumorigenesis and Metastasis. Molecular Cell, 2013, 52, 353-365.	9.7	46
33	The Ku Heterodimer and the Metabolism of Single-Ended DNA Double-Strand Breaks. Cell Reports, 2013, 3, 2033-2045.	6.4	43
34	A Recessive Founder Mutation in Regulator of Telomere Elongation Helicase 1, RTEL1, Underlies Severe Immunodeficiency and Features of Hoyeraal Hreidarsson Syndrome. PLoS Genetics, 2013, 9, e1003695.	3.5	106
35	Higher Than Expected Carrier Frequency Of The Dyskeratosis Congenita RTEL1 p.Arg1264His recessive Founder In Individuals Of Ashkenazi Jewish Ancestry. Blood, 2013, 122, 1228-1228.	1.4	0
36	Chemical Genetics Reveals a Specific Requirement for Cdk2 Activity in the DNA Damage Response and Identifies Nbs1 as a Cdk2 Substrate in Human Cells. PLoS Genetics, 2012, 8, e1002935.	3.5	54

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37	Loss of ATRX, Genome Instability, and an Altered DNA Damage Response Are Hallmarks of the Alternative Lengthening of Telomeres Pathway. PLoS Genetics, 2012, 8, e1002772.	3.5	489
38	Cell cycle- and DNA repair pathway-specific effects of apoptosis on tumor suppression. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 9953-9958.	7.1	55
39	Cohesin Association to Replication Sites Depends on Rad50 and Promotes Fork Restart. Molecular Cell, 2012, 48, 98-108.	9.7	108
40	Whole exome sequencing identifies ATRX mutation as a key molecular determinant in lower-grade glioma. Oncotarget, 2012, 3, 1194-1203.	1.8	241
41	Generation of a Novel, Multi-Stage, Progressive, and Transplantable Model of Multiple Myeloma. Blood, 2012, 120, 327-327.	1.4	0
42	The MRE11 complex: starting from the ends. Nature Reviews Molecular Cell Biology, 2011, 12, 90-103.	37.0	612
43	Functional Interplay of the Mre11 Nuclease and Ku in the Response to Replication-Associated DNA Damage. Molecular and Cellular Biology, 2011, 31, 4379-4389.	2.3	94
44	The Rad50 coiled-coil domain is indispensable for Mre11 complex functions. Nature Structural and Molecular Biology, 2011, 18, 1124-1131.	8.2	88
45	Loss of ATM/Chk2/p53 Pathway Components Accelerates Tumor Development and Contributes toÂRadiation Resistance in Gliomas. Cancer Cell, 2010, 18, 619-629.	16.8	211
46	Long-lived Min Mice Develop Advanced Intestinal Cancers through a Genetically Conservative Pathway. Cancer Research, 2009, 69, 5768-5775.	0.9	43
47	Rad50 Is Dispensable for the Maintenance and Viability of Postmitotic Tissues. Molecular and Cellular Biology, 2009, 29, 483-492.	2.3	41
48	Division of labor: DNA repair and the cell cycle specific functions of the Mre11 complex. Cell Cycle, 2009, 8, 1510-1514.	2.6	7
49	The Mre11 Complex and the Response to Dysfunctional Telomeres. Molecular and Cellular Biology, 2009, 29, 5540-5551.	2.3	59
50	Differential DNA damage signaling accounts for distinct neural apoptotic responses in ATLD and NBS. Genes and Development, 2009, 23, 171-180.	5.9	92
51	Artemis and Nonhomologous End Joining-Independent Influence of DNA-Dependent Protein Kinase Catalytic Subunit on Chromosome Stability. Molecular and Cellular Biology, 2009, 29, 503-514.	2.3	17
52	Taking the time to make important decisions: The checkpoint effector kinases Chk1 and Chk2 and the DNA damage response. DNA Repair, 2009, 8, 1047-1054.	2.8	202
53	Checkpoint response to DNA damage. DNA Repair, 2009, 8, 973-973.	2.8	3
54	NBS1 cooperates with homologous recombination to counteract chromosome breakage during replication. DNA Repair, 2009, 8, 1363-1370.	2.8	8

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55	DNA Replication Reaches the Breaking Point. Cell, 2009, 137, 211-212.	28.9	2
56	Maintenance of the DNA-Damage Checkpoint Requires DNA-Damage-Induced Mediator Protein Oligomerization. Molecular Cell, 2009, 33, 147-159.	9.7	51
57	Roles for NBS1 in Alternative Nonhomologous End-Joining of V(D)J Recombination Intermediates. Molecular Cell, 2009, 34, 13-25.	9.7	98
58	Chk2 Suppresses the Oncogenic Potential of DNA Replication-Associated DNA Damage. Molecular Cell, 2008, 31, 21-32.	9.7	58
59	Working together and apart: The twisted relationship of the Mre11 complex and Chk2 in apoptosis and tumor suppression. Cell Cycle, 2008, 7, 3618-3621.	2.6	11
60	Functional Interactions Between Sae2 and the Mre11 Complex. Genetics, 2008, 178, 711-723.	2.9	51
61	ZIP4H (TEX11) Deficiency in the Mouse Impairs Meiotic Double Strand Break Repair and the Regulation of Crossing Over. PLoS Genetics, 2008, 4, e1000042.	3.5	106
62	DNA Damage Signaling in Hematopoietic Cells: A Role for Mre11 Complex Repair of Topoisomerase Lesions. Cancer Research, 2008, 68, 2186-2193.	0.9	17
63	The Saccharomyces cerevisiae 14-3-3 proteins Bmh1 and Bmh2 directly influence the DNA damage-dependent functions of Rad53. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 2797-2802.	7.1	39
64	CELL SIGNALING: A Touching Response to Damage. Science, 2007, 316, 1138-1139.	12.6	25
65	Mre11 and Ku regulation of double-strand break repair by gene conversion and break-induced replication. DNA Repair, 2007, 6, 797-808.	2.8	25
66	The carboxy terminus of NBS1 is required for induction of apoptosis by the MRE11 complex. Nature, 2007, 447, 218-221.	27.8	109
67	The Mre11 Complex Influences DNA Repair, Synapsis, and Crossing Over in Murine Meiosis. Current Biology, 2007, 17, 373-378.	3.9	179
68	Rad50S alleles of the Mre11 complex: Questions answered and questions raised. Experimental Cell Research, 2006, 312, 2694-2699.	2.6	24
69	Modeling disease in the mouse: Lessons from DNA damage response and cell cycle control genes. Journal of Cellular Biochemistry, 2006, 97, 459-473.	2.6	8
70	Methods for Studying the Cellular Response to DNA Damage: Influence of the Mre11 Complex on Chromosome Metabolism. Methods in Enzymology, 2006, 409, 251-284.	1.0	28
71	At the end, remodeling leads to eviction. Nature Structural and Molecular Biology, 2005, 12, 1028-1029.	8.2	8
72	The Rad50 hook domain is a critical determinant of Mre11 complex functions. Nature Structural and Molecular Biology, 2005, 12, 403-407.	8.2	135

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73	The BRCA1-interacting helicase BRIP1 is deficient in Fanconi anemia. Nature Genetics, 2005, 37, 931-933.	21.4	337
74	Srs2 and Sgs1 DNA Helicases Associate with Mre11 in Different Subcomplexes following Checkpoint Activation and CDK1-Mediated Srs2 Phosphorylation. Molecular and Cellular Biology, 2005, 25, 5738-5751.	2.3	80
75	The <i>Rad50^S</i> allele promotes ATM-dependent DNA damage responses and suppresses ATM deficiency: implications for the Mre11 complex as a DNA damage sensor. Genes and Development, 2005, 19, 3043-3054.	5.9	79
76	RAD50 and NBS1 are breast cancer susceptibility genes associated with genomic instability. Carcinogenesis, 2005, 27, 1593-1599.	2.8	179
77	Activation of the DNA Damage Response by Telomere Attrition: A Passage to Cellular Senescence. Cell Cycle, 2004, 3, 541-544.	2.6	61
78	The Telomeric Protein TRF2 Binds the ATM Kinase and Can Inhibit the ATM-Dependent DNA Damage Response. PLoS Biology, 2004, 2, e240.	5.6	306
79	Distribution and Dynamics of Chromatin Modification Induced by a Defined DNA Double-Strand Break. Current Biology, 2004, 14, 1703-1711.	3.9	458
80	The Mre11 complex and the metabolism of chromosome breaks: the importance of communicating and holding things together. DNA Repair, 2004, 3, 845-854.	2.8	234
81	Association of Mre11p with Double-Strand Break Sites during Yeast Meiosis. Molecular Cell, 2004, 13, 389-401.	9.7	129
82	The cellular response to DNA double-strand breaks: defining the sensors and mediators. Trends in Cell Biology, 2003, 13, 458-462.	7.9	305
83	Checkpoint Failure and Chromosomal Instability without Lymphomagenesis in Mre11ATLD1/ATLD1 Mice. Molecular Cell, 2003, 12, 1511-1523.	9.7	157
84	DNA replication-dependent nuclear dynamics of the Mre11 complex. Molecular Cancer Research, 2003, 1, 207-18.	3.4	147
85	Cancer predisposition and hematopoietic failure in <i>Rad50^{S/S}</i> mice. Genes and Development, 2002, 16, 2237-2251.	5.9	180
86	The DNA damage-dependent intraâ€“S phase checkpoint is regulated by parallel pathways. Nature Genetics, 2002, 30, 290-294.	21.4	350
87	Complementation between N-terminal Saccharomyces cerevisiae mre11 alleles in DNA repair and telomere length maintenance. DNA Repair, 2002, 1, 27-40.	2.8	67
88	A Murine Model of Nijmegen Breakage Syndrome. Current Biology, 2002, 12, 648-653.	3.9	191
89	The Rad50 zinc-hook is a structure joining Mre11 complexes in DNA recombination and repair. Nature, 2002, 418, 562-566.	27.8	485
90	Mre11 Complex and DNA Replication: Linkage to E2F and Sites of DNA Synthesis. Molecular and Cellular Biology, 2001, 21, 6006-6016.	2.3	199

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91	DNA Damage-Dependent Nuclear Dynamics of the Mre11 Complex. Molecular and Cellular Biology, 2001, 21, 281-288.	2.3	369
92	When more is better. Nature Genetics, 2000, 26, 257-258.	21.4	6
93	The Mre11-Rad50-Xrs2 Protein Complex Facilitates Homologous Recombination-Based Double-Strand Break Repair in <i>Saccharomyces cerevisiae</i>. Molecular and Cellular Biology, 1999, 19, 7681-7687.	2.3	251
94	In Situ Visualization of DNA Double-Strand Break Repair in Human Fibroblasts. Science, 1998, 280, 590-592.	12.6	466
95	Alteration of N-Terminal Phosphoesterase Signature Motifs Inactivates Saccharomyces cerevisiae Mre11. Genetics, 1998, 150, 591-600.	2.9	130
96	Nej1 Interacts with Mre11 to Regulate-Tethering and Dna2 Binding at DNA Double-Strand Breaks. SSRN Electronic Journal, 0, , .	0.4	0