

Antony W. Oliver

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3790351/publications.pdf>

Version: 2024-02-01

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	Structure of the human RAD17â€‘RFC clamp loader and 9â€‘1â€‘1 checkpoint clamp bound to a dsDNAâ€‘ssDNA junction. <i>Nucleic Acids Research</i> , 2022, 50, 8279-8289.	6.5	13
2	Uncovering an allosteric mode of action for a selective inhibitor of human Bloom syndrome protein. <i>ELife</i> , 2021, 10, .	2.8	18
3	Nse5/6 is a negative regulator of the ATPase activity of the Smc5/6 complex. <i>Nucleic Acids Research</i> , 2021, 49, 4534-4549.	6.5	22
4	Live-cell single-molecule tracking highlights requirements for stable Smc5/6 chromatin association in vivo. <i>ELife</i> , 2021, 10, .	2.8	23
5	Inhibition of MRN activity by a telomere protein motif. <i>Nature Communications</i> , 2021, 12, 3856.	5.8	20
6	Structural basis for recruitment of the CHK1 DNA damage kinase by the CLASPIN scaffold protein. <i>Structure</i> , 2021, 29, 531-539.e3.	1.6	8
7	Phosphorylation-dependent assembly of DNA damage response systems and the central roles of TOPBP1. <i>DNA Repair</i> , 2021, 108, 103232.	1.3	21
8	A role of the Nse4 kleisin and Nse1/Nse3 KITE subunits in the ATPase cycle of SMC5/6. <i>Scientific Reports</i> , 2020, 10, 9694.	1.6	15
9	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
10	MDC1 Interacts with TOPBP1 to Maintain Chromosomal Stability during Mitosis. <i>Molecular Cell</i> , 2019, 74, 571-583.e8.	4.5	97
11	Are SMC Complexes Loop Extruding Factors? Linking Theory With Fact. <i>BioEssays</i> , 2019, 41, e1800182.	1.2	11
12	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
13	CCRK is a novel signalling hub exploitable in cancer immunotherapy. , 2018, 186, 138-151.		35
14	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
15	DIS3 isoforms vary in their endoribonuclease activity and are differentially expressed within haematological cancers. <i>Biochemical Journal</i> , 2018, 475, 2091-2105.	1.7	12
16	BRCT domains of the DNA damage checkpoint proteins TOPBP1/Rad4 display distinct specificities for phosphopeptide ligands. <i>ELife</i> , 2018, 7, .	2.8	34
17	Specialized interfaces of Smc5/6 control hinge stability and DNA association. <i>Nature Communications</i> , 2017, 8, 14011.	5.8	61
18	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

#	ARTICLE	IF	CITATIONS
19	Identification and Characterization of a Novel Constitutional PIK3CA Mutation in a Child Lacking the Typical Segmental Overgrowth of the PIK3CA-Related Overgrowth Spectrum. Human Mutation, 2016, 37, 242-245.	1.1	11
20	Mode of action of DNA-competitive small molecule inhibitors of tyrosyl DNA phosphodiesterase 2. Biochemical Journal, 2016, 473, 1869-1879.	1.7	30
21	The Ku-binding motif is a conserved module for recruitment and stimulation of non-homologous end-joining proteins. Nature Communications, 2016, 7, 11242.	5.8	57
22	PARP3 is a sensor of nicked nucleosomes and monoribosylates histone H2B Glu2. Nature Communications, 2016, 7, 12404.	5.8	60
23	Chromatin association of the SMC5/6 complex is dependent on binding of its NSE3 subunit to DNA. Nucleic Acids Research, 2016, 44, 1064-1079.	6.5	68
24	Destabilized SMC5/6 complex leads to chromosome breakage syndrome with severe lung disease. Journal of Clinical Investigation, 2016, 126, 2881-2892.	3.9	65
25	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
26	A Novel Role of PALB2 in Lymphoid Tumour Development. Blood, 2016, 128, 5113-5113.	0.6	0
27	ATM Localization and Heterochromatin Repair Depend on Direct Interaction of the 53BP1-BRCT 2 Domain with H2AX. Cell Reports, 2015, 13, 2081-2089.	2.9	61
28	The 3' to 5' Exoribonuclease DIS3: From Structure and Mechanisms to Biological Functions and Role in Human Disease. Biomolecules, 2015, 5, 1515-1539.	1.8	42
29	The XRCC1 phosphate-binding pocket binds poly (ADP-ribose) and is required for XRCC1 function. Nucleic Acids Research, 2015, 43, 6934-6944.	6.5	83
30	Design and discovery of 3-aryl-5-substituted-isoquinolin-1-ones as potent tankyrase inhibitors. MedChemComm, 2015, 6, 1687-1692.	3.5	11
31	PP2A/B55 and Fcp1 Regulate Greatwall and Ensa Dephosphorylation during Mitotic Exit. PLoS Genetics, 2014, 10, e1004004.	1.5	55
32	Quantification of DNA-associated proteins inside eukaryotic cells using single-molecule localization microscopy. Nucleic Acids Research, 2014, 42, e146-e146.	6.5	35
33	TopBP1: A BRCT-scaffold protein functioning in multiple cellular pathways. DNA Repair, 2014, 22, 165-174.	1.3	108
34	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
35	Phosphorylation-Dependent Assembly and Coordination of the DNA Damage Checkpoint Apparatus by Rad4/TopBP1. Molecular Cell, 2013, 51, 723-736.	4.5	27
36	Recombination-restarted replication makes inverted chromosome fusions at inverted repeats. Nature, 2013, 493, 246-249.	13.7	144

#	ARTICLE	IF	CITATIONS
37	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. <i>DNA Repair</i> , 2013, 12, 1011-1023.	1.3	22
38	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
39	The BAH domain of Rsc2 is a histone H3 binding domain. <i>Nucleic Acids Research</i> , 2013, 41, 9168-9182.	6.5	31
40	Fragment-Based Screening Maps Inhibitor Interactions in the ATP-Binding Site of Checkpoint Kinase 2. <i>PLoS ONE</i> , 2013, 8, e65689.	1.1	23
41	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
42	Cancer and the bromodomains of BAF180. <i>Biochemical Society Transactions</i> , 2012, 40, 364-369.	1.6	31
43	APLF promotes the assembly and activity of non-homologous end joining protein complexes. <i>EMBO Journal</i> , 2012, 32, 112-125.	3.5	118
44	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
45	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
46	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
47	The Structural Basis for Substrate Recognition by Mammalian Polynucleotide Kinase 3 ^{â€²} Phosphatase. <i>Molecular Cell</i> , 2011, 44, 385-396.	4.5	32
48	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
49	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
50	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
51	An Artemis polymorphic variant reduces Artemis activity and confers cellular radiosensitivity. <i>DNA Repair</i> , 2010, 9, 1003-1010.	1.3	33
52	Identification and characterisation of 2-aminopyridine inhibitors of checkpoint kinase 2. <i>Bioorganic and Medicinal Chemistry</i> , 2010, 18, 707-718.	1.4	50
53	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
54	Structural basis for recruitment of BRCA2 by PALB2. <i>EMBO Reports</i> , 2009, 10, 990-996.	2.0	154

#	ARTICLE	IF	CITATIONS
55	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
56	Activation segment dimerization: a mechanism for kinase autophosphorylation of non-consensus sites. <i>EMBO Journal</i> , 2008, 27, 704-714.	3.5	147
57	Smc5/6: a link between DNA repair and unidirectional replication?. <i>Nature Reviews Molecular Cell Biology</i> , 2008, 9, 177-182.	16.1	104
58	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
59	Activation segment exchange: a common mechanism of kinase autophosphorylation?. <i>Trends in Biochemical Sciences</i> , 2007, 32, 351-356.	3.7	86
60	Structure of an archaeal PCNA1â€“PCNA2â€“FEN1 complex: elucidating PCNA subunit and client enzyme specificity. <i>Nucleic Acids Research</i> , 2006, 34, 4515-4526.	6.5	64
61	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
62	Crystal structure of the proximal BAH domain of the polybromo protein. <i>Biochemical Journal</i> , 2005, 389, 657-664.	1.7	23
63	Gross Chromosomal Rearrangements and Elevated Recombination at an Inducible Site-Specific Replication Fork Barrier. <i>Cell</i> , 2005, 121, 689-702.	13.5	241
64	Identification and functional analysis of TopBP1 and its homologs. <i>DNA Repair</i> , 2005, 4, 1227-1239.	1.3	147
65	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
66	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
67	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
68	Mrc1 transduces signals of DNA replication stress to activate Rad53. <i>Nature Cell Biology</i> , 2001, 3, 958-965.	4.6	474
69	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
70	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
71	Structural characterization of DNA and RNA sequences recognized by the gene 5 protein of bacteriophage fd. <i>Biochemical Journal</i> , 1999, 339, 525.	1.7	6
72	109 Preferential binding of the fd gene 5 protein to a structured form of the single-stranded DNA sequence d(GT5G4CT4C). <i>Biochemical Society Transactions</i> , 1997, 25, S643-S643.	1.6	2