

John H J Petrini

List of Publications by Year in descending order

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96
papers

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41344

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48315

88
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102
all docs

102
docs citations

102
times ranked

10601
citing authors

#	ARTICLE	IF	CITATIONS
1	The MRE11 complex: starting from the ends. <i>Nature Reviews Molecular Cell Biology</i> , 2011, 12, 90-103.	37.0	612
2	Loss of ATRX, Genome Instability, and an Altered DNA Damage Response Are Hallmarks of the Alternative Lengthening of Telomeres Pathway. <i>PLoS Genetics</i> , 2012, 8, e1002772.	3.5	489
3	The Rad50 zinc-hook is a structure joining Mre11 complexes in DNA recombination and repair. <i>Nature</i> , 2002, 418, 562-566.	27.8	485
4	In Situ Visualization of DNA Double-Strand Break Repair in Human Fibroblasts. <i>Science</i> , 1998, 280, 590-592.	12.6	466
5	Distribution and Dynamics of Chromatin Modification Induced by a Defined DNA Double-Strand Break. <i>Current Biology</i> , 2004, 14, 1703-1711.	3.9	458
6	DNA Damage-Dependent Nuclear Dynamics of the Mre11 Complex. <i>Molecular and Cellular Biology</i> , 2001, 21, 281-288.	2.3	369
7	The DNA damage-dependent intra-S phase checkpoint is regulated by parallel pathways. <i>Nature Genetics</i> , 2002, 30, 290-294.	21.4	350
8	The BRCA1-interacting helicase BRIP1 is deficient in Fanconi anemia. <i>Nature Genetics</i> , 2005, 37, 931-933.	21.4	337
9	The Telomeric Protein TRF2 Binds the ATM Kinase and Can Inhibit the ATM-Dependent DNA Damage Response. <i>PLoS Biology</i> , 2004, 2, e240.	5.6	306
10	The cellular response to DNA double-strand breaks: defining the sensors and mediators. <i>Trends in Cell Biology</i> , 2003, 13, 458-462.	7.9	305
11	The Mre11-Rad50-Xrs2 Protein Complex Facilitates Homologous Recombination-Based Double-Strand Break Repair in <i>Saccharomyces cerevisiae</i> . <i>Molecular and Cellular Biology</i> , 1999, 19, 7681-7687.	2.3	251
12	Whole exome sequencing identifies ATRX mutation as a key molecular determinant in lower-grade glioma. <i>Oncotarget</i> , 2012, 3, 1194-1203.	1.8	241
13	The Mre11 complex and the metabolism of chromosome breaks: the importance of communicating and holding things together. <i>DNA Repair</i> , 2004, 3, 845-854.	2.8	234
14	Loss of ATM/Chk2/p53 Pathway Components Accelerates Tumor Development and Contributes to Radiation Resistance in Gliomas. <i>Cancer Cell</i> , 2010, 18, 619-629.	16.8	211
15	Taking the time to make important decisions: The checkpoint effector kinases Chk1 and Chk2 and the DNA damage response. <i>DNA Repair</i> , 2009, 8, 1047-1054.	2.8	202
16	Mre11 Complex and DNA Replication: Linkage to E2F and Sites of DNA Synthesis. <i>Molecular and Cellular Biology</i> , 2001, 21, 6006-6016.	2.3	199
17	A Murine Model of Nijmegen Breakage Syndrome. <i>Current Biology</i> , 2002, 12, 648-653.	3.9	191
18	Cancer predisposition and hematopoietic failure in <i>Rad50^{S/S}</i> mice. <i>Genes and Development</i> , 2002, 16, 2237-2251.	5.9	180

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19	RAD50 and NBS1 are breast cancer susceptibility genes associated with genomic instability. <i>Carcinogenesis</i> , 2005, 27, 1593-1599.	2.8	179
20	The Mre11 Complex Influences DNA Repair, Synapsis, and Crossing Over in Murine Meiosis. <i>Current Biology</i> , 2007, 17, 373-378.	3.9	179
21	Checkpoint Failure and Chromosomal Instability without Lymphomagenesis in Mre11ATLD1/ATLD1 Mice. <i>Molecular Cell</i> , 2003, 12, 1511-1523.	9.7	157
22	DNA replication-dependent nuclear dynamics of the Mre11 complex. <i>Molecular Cancer Research</i> , 2003, 1, 207-18.	3.4	147
23	TRF2 Recruits RTEL1 to Telomeres in S Phase to Promote T-Loop Unwinding. <i>Molecular Cell</i> , 2015, 57, 622-635.	9.7	143
24	The Rad50 hook domain is a critical determinant of Mre11 complex functions. <i>Nature Structural and Molecular Biology</i> , 2005, 12, 403-407.	8.2	135
25	Rad50-CARD9 interactions link cytosolic DNA sensing to IL-1 β production. <i>Nature Immunology</i> , 2014, 15, 538-545.	14.5	132
26	Alteration of N-Terminal Phosphoesterase Signature Motifs Inactivates <i>Saccharomyces cerevisiae</i> Mre11. <i>Genetics</i> , 1998, 150, 591-600.	2.9	130
27	Association of Mre11p with Double-Strand Break Sites during Yeast Meiosis. <i>Molecular Cell</i> , 2004, 13, 389-401.	9.7	129
28	Aberrant topoisomerase-1 DNA lesions are pathogenic in neurodegenerative genome instability syndromes. <i>Nature Neuroscience</i> , 2014, 17, 813-821.	14.8	128
29	Synthetic Lethality in ATM-Deficient <i>rad50</i> -Mutant Tumors Underlies Outlier Response to Cancer Therapy. <i>Cancer Discovery</i> , 2014, 4, 1014-1021.	9.4	114
30	The carboxy terminus of NBS1 is required for induction of apoptosis by the MRE11 complex. <i>Nature</i> , 2007, 447, 218-221.	27.8	109
31	Cohesin Association to Replication Sites Depends on Rad50 and Promotes Fork Restart. <i>Molecular Cell</i> , 2012, 48, 98-108.	9.7	108
32	ZIP4H (TEX11) Deficiency in the Mouse Impairs Meiotic Double Strand Break Repair and the Regulation of Crossing Over. <i>PLoS Genetics</i> , 2008, 4, e1000042.	3.5	106
33	A Recessive Founder Mutation in Regulator of Telomere Elongation Helicase 1, RTEL1, Underlies Severe Immunodeficiency and Features of Hoyeraal Hreidarsson Syndrome. <i>PLoS Genetics</i> , 2013, 9, e1003695.	3.5	106
34	Massively parallel sequencing of phyllodes tumours of the breast reveals actionable mutations, and <i>TERT</i> promoter hotspot mutations and <i>TERT</i> gene amplification as likely drivers of progression. <i>Journal of Pathology</i> , 2016, 238, 508-518.	4.5	102
35	Roles for NBS1 in Alternative Nonhomologous End-Joining of V(D)J Recombination Intermediates. <i>Molecular Cell</i> , 2009, 34, 13-25.	9.7	98
36	Functional Interplay of the Mre11 Nuclease and Ku in the Response to Replication-Associated DNA Damage. <i>Molecular and Cellular Biology</i> , 2011, 31, 4379-4389.	2.3	94

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37	Tumour predisposition and cancer syndromes as models to study gene-environment interactions. <i>Nature Reviews Cancer</i> , 2020, 20, 533-549.	28.4	93
38	Differential DNA damage signaling accounts for distinct neural apoptotic responses in ATLD and NBS. <i>Genes and Development</i> , 2009, 23, 171-180.	5.9	92
39	The Rad50 coiled-coil domain is indispensable for Mre11 complex functions. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 1124-1131.	8.2	88
40	Srs2 and Sgs1 DNA Helicases Associate with Mre11 in Different Subcomplexes following Checkpoint Activation and CDK1-Mediated Srs2 Phosphorylation. <i>Molecular and Cellular Biology</i> , 2005, 25, 5738-5751.	2.3	80
41	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. <i>Genes and Development</i> , 2005, 19, 3043-3054.	5.9	79
42	Complementation between N-terminal <i>Saccharomyces cerevisiae</i> mre11 alleles in DNA repair and telomere length maintenance. <i>DNA Repair</i> , 2002, 1, 27-40.	2.8	67
43	Eukaryotic Rad50 functions as a rod-shaped dimer. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 248-257.	8.2	63
44	Activation of the DNA Damage Response by Telomere Attrition: A Passage to Cellular Senescence. <i>Cell Cycle</i> , 2004, 3, 541-544.	2.6	61
45	RTEL1 suppresses G-quadruplex-associated R-loops at difficult-to-replicate loci in the human genome. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 424-437.	8.2	60
46	The Mre11 Complex and the Response to Dysfunctional Telomeres. <i>Molecular and Cellular Biology</i> , 2009, 29, 5540-5551.	2.3	59
47	Chk2 Suppresses the Oncogenic Potential of DNA Replication-Associated DNA Damage. <i>Molecular Cell</i> , 2008, 31, 21-32.	9.7	58
48	Cell cycle- and DNA repair pathway-specific effects of apoptosis on tumor suppression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 9953-9958.	7.1	55
49	Chemical Genetics Reveals a Specific Requirement for Cdk2 Activity in the DNA Damage Response and Identifies Nbs1 as a Cdk2 Substrate in Human Cells. <i>PLoS Genetics</i> , 2012, 8, e1002935.	3.5	54
50	Functional Interactions Between Sae2 and the Mre11 Complex. <i>Genetics</i> , 2008, 178, 711-723.	2.9	51
51	Maintenance of the DNA-Damage Checkpoint Requires DNA-Damage-Induced Mediator Protein Oligomerization. <i>Molecular Cell</i> , 2009, 33, 147-159.	9.7	51
52	Therapeutic targeting of PGBD5-induced DNA repair dependency in pediatric solid tumors. <i>Science Translational Medicine</i> , 2017, 9, .	12.4	48
53	The Mre11 Complex Suppresses Oncogene-Driven Breast Tumorigenesis and Metastasis. <i>Molecular Cell</i> , 2013, 52, 353-365.	9.7	46
54	Interdependence of the Rad50 Hook and Globular Domain Functions. <i>Molecular Cell</i> , 2015, 57, 479-491.	9.7	46

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55	Long-lived Min Mice Develop Advanced Intestinal Cancers through a Genetically Conservative Pathway. <i>Cancer Research</i> , 2009, 69, 5768-5775.	0.9	43
56	The Ku Heterodimer and the Metabolism of Single-Ended DNA Double-Strand Breaks. <i>Cell Reports</i> , 2013, 3, 2033-2045.	6.4	43
57	The Rad50 hook domain regulates DNA damage signaling and tumorigenesis. <i>Genes and Development</i> , 2014, 28, 451-462.	5.9	43
58	Rad50 Is Dispensable for the Maintenance and Viability of Postmitotic Tissues. <i>Molecular and Cellular Biology</i> , 2009, 29, 483-492.	2.3	41
59	The <i>Saccharomyces cerevisiae</i> 14-3-3 proteins Bmh1 and Bmh2 directly influence the DNA damage-dependent functions of Rad53. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 2797-2802.	7.1	39
60	The Mre11-Nbs1 Interface Is Essential for Viability and Tumor Suppression. <i>Cell Reports</i> , 2017, 18, 496-507.	6.4	39
61	RTEL1 influences the abundance and localization of TERRA RNA. <i>Nature Communications</i> , 2021, 12, 3016.	12.8	30
62	A Damage-Independent Role for 53BP1 that Impacts Break Order and Igh Architecture during Class Switch Recombination. <i>Cell Reports</i> , 2016, 16, 48-55.	6.4	29
63	A P53-Independent DNA Damage Response Suppresses Oncogenic Proliferation and Genome Instability. <i>Cell Reports</i> , 2020, 30, 1385-1399.e7.	6.4	29
64	Methods for Studying the Cellular Response to DNA Damage: Influence of the Mre11 Complex on Chromosome Metabolism. <i>Methods in Enzymology</i> , 2006, 409, 251-284.	1.0	28
65	Nej1 Interacts with Mre11 to Regulate Tethering and Dna2 Binding at DNA Double-Strand Breaks. <i>Cell Reports</i> , 2019, 28, 1564-1573.e3.	6.4	27
66	CELL SIGNALING: A Touching Response to Damage. <i>Science</i> , 2007, 316, 1138-1139.	12.6	25
67	Mre11 and Ku regulation of double-strand break repair by gene conversion and break-induced replication. <i>DNA Repair</i> , 2007, 6, 797-808.	2.8	25
68	Rad50S alleles of the Mre11 complex: Questions answered and questions raised. <i>Experimental Cell Research</i> , 2006, 312, 2694-2699.	2.6	24
69	The telomere-binding protein Rif2 and ATP-bound Rad50 have opposing roles in the activation of yeast Tel1ATM kinase. <i>Journal of Biological Chemistry</i> , 2019, 294, 18846-18852.	3.4	19
70	DNA Damage Signaling in Hematopoietic Cells: A Role for Mre11 Complex Repair of Topoisomerase Lesions. <i>Cancer Research</i> , 2008, 68, 2186-2193.	0.9	17
71	Artemis and Nonhomologous End Joining-Independent Influence of DNA-Dependent Protein Kinase Catalytic Subunit on Chromosome Stability. <i>Molecular and Cellular Biology</i> , 2009, 29, 503-514.	2.3	17
72	Functions of the MRE11 complex in the development and maintenance of oocytes. <i>Chromosoma</i> , 2016, 125, 151-162.	2.2	17

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73	Modeling cancer genomic data in yeast reveals selection against ATM function during tumorigenesis. PLoS Genetics, 2020, 16, e1008422.	3.5	17
74	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
75	Defining ATM-Independent Functions of the Mre11 Complex with a Novel Mouse Model. Molecular Cancer Research, 2016, 14, 185-195.	3.4	9
76	At the end, remodeling leads to eviction. Nature Structural and Molecular Biology, 2005, 12, 1028-1029.	8.2	8
77	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
78	NBS1 cooperates with homologous recombination to counteract chromosome breakage during replication. DNA Repair, 2009, 8, 1363-1370.	2.8	8
79	Nbs1-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
80	Mouse DCUN1D1 (SCCRO) is required for spermatogenetic individualization. PLoS ONE, 2019, 14, e0209995.	2.5	8
81	Division of labor: DNA repair and the cell cycle specific functions of the Mre11 complex. Cell Cycle, 2009, 8, 1510-1514.	2.6	7
82	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
83	When more is better. Nature Genetics, 2000, 26, 257-258.	21.4	6
84	Generation of a novel, multi-stage, progressive, and transplantable model of plasma cell neoplasms. Scientific Reports, 2016, 6, 22760.	3.3	4
85	Oncogene-induced DNA damage: cyclic AMP steps into the ring. Journal of Clinical Investigation, 2020, 130, 5668-5670.	8.2	4
86	Checkpoint response to DNA damage. DNA Repair, 2009, 8, 973-973.	2.8	3
87	DNA Replication Reaches the Breaking Point. Cell, 2009, 137, 211-212.	28.9	2
88	Generation of a Novel, Multi-Stage, Progressive, and Transplantable Model of Multiple Myeloma. Blood, 2012, 120, 327-327.	1.4	0
89	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
90	Nej1 Interacts with Mre11 to Regulate-Tethering and Dna2 Binding at DNA Double-Strand Breaks. SSRN Electronic Journal, 0, , .	0.4	0

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91	Modeling cancer genomic data in yeast reveals selection against ATM function during tumorigenesis. , 2020, 16, e1008422.		0
92	Modeling cancer genomic data in yeast reveals selection against ATM function during tumorigenesis. , 2020, 16, e1008422.		0
93	Modeling cancer genomic data in yeast reveals selection against ATM function during tumorigenesis. , 2020, 16, e1008422.		0
94	Modeling cancer genomic data in yeast reveals selection against ATM function during tumorigenesis. , 2020, 16, e1008422.		0
95	Modeling cancer genomic data in yeast reveals selection against ATM function during tumorigenesis. , 2020, 16, e1008422.		0
96	Modeling cancer genomic data in yeast reveals selection against ATM function during tumorigenesis. , 2020, 16, e1008422.		0