

Thomas E Wilson

List of Publications by Year in descending order

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55
papers

4,917
citations

159585

30
h-index

161849

54
g-index

59
all docs

59
docs citations

59
times ranked

5371
citing authors

#	ARTICLE	IF	CITATIONS
1	Activity of DNA ligase IV stimulated by complex formation with XRCC4 protein in mammalian cells. <i>Nature</i> , 1997, 388, 492-495.	27.8	586
2	Yeast DNA ligase IV mediates non-homologous DNA end joining. <i>Nature</i> , 1997, 388, 495-498.	27.8	381
3	Nonhomologous End Joining in Yeast. <i>Annual Review of Genetics</i> , 2005, 39, 431-451.	7.6	353
4	Participation of Non-Zinc Finger Residues in DNA Binding by Two Nuclear Orphan Receptors. <i>Science</i> , 1992, 256, 107-110.	12.6	325
5	Repair of Double-Strand Breaks by End Joining. <i>Cold Spring Harbor Perspectives in Biology</i> , 2013, 5, a012757-a012757.	5.5	309
6	Rate of elongation by RNA polymerase II is associated with specific gene features and epigenetic modifications. <i>Genome Research</i> , 2014, 24, 896-905.	5.5	229
7	Yeast Tdp1 and Rad1-Rad10 function as redundant pathways for repairing Top1 replicative damage. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 13669-13674.	7.1	203
8	Mycobacterial Ku and Ligase Proteins Constitute a Two-Component NHEJ Repair Machine. <i>Science</i> , 2004, 306, 683-685.	12.6	193
9	Efficient Processing of DNA Ends during Yeast Nonhomologous End Joining. <i>Journal of Biological Chemistry</i> , 1999, 274, 23599-23609.	3.4	187
10	Fragile sites in cancer: more than meets the eye. <i>Nature Reviews Cancer</i> , 2017, 17, 489-501.	28.4	187
11	Large transcription units unify copy number variants and common fragile sites arising under replication stress. <i>Genome Research</i> , 2015, 25, 189-200.	5.5	152
12	Use of Bru-Seq and BruChase-Seq for genome-wide assessment of the synthesis and stability of RNA. <i>Methods</i> , 2014, 67, 45-54.	3.8	145
13	Recruitment and Dissociation of Nonhomologous End Joining Proteins at a DNA Double-Strand Break in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2008, 178, 1237-1249.	2.9	115
14	Coordinated regulation of synthesis and stability of RNA during the acute TNF-induced proinflammatory response. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 2240-2245.	7.1	112
15	Rejoining of DNA Double-Strand Breaks as a Function of Overhang Length. <i>Molecular and Cellular Biology</i> , 2005, 25, 896-906.	2.3	98
16	DNA Joint Dependence of Pol X Family Polymerase Action in Nonhomologous End Joining. <i>Journal of Biological Chemistry</i> , 2005, 280, 29030-29037.	3.4	95
17	Enhancement of <i>Saccharomyces cerevisiae</i> End-Joining Efficiency by Cell Growth Stage but Not by Impairment of Recombination. <i>Genetics</i> , 2002, 161, 1015-1027.	2.9	94
18	Genome-wide de novo L1 Retrotransposition Connects Endonuclease Activity with Replication. <i>Cell</i> , 2019, 177, 837-851.e28.	28.9	88

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19	Hydroxyurea induces de novo copy number variants in human cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 17360-17365.	7.1	82
20	Repair of DNA Strand Breaks by the Overlapping Functions of Lesion-Specific and Non-Lesion-Specific DNA 3' Phosphatases. <i>Molecular and Cellular Biology</i> , 2001, 21, 7191-7198.	2.3	80
21	Recruitment of <i>Saccharomyces cerevisiae</i> Dnl4-Lif1 Complex to a Double-Strand Break Requires Interactions With Yku80 and the Xrs2 FHA Domain. <i>Genetics</i> , 2008, 180, 1809-1819.	2.9	74
22	Mutations of the Yku80 C Terminus and Xrs2 FHA Domain Specifically Block Yeast Nonhomologous End Joining. <i>Molecular and Cellular Biology</i> , 2005, 25, 10782-10790.	2.3	70
23	Non-homologous end-joining: bacteria join the chromosome breakdance. <i>Trends in Biochemical Sciences</i> , 2003, 28, 62-66.	7.5	65
24	Uncoupling of 3'-Phosphatase and 5'-Kinase Functions in Budding Yeast. <i>Journal of Biological Chemistry</i> , 2001, 276, 15073-15081.	3.4	55
25	Modes of interaction among yeast Nej1, Lif1 and Dnl4 proteins and comparison to human XLF, XRCC4 and Lig4. <i>DNA Repair</i> , 2007, 6, 1507-1516.	2.8	55
26	A Genomics-Based Screen for Yeast Mutants With an Altered Recombination/End-Joining Repair Ratio. <i>Genetics</i> , 2002, 162, 677-688.	2.9	53
27	De Novo CNV Formation in Mouse Embryonic Stem Cells Occurs in the Absence of Xrcc4-Dependent Nonhomologous End Joining. <i>PLoS Genetics</i> , 2012, 8, e1002981.	3.5	51
28	Mycobacteriophage Exploit NHEJ to Facilitate Genome Circularization. <i>Molecular Cell</i> , 2006, 23, 743-748.	9.7	45
29	Copy number variants are produced in response to low-dose ionizing radiation in cultured cells. <i>Environmental and Molecular Mutagenesis</i> , 2014, 55, 103-113.	2.2	41
30	The Role of Yeast DNA 3'-Phosphatase Tpp1 and Rad1/Rad10 Endonuclease in Processing Spontaneous and Induced Base Lesions. <i>Journal of Biological Chemistry</i> , 2003, 278, 31434-31443.	3.4	38
31	Transcriptional and post-transcriptional regulation of the ionizing radiation response by ATM and p53. <i>Scientific Reports</i> , 2017, 7, 43598.	3.3	31
32	Overhang polarity of chromosomal double-strand breaks impacts kinetics and fidelity of yeast non-homologous end joining. <i>Nucleic Acids Research</i> , 2016, 44, 2769-2781.	14.5	30
33	Identifying transcription start sites and active enhancer elements using BruUV-seq. <i>Scientific Reports</i> , 2016, 5, 17978.	3.3	27
34	<i>Saccharomyces cerevisiae</i> DNA Ligase IV Supports Imprecise End Joining Independently of Its Catalytic Activity. <i>PLoS Genetics</i> , 2013, 9, e1003599.	3.5	26
35	Release from Myosin V via Regulated Recruitment of an E3 Ubiquitin Ligase Controls Organelle Localization. <i>Developmental Cell</i> , 2014, 28, 520-533.	7.0	25
36	Pooled Segregant Sequencing Reveals Genetic Determinants of Yeast Pseudohyphal Growth. <i>PLoS Genetics</i> , 2014, 10, e1004570.	3.5	24

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37	Genetic interactions between HNT3/Aprataxin and RAD27/FEN1 suggest parallel pathways for 5' end processing during base excision repair. <i>DNA Repair</i> , 2010, 9, 690-699.	2.8	23
38	Evidence that base stacking potential in annealed 3' overhangs determines polymerase utilization in yeast nonhomologous end joining. <i>DNA Repair</i> , 2008, 7, 67-76.	2.8	19
39	Frequency of DNA end joining <i>in trans</i> is not determined by the predamage spatial proximity of double-strand breaks in yeast. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 9481-9490.	7.1	16
40	Cotranscriptional splicing efficiencies differ within genes and between cell types. <i>Rna</i> , 2021, 27, 829-840.	3.5	16
41	Locus-specific transcription silencing at the <i>FHIT</i> gene suppresses replication stress-induced copy number variant formation and associated replication delay. <i>Nucleic Acids Research</i> , 2021, 49, 7507-7524.	14.5	16
42	Double-strand breaks in motion: implications for chromosomal rearrangement. <i>Current Genetics</i> , 2020, 66, 1-6.	1.7	13
43	Breaks in the brain. <i>Nature</i> , 2016, 532, 46-47.	27.8	11
44	Characterization of novel primary miRNA transcription units in human cells using Bru-seq nascent RNA sequencing. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqz014.	3.2	10
45	Abrogation of the Chk1-Pds1 Checkpoint Leads to Tolerance of Persistent Single-Strand Breaks in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2005, 169, 1833-1844.	2.9	9
46	Yeast DNA ligase IV mutations reveal a nonhomologous end joining function of BRCT1 distinct from XRCC4/Lif1 binding. <i>DNA Repair</i> , 2014, 24, 37-45.	2.8	8
47	Bur1 functions with TORC1 for vacuole-mediated cell cycle progression. <i>EMBO Reports</i> , 2022, 23, e53477.	4.5	8
48	Identification of Suppressor of Clathrin Deficiency-1 (<i>SCD1</i>) and Its Connection to Clathrin-Mediated Endocytosis in <i>Saccharomyces cerevisiae</i> . <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 867-877.	1.8	7
49	Mapping yeast mitotic 5' resection at base resolution reveals the sequence and positional dependence of nucleases <i>in vivo</i> . <i>Nucleic Acids Research</i> , 2021, 49, 12607-12621.	14.5	7
50	Nonhomologous end-joining: mechanisms, conservation and relationship to illegitimate recombination. <i>Topics in Current Genetics</i> , 2007, , 487-513.	0.7	7
51	Mechanisms of glycosylase induced genomic instability. <i>PLoS ONE</i> , 2017, 12, e0174041.	2.5	7
52	Effects of hydroxyurea on CNV induction in the mouse germline. <i>Environmental and Molecular Mutagenesis</i> , 2018, 59, 698-714.	2.2	5
53	Twin peaks: finding fragile sites with MiDAS-seq. <i>Cell Research</i> , 2020, 30, 944-945.	12.0	4
54	Building on the past, shaping the future: The environmental mutagenesis and genomics society. <i>Environmental and Molecular Mutagenesis</i> , 2013, 54, 153-157.	2.2	2

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55	Nonhomologous End-Joining: Mechanisms, Conservation and Relationship to Illegitimate Recombination. , 2006, , 487-513.		1