Aidan J Doherty

List of Publications by Year
in descending order

72 papers	5,363 citations	76294 40 h-index	85498 71 g-index
75 all docs	75 docs citations	75 times ranked	4380 citing authors

#	ARTICLE	IF	CITATIONS
1	Molecular basis for the initiation of DNA primer synthesis. Nature, 2022, 605, 767-773.	13.7	11
2	DNA repair | Nonhomologous End-Joining in Bacteria. , 2021, , 289-295.		0
3	Repriming DNA synthesis: an intrinsic restart pathway that maintains efficient genome replication. Nucleic Acids Research, 2021, 49, 4831-4847.	6.5	28
4	CRISPR-Associated Primase-Polymerases are implicated in prokaryotic CRISPR-Cas adaptation. Nature Communications, 2021, 12, 3690.	5.8	12
5	PLK1 regulates the PrimPol damage tolerance pathway during the cell cycle. Science Advances, 2021, 7, eabh1004.	4.7	10
6	PrimPol-dependent single-stranded gap formation mediates homologous recombination at bulky DNA adducts. Nature Communications, 2020, 11, 5863.	5.8	69
7	Molecular basis for DNA repair synthesis on short gaps by mycobacterial Primase-Polymerase C. Nature Communications, 2020, 11, 4196.	5.8	9
8	Mitochondrial genetic variation is enriched in G-quadruplex regions that stall DNA synthesis in vitro. Human Molecular Genetics, 2020, 29, 1292-1309.	1.4	36
9	PrimPol is required for the maintenance of efficient nuclear and mitochondrial DNA replication in human cells. Nucleic Acids Research, 2019, 47, 4026-4038.	6.5	42
10	PDIP38/PolDIP2 controls the DNA damage tolerance pathways by increasing the relative usage of translesion DNA synthesis over template switching. PLoS ONE, 2019, 14, e0213383.	1.1	15
11	Râ€loop formation during S phase is restricted by PrimPolâ€mediated repriming. EMBO Journal, 2019, 38, .	3.5	77
12	EXD2 governs germ stem cell homeostasis and lifespan by promoting mitoribosome integrity and translation. Nature Cell Biology, 2018, 20, 162-174.	4.6	31
13	The involvement of tau in nucleolar transcription and the stress response. Acta Neuropathologica Communications, 2018, 6, 70.	2.4	74
14	The Involvement of AÎ²42 and Tau in Nucleolar and Protein Synthesis Machinery Dysfunction. Frontiers in Cellular Neuroscience, 2018, 12, 220.	1.8	29
15	Mitochondrial DNA replication: a PrimPol perspective. Biochemical Society Transactions, 2017, 45, 513-529.	1.6	36
16	Molecular basis for PrimPol recruitment to replication forks by RPA. Nature Communications, 2017, 8, 15222.	5.8	82
17	DNA Ligase C and Prim-PolC participate in base excision repair in mycobacteria. Nature Communications, 2017, 8, 1251.	5.8	25
18	Current and Emerging Assays for Studying the Primer Synthesis Activities of DNA Primases. Methods in Enzymology, 2017, 591, 327-353.	0.4	4

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19	PrimPolâ€"Prime Time to Reprime. Genes, 2017, 8, 20.	1.0	56
20	Repriming by PrimPol is critical for DNA replication restart downstream of lesions and chain-terminating nucleosides. Cell Cycle, 2016, 15, 1997-2008.	1.3	88
21	PolDIP2 interacts with human PrimPol and enhances its DNA polymerase activities. Nucleic Acids Research, 2016, 44, 3317-3329.	6.5	59
22	PrimPol Is Required for Replicative Tolerance of G Quadruplexes in Vertebrate Cells. Molecular Cell, 2016, 61, 161-169.	4.5	146
23	PrimPol-deficient cells exhibit a pronounced G2 checkpoint response following UV damage. Cell Cycle, 2016, 15, 908-918.	1.3	25
24	Molecular basis for DNA strand displacement by NHEJ repair polymerases. Nucleic Acids Research, 2016, 44, 2173-2186.	6.5	24
25	Archaeal replicative primases can perform translesion DNA synthesis. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E633-8.	3.3	24
26	Primase-polymerases are a functionally diverse superfamily of replication and repair enzymes. Nucleic Acids Research, 2015, 43, 6651-6664.	6.5	79
27	Human PrimPol is a highly error-prone polymerase regulated by single-stranded DNA binding proteins. Nucleic Acids Research, 2015, 43, 1056-1068.	6.5	93
28	Author Response: PRIMPOL Mutation: Functional Study Does Not Always Reveal the Truth. Investigative Ophthalmology and Visual Science, 2015, 56, 1183-1183.	3.3	3
29	Cdk1 Restrains NHEJ through Phosphorylation of XRCC4-like Factor Xlf1. Cell Reports, 2014, 9, 2011-2017.	2.9	18
30	Human PrimPol mutation associated with high myopia has a DNA replication defect. Nucleic Acids Research, 2014, 42, 12102-12111.	6.5	39
31	An archaeal family-B DNA polymerase variant able to replicate past DNA damage: occurrence of replicative and translesion synthesis polymerases within the B family. Nucleic Acids Research, 2014, 42, 9949-9963.	6.5	11
32	PrimPolâ€"A new polymerase on the block. Molecular and Cellular Oncology, 2014, 1, e960754.	0.3	35
33	Molecular dissection of the domain architecture and catalytic activities of human PrimPol. Nucleic Acids Research, 2014, 42, 5830-5845.	6.5	94
34	Evaluation of DNA Primase DnaG as a Potential Target for Antibiotics. Antimicrobial Agents and Chemotherapy, 2014, 58, 1699-1706.	1.4	20
35	PPL2 Translesion Polymerase Is Essential for the Completion of Chromosomal DNA Replication in the African Trypanosome. Molecular Cell, 2013, 52, 554-565.	4.5	54
36	PrimPol Bypasses UV Photoproducts during Eukaryotic Chromosomal DNA Replication. Molecular Cell, 2013, 52, 566-573.	4.5	235

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37	Molecular Basis for DNA Double-Strand Break Annealing and Primer Extension by an NHEJ DNA Polymerase. Cell Reports, 2013, 5, 1108-1120.	2.9	31
38	Ribonucleolytic resection is required for repair of strand displaced nonhomologous end-joining intermediates. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E1984-91.	3.3	44
39	Structure of a Preternary Complex Involving a Prokaryotic NHEJ DNA Polymerase. Molecular Cell, 2011, 41, 221-231.	4.5	43
40	Characterization of the roles of the catalytic domains of Mycobacterium tuberculosis ligase D in Ku-dependent error-prone DNA end joining. Mutagenesis, 2010, 25, 473-481.	1.0	22
41	The Direct Interaction between 53BP1 and MDC1 Is Required for the Recruitment of 53BP1 to Sites of Damage. Journal of Biological Chemistry, 2009, 284, 426-435.	1.6	55
42	Repairing DNA double-strand breaks by the prokaryotic non-homologous end-joining pathway. Biochemical Society Transactions, 2009, 37, 539-545.	1.6	35
43	Structure of a NHEJ Polymerase-Mediated DNA Synaptic Complex. Science, 2007, 318, 456-459.	6.0	78
44	Role of DNA Repair by Nonhomologous-End Joining in Bacillus subtilis Spore Resistance to Extreme Dryness, Mono- and Polychromatic UV, and Ionizing Radiation. Journal of Bacteriology, 2007, 189, 3306-3311.	1.0	139
45	Structure and Function of a Mycobacterial NHEJ DNA Repair Polymerase. Journal of Molecular Biology, 2007, 366, 391-405.	2.0	81
46	Nonhomologous End-Joining in Bacteria: A Microbial Perspective. Annual Review of Microbiology, 2007, 61, 259-282.	2.9	140
47	NHEJ protects mycobacteria in stationary phase against the harmful effects of desiccation. DNA Repair, 2007, 6, 1271-1276.	1.3	80
48	Expression of Mycobacterium tuberculosis Ku and Ligase D in Escherichia coli results in RecA and RecB-independent DNA end-joining at regions of microhomology. DNA Repair, 2007, 6, 1413-1424.	1.3	38
49	Identification of a novel motif in DNA ligases exemplified by DNA ligase IV. DNA Repair, 2006, 5, 788-798.	1.3	19
50	Mycobacteriophage Exploit NHEJ to Facilitate Genome Circularization. Molecular Cell, 2006, 23, 743-748.	4.5	45
51	Making Ends Meet: Repairing Breaks in Bacterial DNA by Non-Homologous End-Joining. PLoS Genetics, 2006, 2, e8.	1.5	166
52	Evolutionary and Functional Conservation of the DNA Non-homologous End-joining Protein, XLF/Cernunnos*. Journal of Biological Chemistry, 2006, 281, 37517-37526.	1.6	74
53	Binding of EMSY to HP1Î²: implications for recruitment of HP1Î² and BS69. EMBO Reports, 2005, 6, 675-680.	2.0	29
54	New Insights into NHEJ Repair Processes in Prokaryotes. Cell Cycle, 2005, 4, 675-678.	1.3	36

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55	Crystal Structure of the ENT Domain of Human EMSY. Journal of Molecular Biology, 2005, 350, 964-973.	2.0	24
56	Domain Structure of a NHEJ DNA Repair Ligase from Mycobacterium tuberculosis. Journal of Molecular Biology, 2005, 351, 531-544.	2.0	55
57	DNA Toroids: Framework for DNA Repair in Deinococcus radiodurans and in Germinating Bacterial Spores. Journal of Bacteriology, 2004, 186, 5973-5977.	1.0	50
58	Mycobacterial Ku and Ligase Proteins Constitute a Two-Component NHEJ Repair Machine. Science, 2004, 306, 683-685.	6.0	193
59	The Gam protein of bacteriophage Mu is an orthologue of eukaryotic Ku. EMBO Reports, 2003, 4, 47-52.	2.0	76
60	EMSY Links the BRCA2 Pathway to Sporadic Breast and Ovarian Cancer. Cell, 2003, 115, 523-535.	13.5	389
61	Ku Stimulation of DNA Ligase IV-dependent Ligation Requires Inward Movement along the DNA Molecule. Journal of Biological Chemistry, 2003, 278, 22466-22474.	1.6	69
62	Potential Role for 53BP1 in DNA End-joining Repair through Direct Interaction with DNA. Journal of Biological Chemistry, 2003, 278, 36487-36495.	1.6	133
63	Identification of a DNA Nonhomologous End-Joining Complex in Bacteria. Science, 2002, 297, 1686-1689.	6.0	284
64	Purification, crystallization and preliminary X-ray analysis of the BRCT domains of human 53BP1 bound to the p53 tumour suppressor. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 1826-1829.	2.5	9
65	Crystal structure of human 53BP1 BRCT domains bound to p53 tumour suppressor. EMBO Journal, 2002, 21, 3863-3872.	3.5	161
66	Identification of bacterial homologues of the Ku DNA repair proteins. FEBS Letters, 2001, 500, 186-188.	1.3	124
67	A family of DNA repair ligases in bacteria?. FEBS Letters, 2001, 505, 340-342.	1.3	61
68	DNA repair: How Ku makes ends meet. Current Biology, 2001, 11, R920-R924.	1.8	95
69	Cellular and Biochemical Impact of a Mutation in DNA Ligase IV Conferring Clinical Radiosensitivity. Journal of Biological Chemistry, 2001, 276, 31124-31132.	1.6	116
70	Structural and mechanistic conservation in DNA ligases. Nucleic Acids Research, 2000, 28, 4051-4058.	6.5	147
71	X-Ray Crystallography Reveals a Large Conformational Change during Guanyl Transfer by mRNA Capping Enzymes. Cell, 1997, 89, 545-553.	13.5	260
72	Crystal Structure of an ATP-Dependent DNA Ligase from Bacteriophage T7. Cell, 1996, 85, 607-615.	13.5	261