

# Antony W. Oliver

## List of Publications by Year in descending order

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72  
papers

4,778  
citations

94269

37  
h-index

102304

66  
g-index

85  
all docs

85  
docs citations

85  
times ranked

6080  
citing authors

#	ARTICLE	IF	CITATIONS
1	Mrc1 transduces signals of DNA replication stress to activate Rad53. <i>Nature Cell Biology</i> , 2001, 3, 958-965.	4.6	474
2	Gross Chromosomal Rearrangements and Elevated Recombination at an Inducible Site-Specific Replication Fork Barrier. <i>Cell</i> , 2005, 121, 689-702.	13.5	241
3	The zinc-finger domains of PARP1 cooperate to recognize DNA strand breaks. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 685-692.	3.6	214
4	A Supramodular FHA/BRCT-Repeat Architecture Mediates Nbs1 Adaptor Function in Response to DNA Damage. <i>Cell</i> , 2009, 139, 100-111.	13.5	157
5	Structural basis for recruitment of BRCA2 by PALB2. <i>EMBO Reports</i> , 2009, 10, 990-996.	2.0	154
6	Identification and functional analysis of TopBP1 and its homologs. <i>DNA Repair</i> , 2005, 4, 1227-1239.	1.3	147
7	Activation segment dimerization: a mechanism for kinase autophosphorylation of non-consensus sites. <i>EMBO Journal</i> , 2008, 27, 704-714.	3.5	147
8	Recombination-restarted replication makes inverted chromosome fusions at inverted repeats. <i>Nature</i> , 2013, 493, 246-249.	13.7	144
9	Chk1 activation requires Rad9 S/TQ-site phosphorylation to promote association with C-terminal BRCT domains of Rad4TOPBP1. <i>Genes and Development</i> , 2004, 18, 1154-1164.	2.7	140
10	Regulation of DNA Replication through Sld3-Dpb11 Interaction Is Conserved from Yeast to Humans. <i>Current Biology</i> , 2011, 21, 1152-1157.	1.8	135
11	Trans-activation of the DNA-damage signalling protein kinase Chk2 by T-loop exchange. <i>EMBO Journal</i> , 2006, 25, 3179-3190.	3.5	131
12	APLF promotes the assembly and activity of non-homologous end joining protein complexes. <i>EMBO Journal</i> , 2012, 32, 112-125.	3.5	118
13	TopBP1: A BRCT-scaffold protein functioning in multiple cellular pathways. <i>DNA Repair</i> , 2014, 22, 165-174.	1.3	108
14	Smc5/6: a link between DNA repair and unidirectional replication?. <i>Nature Reviews Molecular Cell Biology</i> , 2008, 9, 177-182.	16.1	104
15	Crystal structure of the catalytic fragment of murine poly(ADP-ribose) polymerase-2. <i>Nucleic Acids Research</i> , 2004, 32, 456-464.	6.5	101
16	MDC1 Interacts with TOPBP1 to Maintain Chromosomal Stability during Mitosis. <i>Molecular Cell</i> , 2019, 74, 571-583.e8.	4.5	97
17	CCT241533 Is a Potent and Selective Inhibitor of CHK2 that Potentiates the Cytotoxicity of PARP Inhibitors. <i>Cancer Research</i> , 2011, 71, 463-472.	0.4	96
18	Activation segment exchange: a common mechanism of kinase autophosphorylation?. <i>Trends in Biochemical Sciences</i> , 2007, 32, 351-356.	3.7	86

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19	The XRCC1 phosphate-binding pocket binds poly (ADP-ribose) and is required for XRCC1 function. <i>Nucleic Acids Research</i> , 2015, 43, 6934-6944.	6.5	83
20	Gene tagging and gene replacement using recombinase-mediated cassette exchange in <i>Schizosaccharomyces pombe</i> . <i>Gene</i> , 2008, 407, 63-74.	1.0	75
21	Specific recognition of a multiply phosphorylated motif in the DNA repair scaffold XRCC1 by the FHA domain of human PNK. <i>Nucleic Acids Research</i> , 2009, 37, 1701-1712.	6.5	75
22	The ASCIZ-DYNLL1 axis promotes 53BP1-dependent non-homologous end joining and PARP inhibitor sensitivity. <i>Nature Communications</i> , 2018, 9, 5406.	5.8	74
23	Structure and function of the Rad9-binding region of the DNA-damage checkpoint adaptor TopBP1. <i>Nucleic Acids Research</i> , 2011, 39, 313-324.	6.5	72
24	Chromatin association of the SMC5/6 complex is dependent on binding of its NSE3 subunit to DNA. <i>Nucleic Acids Research</i> , 2016, 44, 1064-1079.	6.5	68
25	Destabilized SMC5/6 complex leads to chromosome breakage syndrome with severe lung disease. <i>Journal of Clinical Investigation</i> , 2016, 126, 2881-2892.	3.9	65
26	Structure of an archaeal PCNA1-PCNA2-FEN1 complex: elucidating PCNA subunit and client enzyme specificity. <i>Nucleic Acids Research</i> , 2006, 34, 4515-4526.	6.5	64
27	Rad62 Protein Functionally and Physically Associates with the Smc5/Smc6 Protein Complex and Is Required for Chromosome Integrity and Recombination Repair in Fission Yeast. <i>Molecular and Cellular Biology</i> , 2004, 24, 9401-9413.	1.1	63
28	ATM Localization and Heterochromatin Repair Depend on Direct Interaction of the 53BP1-BRCT 2 Domain with H2AX. <i>Cell Reports</i> , 2015, 13, 2081-2089.	2.9	61
29	Specialized interfaces of Smc5/6 control hinge stability and DNA association. <i>Nature Communications</i> , 2017, 8, 14011.	5.8	61
30	PARP3 is a sensor of nicked nucleosomes and monoribosylates histone H2B <sup>Glu2</sup> . <i>Nature Communications</i> , 2016, 7, 12404.	5.8	60
31	Efficient Single-Strand Break Repair Requires Binding to Both Poly(ADP-Ribose) and DNA by the Central BRCT Domain of XRCC1. <i>Cell Reports</i> , 2019, 26, 573-581.e5.	2.9	58
32	The Ku-binding motif is a conserved module for recruitment and stimulation of non-homologous end-joining proteins. <i>Nature Communications</i> , 2016, 7, 11242.	5.8	57
33	An Essential Function for the ATR-Activation-Domain (AAD) of TopBP1 in Mouse Development and Cellular Senescence. <i>PLoS Genetics</i> , 2013, 9, e1003702.	1.5	56
34	PP2A/B55 and Fcp1 Regulate Greatwall and Ensa Dephosphorylation during Mitotic Exit. <i>PLoS Genetics</i> , 2014, 10, e1004004.	1.5	55
35	Identification and characterisation of 2-aminopyridine inhibitors of checkpoint kinase 2. <i>Bioorganic and Medicinal Chemistry</i> , 2010, 18, 707-718.	1.4	50
36	Preferential binding of fd gene 5 protein to tetraplex nucleic acid structures 1 Edited by A. Klug. <i>Journal of Molecular Biology</i> , 2000, 301, 575-584.	2.0	46

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37	Structure-Based Design of Potent and Selective 2-(Quinazolin-2-yl)phenol Inhibitors of Checkpoint Kinase 2. <i>Journal of Medicinal Chemistry</i> , 2011, 54, 580-590.	2.9	46
38	Regulation of gene expression at the fission yeast <i>Schizosaccharomyces pombe</i> <i>urg1</i> locus. <i>Gene</i> , 2011, 484, 75-85.	1.0	42
39	The 3' to 5' Exoribonuclease DIS3: From Structure and Mechanisms to Biological Functions and Role in Human Disease. <i>Biomolecules</i> , 2015, 5, 1515-1539.	1.8	42
40	Phosphorylation-mediated interactions with TOPBP1 couple 53BP1 and 9-1-1 to control the G1 DNA damage checkpoint. <i>ELife</i> , 2019, 8, .	2.8	40
41	Quantification of DNA-associated proteins inside eukaryotic cells using single-molecule localization microscopy. <i>Nucleic Acids Research</i> , 2014, 42, e146-e146.	6.5	35
42	CCRK is a novel signalling hub exploitable in cancer immunotherapy. , 2018, 186, 138-151.		35
43	BRCT domains of the DNA damage checkpoint proteins TOPBP1/Rad4 display distinct specificities for phosphopeptide ligands. <i>ELife</i> , 2018, 7, .	2.8	34
44	An Artemis polymorphic variant reduces Artemis activity and confers cellular radiosensitivity. <i>DNA Repair</i> , 2010, 9, 1003-1010.	1.3	33
45	The Structural Basis for Substrate Recognition by Mammalian Polynucleotide Kinase 3 <sup>â€²</sup> Phosphatase. <i>Molecular Cell</i> , 2011, 44, 385-396.	4.5	32
46	Cancer and the bromodomains of BAF180. <i>Biochemical Society Transactions</i> , 2012, 40, 364-369.	1.6	31
47	The BAH domain of Rsc2 is a histone H3 binding domain. <i>Nucleic Acids Research</i> , 2013, 41, 9168-9182.	6.5	31
48	A first generation inhibitor of human Greatwall kinase, enabled by structural and functional characterisation of a minimal kinase domain construct. <i>Oncotarget</i> , 2016, 7, 71182-71197.	0.8	30
49	Mode of action of DNA-competitive small molecule inhibitors of tyrosyl DNA phosphodiesterase 2. <i>Biochemical Journal</i> , 2016, 473, 1869-1879.	1.7	30
50	Phosphorylation-Dependent Assembly and Coordination of the DNA Damage Checkpoint Apparatus by Rad4TopBP1. <i>Molecular Cell</i> , 2013, 51, 723-736.	4.5	27
51	The Rad4TopBP1 ATR-Activation Domain Functions in G1/S Phase in a Chromatin-Dependent Manner. <i>PLoS Genetics</i> , 2012, 8, e1002801.	1.5	24
52	Structural characterization of DNA and RNA sequences recognized by the gene 5 protein of bacteriophage fd. <i>Biochemical Journal</i> , 1999, 339, 525-531.	1.7	23
53	Crystal structure of the proximal BAH domain of the polybromo protein. <i>Biochemical Journal</i> , 2005, 389, 657-664.	1.7	23
54	Live-cell single-molecule tracking highlights requirements for stable Smc5/6 chromatin association in vivo. <i>ELife</i> , 2021, 10, .	2.8	23

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55	Fragment-Based Screening Maps Inhibitor Interactions in the ATP-Binding Site of Checkpoint Kinase 2. PLoS ONE, 2013, 8, e65689.	1.1	23
56	The conserved Fanconi anemia nuclease Fan1 and the SUMO E3 ligase Pli1 act in two novel Pso2-independent pathways of DNA interstrand crosslink repair in yeast. DNA Repair, 2013, 12, 1011-1023.	1.3	22
57	Nse5/6 is a negative regulator of the ATPase activity of the Smc5/6 complex. Nucleic Acids Research, 2021, 49, 4534-4549.	6.5	22
58	Phosphorylation-dependent assembly of DNA damage response systems and the central roles of TOPBP1. DNA Repair, 2021, 108, 103232.	1.3	21
59	Inhibition of MRN activity by a telomere protein motif. Nature Communications, 2021, 12, 3856.	5.8	20
60	A Hypomorphic PALB2 Allele Gives Rise to an Unusual Form of FA-N Associated with Lymphoid Tumour Development. PLoS Genetics, 2016, 12, e1005945.	1.5	19
61	Uncovering an allosteric mode of action for a selective inhibitor of human Bloom syndrome protein. ELife, 2021, 10, .	2.8	18
62	A role of the Nse4 kleisin and Nse1/Nse3 KITE subunits in the ATPase cycle of SMC5/6. Scientific Reports, 2020, 10, 9694.	1.6	15
63	Development of an oligonucleotide-based fluorescence assay for the identification of tyrosyl-DNA phosphodiesterase 1 (TDP1) inhibitors. Analytical Biochemistry, 2014, 454, 17-22.	1.1	14
64	Structure of the human RAD17â€‘RFC clamp loader and 9â€‘1â€‘1 checkpoint clamp bound to a dsDNAâ€‘ssDNA junction. Nucleic Acids Research, 2022, 50, 8279-8289.	6.5	13
65	DIS3 isoforms vary in their endoribonuclease activity and are differentially expressed within haematological cancers. Biochemical Journal, 2018, 475, 2091-2105.	1.7	12
66	Design and discovery of 3-aryl-5-substituted-isoquinolin-1-ones as potent tankyrase inhibitors. MedChemComm, 2015, 6, 1687-1692.	3.5	11
67	Identification and Characterization of a Novel Constitutional PIK3CA Mutation in a Child Lacking the Typical Segmental Overgrowth of â€‘PIK3CA-Related Overgrowth Spectrumâ€‘. Human Mutation, 2016, 37, 242-245.	1.1	11
68	Are SMC Complexes Loop Extruding Factors? Linking Theory With Fact. BioEssays, 2019, 41, e1800182.	1.2	11
69	Structural basis for recruitment of the CHK1 DNA damage kinase by the CLASPIN scaffold protein. Structure, 2021, 29, 531-539.e3.	1.6	8
70	Structural characterization of DNA and RNA sequences recognized by the gene 5 protein of bacteriophage fd. Biochemical Journal, 1999, 339, 525.	1.7	6
71	109 Preferential binding of the fd gene 5 protein to a structured form of the single-stranded DNA sequence d(GT5G4CT4C). Biochemical Society Transactions, 1997, 25, S643-S643.	1.6	2
72	A Novel Role of PALB2 in Lymphoid Tumour Development. Blood, 2016, 128, 5113-5113.	0.6	0