

R Scott Williams

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

52 papers	3,530 citations	28 h-index	52 g-index
52 ext. papers	4,013 ext. citations	15 avg, IF	4.97 L-index

#	Paper	IF	Citations
52	The three-component helicase/primase complex of herpes simplex virus-1. <i>Open Biology</i> , 2021 , 11, 210011	11.1	0
51	LIG1 syndrome mutations remodel a cooperative network of ligand binding interactions to compromise ligation efficiency. <i>Nucleic Acids Research</i> , 2021 , 49, 1619-1630	20.1	2
50	High-fidelity DNA ligation enforces accurate Okazaki fragment maturation during DNA replication. <i>Nature Communications</i> , 2021 , 12, 482	17.4	3
49	Ubiquitin stimulated reversal of topoisomerase 2 DNA-protein crosslinks by TDP2. <i>Nucleic Acids Research</i> , 2020 , 48, 6310-6325	20.1	6
48	Two-tiered enforcement of high-fidelity DNA ligation. <i>Nature Communications</i> , 2019 , 10, 5431	17.4	10
47	Ctp1 protein-DNA filaments promote DNA bridging and DNA double-strand break repair. <i>Journal of Biological Chemistry</i> , 2019 , 294, 3312-3320	5.4	17
46	Selectable high-yield recombinant protein production in human cells using a GFP/YFP nanobody affinity support. <i>Protein Science</i> , 2018 , 27, 1083-1092	6.3	15
45	Structures of DNA-bound human ligase IV catalytic core reveal insights into substrate binding and catalysis. <i>Nature Communications</i> , 2018 , 9, 2642	17.4	23
44	Regulatory control of DNA end resection by Sae2 phosphorylation. <i>Nature Communications</i> , 2018 , 9, 4016	17.4	41
43	Mechanism of APTX nicked DNA sensing and pleiotropic inactivation in neurodegenerative disease. <i>EMBO Journal</i> , 2018 , 37,	13	8
42	CtIP/Ctp1/Sae2, molecular form fit for function. <i>DNA Repair</i> , 2017 , 56, 109-117	4.3	35
41	APE2 Zf-GRF facilitates 3X5Xresection of DNA damage following oxidative stress. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, 304-309	11.5	28
40	ZATT (ZNF451)-mediated resolution of topoisomerase 2 DNA-protein cross-links. <i>Science</i> , 2017 , 357, 1412-1416	33.3	76
39	Structure of the sirtuin-linked macrodomain SAV0325 from Staphylococcus aureus. <i>Protein Science</i> , 2016 , 25, 1682-91	6.3	10
38	Reversal of DNA damage induced Topoisomerase 2 DNA-protein crosslinks by Tdp2. <i>Nucleic Acids Research</i> , 2016 , 44, 3829-44	20.1	17
37	Molecular underpinnings of Aprataxin RNA/DNA deadenylase function and dysfunction in neurological disease. <i>Progress in Biophysics and Molecular Biology</i> , 2015 , 117, 157-165	4.7	12
36	Recognition and repair of chemically heterogeneous structures at DNA ends. <i>Environmental and Molecular Mutagenesis</i> , 2015 , 56, 1-21	3.2	58

35	Tetrameric Ctp1 coordinates DNA binding and DNA bridging in DNA double-strand-break repair. <i>Nature Structural and Molecular Biology</i> , 2015 , 22, 158-66	17.6	50
34	Aprataxin resolves adenylated RNA-DNA junctions to maintain genome integrity. <i>Nature</i> , 2014 , 506, 111-5	50.4	74
33	ATP-driven Rad50 conformations regulate DNA tethering, end resection, and ATM checkpoint signaling. <i>EMBO Journal</i> , 2014 , 33, 482-500	13	111
32	Ribonucleotide triggered DNA damage and RNA-DNA damage responses. <i>RNA Biology</i> , 2014 , 11, 1340-6	4.8	19
31	Proteolytic degradation of topoisomerase II (Top2) enables the processing of Top2-DNA and Top2-RNA covalent complexes by tyrosyl-DNA-phosphodiesterase 2 (TDP2). <i>Journal of Biological Chemistry</i> , 2014 , 289, 17960-9	5.4	84
30	Deficiency of terminal ADP-ribose protein glycohydrolase TARG1/C6orf130 in neurodegenerative disease. <i>EMBO Journal</i> , 2013 , 32, 1225-37	13	215
29	A mutation in the FHA domain of <i>Coprinus cinereus</i> Nbs1 Leads to Spo11-independent meiotic recombination and chromosome segregation. <i>G3: Genes, Genomes, Genetics</i> , 2013 , 3, 1927-43	3.2	12
28	Mechanism of repair of 5Xtopoisomerase II-DNA adducts by mammalian tyrosyl-DNA phosphodiesterase 2. <i>Nature Structural and Molecular Biology</i> , 2012 , 19, 1363-71	17.6	55
27	FEN nucleases: bind, bend, fray, cut. <i>Cell</i> , 2011 , 145, 171-2	56.2	15
26	ABC ATPase signature helices in Rad50 link nucleotide state to Mre11 interface for DNA repair. <i>Nature Structural and Molecular Biology</i> , 2011 , 18, 423-31	17.6	129
25	Structure of an aprataxin-DNA complex with insights into AOA1 neurodegenerative disease. <i>Nature Structural and Molecular Biology</i> , 2011 , 18, 1189-95	17.6	35
24	Development of a novel assay for human tyrosyl DNA phosphodiesterase 2. <i>Analytical Biochemistry</i> , 2011 , 416, 112-6	3.1	16
23	DNA end processing by polynucleotide kinase/phosphatase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 20855-6	11.5	13
22	gammaH2A binds Brc1 to maintain genome integrity during S-phase. <i>EMBO Journal</i> , 2010 , 29, 1136-48	13	67
21	Comprehensive analysis of missense variations in the BRCT domain of BRCA1 by structural and functional assays. <i>Cancer Research</i> , 2010 , 70, 4880-90	10.1	113
20	Nbs1 flexibly tethers Ctp1 and Mre11-Rad50 to coordinate DNA double-strand break processing and repair. <i>Cell</i> , 2009 , 139, 87-99	56.2	242
19	Mre11 dimers coordinate DNA end bridging and nuclease processing in double-strand-break repair. <i>Cell</i> , 2008 , 135, 97-109	56.2	358
18	A charged performance by gp17 in viral packaging. <i>Cell</i> , 2008 , 135, 1169-71	56.2	4

17	The BARD1 C-terminal domain structure and interactions with polyadenylation factor CstF-50. <i>Biochemistry</i> , 2008 , 47, 11446-56	3.2	24
16	Coprinus cinereus rad50 mutants reveal an essential structural role for Rad50 in axial element and synaptonemal complex formation, homolog pairing and meiotic recombination. <i>Genetics</i> , 2008 , 180, 1889-907	16	
15	Mre11-Rad50-Nbs1 is a keystone complex connecting DNA repair machinery, double-strand break signaling, and the chromatin template. <i>Biochemistry and Cell Biology</i> , 2007 , 85, 509-20	3.6	305
14	Learning our ABCs: Rad50 directs MRN repair functions via adenylate kinase activity from the conserved ATP binding cassette. <i>Molecular Cell</i> , 2007 , 25, 789-91	17.6	5
13	BRCA1 DNA-binding activity is stimulated by BARD1. <i>Cancer Research</i> , 2006 , 66, 2012-8	10.1	40
12	Structural basis for phosphorylation-dependent signaling in the DNA-damage response. <i>Biochemistry and Cell Biology</i> , 2005 , 83, 721-7	3.6	32
11	The molecular architecture of the mammalian DNA repair enzyme, polynucleotide kinase. <i>Molecular Cell</i> , 2005 , 17, 657-70	17.6	167
10	A nanomachine for making ends meet: MRN is a flexing scaffold for the repair of DNA double-strand breaks. <i>Molecular Cell</i> , 2005 , 19, 724-6	17.6	30
9	Dimerization of CtIP, a BRCA1- and CtBP-interacting protein, is mediated by an N-terminal coiled-coil motif. <i>Journal of Biological Chemistry</i> , 2004 , 279, 26932-8	5.4	42
8	Structural basis of phosphopeptide recognition by the BRCT domain of BRCA1. <i>Nature Structural and Molecular Biology</i> , 2004 , 11, 519-25	17.6	183
7	Interactions between BRCT repeats and phosphoproteins: tangled up in two. <i>Trends in Biochemical Sciences</i> , 2004 , 29, 579-85	10.3	178
6	Structural consequences of a cancer-causing BRCA1-BRCT missense mutation. <i>Journal of Biological Chemistry</i> , 2003 , 278, 2630-5	5.4	72
5	Detection of protein folding defects caused by BRCA1-BRCT truncation and missense mutations. <i>Journal of Biological Chemistry</i> , 2003 , 278, 53007-16	5.4	91
4	Crystal structure of the BRCT repeat region from the breast cancer-associated protein BRCA1. <i>Nature Structural Biology</i> , 2001 , 8, 838-42		201
3	Structure of a conjugating enzyme-ubiquitin thiolester intermediate reveals a novel role for the ubiquitin tail. <i>Structure</i> , 2001 , 9, 897-904	5.2	144
2	Molecular genetic analysis of the region containing the essential <i>Pseudomonas aeruginosa</i> asd gene encoding aspartate-beta-semialdehyde dehydrogenase. <i>Microbiology (United Kingdom)</i> , 1997 , 143 (Pt 3), 899-907	2.9	24
1	A genetic map of the response to DNA damage in human cells		3