Daniel Durocher

List of Publications by Year
in descending order

126 papers	24,156 citations	14655 66 h-index	19190 118 g-index
143 all docs	143 docs citations	143 times ranked	26896 citing authors

#	Article	IF	Citations
1	RIF1 acts in DNA repair through phosphopeptide recognition of 53BP1. Molecular Cell, 2022, 82, 1359-1371.e9.	9.7	14
2	CCNE1 amplification is synthetic lethal with PKMYT1 kinase inhibition. Nature, 2022, 604, 749-756.	27.8	60
3	The CIP2A-TOPBP1 complex safeguards chromosomal stability during mitosis. Nature Communications, 2022, 13, .	12.8	20
4	Genome-scale chemogenomic CRISPR screens in human cells using the TKOv3 library. STAR Protocols, 2021, 2, 100321.	1.2	22
5	Synthetic Lethality in Cancer Therapeutics: The Next Generation. Cancer Discovery, 2021, 11, 1626-1635.	9.4	91
6	Lineage-defined leiomyosarcoma subtypes emerge years before diagnosis and determine patient survival. Nature Communications, 2021, 12, 4496.	12.8	28
7	Two redundant ubiquitinâ€dependent pathways of BRCA1 localization to DNA damage sites. EMBO Reports, 2021, 22, e53679.	4.5	11
8	The CIP2Aâ€“TOPBP1 axis safeguards chromosome stability and is a synthetic lethal target for BRCA-mutated cancer. Nature Cancer, 2021, 2, 1357-1371.	13.2	55
9	FAM72A antagonizes UNG2 to promote mutagenic repair during antibody maturation. Nature, 2021, 600, 324-328.	27.8	29
10	Functional characterization of a PROTAC directed against BRAF mutant V600E. Nature Chemical Biology, 2020, 16, 1170-1178.	8.0	80
11	A substrate binding model for the KEOPS tRNA modifying complex. Nature Communications, 2020, 11, 6233.	12.8	21
12	Endogenous DNA 3â€² Blocks Are Vulnerabilities for BRCA1 and BRCA2 Deficiency and Are Reversed by the APE2 Nuclease. Molecular Cell, 2020, 78, 1152-1165.e8.	9.7	69
13	A Genetic Map of the Response to DNA Damage in Human Cells. Cell, 2020, 182, 481-496.e21.	28.9	324
14	<scp>SHLD</scp> 2 promotes class switch recombination by preventing inactivating deletions within the Igh locus. EMBO Reports, 2020, 21, e49823.	4.5	20
15	Identifying chemogenetic interactions from CRISPR screens with drugZ. Genome Medicine, 2019, 11, 52.	8.2	127
16	Control of homologous recombination by the HROBâ€“MCM8â€“MCM9 pathway. Genes and Development, 2019, 33, 1397-1415.	5.9	55
17	A consensus set of genetic vulnerabilities to ATR inhibition. Open Biology, 2019, 9, 190156.	3.6	81
18	BRCA1 Haploinsufficiency Is Masked by RNF168-Mediated Chromatin Ubiquitylation. Molecular Cell, 2019, 73, 1267-1281.e7.	9.7	78

#	Article	IF	Citations
19	Shieldin â€“ the protector of <scp>DNA</scp> ends. EMBO Reports, 2019, 20, .	4.5	169
20	Abstract PL03-03: Navigating gene-gene and drug-gene interaction landscapes underpinning the DNA damage response. , 2019, , .		0
21	Mapping <scp>DNA</scp> damageâ€dependent genetic interactions in yeast via party mating and barcode fusion genetics. Molecular Systems Biology, 2018, 14, e7985.	7.2	25
22	CRISPR screens identify genomic ribonucleotides as a source of PARP-trapping lesions. Nature, 2018, 559, 285-289.	27.8	297
23	53BP1â€“RIF1â€“shieldin counteracts DSB resection through CST- and Polα-dependent fill-in. Nature, 2018, 560, 112-116.	27.8	313
24	The shieldin complex mediates 53BP1-dependent DNA repair. Nature, 2018, 560, 117-121.	27.8	445
25	Inhibition of 53BP1 favors homology-dependent DNA repair and increases CRISPRâ€“Cas9 genome-editing efficiency. Nature Biotechnology, 2018, 36, 95-102.	17.5	206
26	ZMYM3 regulates BRCA1 localization at damaged chromatin to promote DNA repair. Genes and Development, 2017, 31, 260-274.	5.9	65
27	The control of DNA repair by the cell cycle. Nature Cell Biology, 2017, 19, 1-9.	10.3	549
28	Reading chromatin signatures after DNA double-strand breaks. Philosophical Transactions of the Royal Society B: Biological Sciences, 2017, 372, 20160280.	4.0	49
29	ATM and CDK2 control chromatin remodeler CSB to inhibit RIF1 in DSB repair pathway choice. Nature Communications, 2017, 8, 1921.	12.8	51
30	Evaluation and Design of Genome-Wide CRISPR/SpCas9 Knockout Screens. G3: Genes, Genomes, Genetics, 2017, 7, 2719-2727.	1.8	417
31	Association of Distinct Mutational Signatures With Correlates of Increased Immune Activity in Pancreatic Ductal Adenocarcinoma. JAMA Oncology, 2017, 3, 774.	7.1	221
32	Proteomic analysis of the human KEOPS complex identifies C14ORF142 as a core subunit homologous to yeast Gon7. Nucleic Acids Research, 2017, 45, 805-817.	14.5	49
33	A sharp Pif1-dependent threshold separates DNA double-strand breaks from critically short telomeres. ELife, 2017, 6, .	6.0	22
34	The RNF168 paralog RNF169 defines a new class of ubiquitylated histone reader involved in the response to DNA damage. ELife, 2017, 6, .	6.0	44
35	The TIP60 Complex Regulates Bivalent Chromatin Recognition by 53BP1 through Direct H4K20me Binding and H2AK15 Acetylation. Molecular Cell, 2016, 62, 409-421.	9.7	198
36	Excess Polι functions in response to replicative stress in homologous recombination-proficient cancer cells. Biology Open, 2016, 5, 1485-1492.	1.2	22

#	Article	IF	Citations
37	53BP1 Goes Back to Its p53 Roots. Molecular Cell, 2016, 64, 3-4.	9.7	5
38	The structural basis of modified nucleosome recognition by 53BP1. Nature, 2016, 536, 100-103.	27.8	201
39	Structural and functional characterization of KEOPS dimerization by Pcc1 and its role in t⁶A biosynthesis. Nucleic Acids Research, 2016, 44, 6971-6980.	14.5	26
40	HELB Is a Feedback Inhibitor of DNA End Resection. Molecular Cell, 2016, 61, 405-418.	9.7	119
41	DNA damage signalling targets the kinetochore to promote chromatin mobility. Nature Cell Biology, 2016, 18, 281-290.	10.3	82
42	A mechanism for the suppression of homologous recombination in G1 cells. Nature, 2015, 528, 422-426.	27.8	409
43	Perinuclear tethers license telomeric DSBs for a broad kinesin- and NPC-dependent DNA repair process. Nature Communications, 2015, 6, 7742.	12.8	76
44	MAD2L2 controls DNA repair at telomeres and DNA breaks by inhibiting 5â€² end resection. Nature, 2015, 521, 537-540.	27.8	253
45	Analysis of the Histone H3.1 Interactome: A Suitable Chaperone for the Right Event. Molecular Cell, 2015, 60, 697-709.	9.7	61
46	High-Resolution CRISPR Screens Reveal Fitness Genes and Genotype-Specific Cancer Liabilities. Cell, 2015, 163, 1515-1526.	28.9	1,339
47	Nucleosome Acidic Patch Promotes RNF168- and RING1B/BMI1-Dependent H2AX and H2A Ubiquitination and DNA Damage Signaling. PLoS Genetics, 2014, 10, e1004178.	3.5	83
48	Mitosis Inhibits DNA Double-Strand Break Repair to Guard Against Telomere Fusions. Science, 2014, 344, 189-193.	12.6	280
49	Structure and mechanism of action of the hydroxyâ€“arylâ€“aldehyde class of IRE1 endoribonuclease inhibitors. Nature Communications, 2014, 5, 4202.	12.8	108
50	Structural basis of Rad53 kinase activation by dimerization and activation segment exchange. Cellular Signalling, 2014, 26, 1825-1836.	3.6	16
51	RNF8-Independent Lys63 Poly-Ubiquitylation Prevents Genomic Instability in Response to Replication-Associated DNA Damage. PLoS ONE, 2014, 9, e89997.	2.5	1
52	The CRAPome: a contaminant repository for affinity purificationâ€“mass spectrometry data. Nature Methods, 2013, 10, 730-736.	19.0	1,353
53	Push back to respond better: regulatory inhibition of the DNA double-strand break response. Nature Reviews Molecular Cell Biology, 2013, 14, 661-672.	37.0	154
54	A Strategy for Modulation of Enzymes in the Ubiquitin System. Science, 2013, 339, 590-595.	12.6	257

#	Article	IF	Citations
55	Regulation of DNA Damage Responses by Ubiquitin and SUMO. Molecular Cell, 2013, 49, 795-807.	9.7	522
56	A Cell Cycle-Dependent Regulatory Circuit Composed of 53BP1-RIF1 and BRCA1-CtIP Controls DNA Repair Pathway Choice. Molecular Cell, 2013, 49, 872-883.	9.7	742
57	53BP1 is a reader of the DNA-damage-induced H2A Lys 15 ubiquitin mark. Nature, 2013, 499, 50-54.	27.8	580
58	DNA repair pathway choiceâ€"a PTIP of the hat to 53BP1. EMBO Reports, 2013, 14, 665-666.	4.5	31
59	Reconstitution and characterization of eukaryotic N6-threonylcarbamoylation of tRNA using a minimal enzyme system. Nucleic Acids Research, 2013, 41, 6332-6346.	14.5	68
60	Regulatory ubiquitylation during the response to DNA doubleâ€strand breaks. FASEB Journal, 2013, 27, 334.3.	0.5	0
61	Interaction Proteomics Identify NEURL4 and the HECT E3 Ligase HERC2 as Novel Modulators of Centrosome Architecture. Molecular and Cellular Proteomics, 2012, 11, M111.014233.	3.8	57
62	RMI1 Promotes DNA Replication Fork Progression and Recovery from Replication Fork Stress. Molecular and Cellular Biology, 2012, 32, 3054-3064.	2.3	24
63	OTUB1 Co-opts Lys48-Linked Ubiquitin Recognition to Suppress E2 Enzyme Function. Molecular Cell, 2012, 45, 384-397.	9.7	174
64	OTUB1 Co-opts Lys48-Linked Ubiquitin Recognition to Suppress E2 Enzyme Function. Molecular Cell, 2012, 46, 549.	9.7	3
65	Tandem Protein Interaction Modules Organize the Ubiquitin-Dependent Response to DNA Double-Strand Breaks. Molecular Cell, 2012, 47, 383-395.	9.7	124
66	An Allosteric Inhibitor of the Human Cdc34ÂUbiquitin-Conjugating Enzyme. Cell, 2011, 145, 1075-1087.	28.9	203
67	Srs2 enables checkpoint recovery by promoting disassembly of DNA damage foci from chromatin. DNA Repair, 2011, 10, 1213-1222.	2.8	26
68	Potent and Selective Inhibitors of the Inositol-requiring Enzyme 1 Endoribonuclease. Journal of Biological Chemistry, 2011, 286, 12743-12755.	3.4	190
69	Uroporphyrinogen Decarboxylase Is a Radiosensitizing Target for Head and Neck Cancer. Science Translational Medicine, 2011, 3, 67ra7.	12.4	32
70	MRE11 promotes AKT phosphorylation in direct response to DNA double-strand breaks. Cell Cycle, 2011, 10, 2218-2232.	2.6	111
71	Genomic Instability, Defective Spermatogenesis, Immunodeficiency, and Cancer in a Mouse Model of the RIDDLE Syndrome. PLoS Genetics, 2011, 7, e1001381.	3.5	73
72	A siRNA-Based Screen for Genes Involved in Chromosome End Protection. PLoS ONE, 2011, 6, e21407.	2.5	12

#	Article	IF	Citations
73	The ubiquitous role of ubiquitin in the DNA damage response. DNA Repair, 2010, 9, 1229-1240.	2.8	188
74	Systematic identification of fragile sites via genome-wide location analysis of Î³-H2AX. Nature Structural and Molecular Biology, 2010, 17, 299-305.	8.2	167
75	A viral E3 ligase targets RNF8 and RNF168 to control histone ubiquitination and DNA damage responses. EMBO Journal, 2010, 29, 943-955.	7.8	162
76	Non-canonical inhibition of DNA damage-dependent ubiquitination by OTUB1. Nature, 2010, 466, 941-946.	27.8	316
77	De novo telomere formation is suppressed by the Mec1-dependent inhibition of Cdc13 accumulation at DNA breaks. Genes and Development, 2010, 24, 502-515.	5.9	73
78	Rnf8 deficiency impairs class switch recombination, spermatogenesis, and genomic integrity and predisposes for cancer. Journal of Experimental Medicine, 2010, 207, 983-997.	8.5	112
79	The RNF8/RNF168 ubiquitin ligase cascade facilitates class switch recombination. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 809-814.	7.1	70
80	CDC5 Inhibits the Hyperphosphorylation of the Checkpoint Kinase Rad53, Leading to Checkpoint Adaptation. PLoS Biology, 2010, 8, e1000286.	5.6	50
81	DNA Repair Has a New FAN1 Club. Molecular Cell, 2010, 39, 167-169.	9.7	14
82	The MMS22L-TONSL Complex Mediates Recovery from Replication Stress and Homologous Recombination. Molecular Cell, 2010, 40, 619-631.	9.7	106
83	Rnf8 deficiency impairs class switch recombination, spermatogenesis, and genomic integrity and predisposes for cancer. Journal of Cell Biology, 2010, 189, i6-i6.	5.2	0
84	Regulatory ubiquitylation in response to DNA double-strand breaks. DNA Repair, 2009, 8, 436-443.	2.8	173
85	RNF168 Binds and Amplifies Ubiquitin Conjugates on Damaged Chromosomes to Allow Accumulation of Repair Proteins. Cell, 2009, 136, 435-446.	28.9	784
86	The RIDDLE Syndrome Protein Mediates a Ubiquitin-Dependent Signaling Cascade at Sites of DNA Damage. Cell, 2009, 136, 420-434.	28.9	673
87	DNA Damage Sensing and Signaling. , 2009, , 1-24.		1
88	PP4 is a Î³H2AX phosphatase required for recovery from the DNA damage checkpoint. EMBO Reports, 2008, 9, 1019-1026.	4.5	179
89	PP4 is a Î³H2AX phosphatase required for recovery from the DNA damage checkpoint. EMBO Reports, 2008, 9, 1251-1251.	4.5	0
90	APLF (C2orf13) facilitates nonhomologous end-joining and undergoes ATM-dependent hyperphosphorylation following ionizing radiation. DNA Repair, 2008, 7, 292-302.	2.8	83

#	Article	IF	Citations
91	Engineering a DNA damage response without DNA damage. Genome Biology, 2008, 9, 227.	9.6	1
92	Dun1 Counts on Rad53 to Be Turned On. Molecular Cell, 2008, 31, 1-2.	9.7	9
93	Atomic Structure of the KEOPS Complex: An Ancient Protein Kinase-Containing Molecular Machine. Molecular Cell, 2008, 32, 259-275.	9.7	87
94	Rad6-Rad18 Mediates a Eukaryotic SOS Response by Ubiquitinating the 9-1-1 Checkpoint Clamp. Cell, 2008, 133, 601-611.	28.9	72
95	Significant conservation of synthetic lethal genetic interaction networks between distantly related eukaryotes. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 16653-16658.	7.1	165
96	A Genomewide Suppressor and Enhancer Analysis of cdc13-1 Reveals Varied Cellular Processes Influencing Telomere Capping in Saccharomyces cerevisiae. Genetics, 2008, 180, 2251-2266.	2.9	70
97	A Screen for Suppressors of Gross Chromosomal Rearrangements Identifies a Conserved Role for PLP in Preventing DNA Lesions. PLoS Genetics, 2007, 3, e134.	3.5	55
98	Orchestration of the DNA-Damage Response by the RNF8 Ubiquitin Ligase. Science, 2007, 318, 1637-1640.	12.6	800
99	A Genome-Wide Screen Identifies the Evolutionarily Conserved KEOPS Complex as a Telomere Regulator. Cell, 2006, 124, 1155-1168.	28.9	158
100	Chromatin and DNA repair: the benefits of relaxation. Nature Cell Biology, 2006, 8, 9-10.	10.3	39
101	A phosphatase complex that dephosphorylates Î³H2AX regulates DNA damage checkpoint recovery. Nature, 2006, 439, 497-501.	27.8	439
102	DNA Repair: DNA Polymerase Î¶ and Rev1 Break in. Current Biology, 2006, 16, R296-R299.	3.9	9
103	Telomere Protection: An Act of God. Current Biology, 2006, 16, R544-R546.	3.9	6
104	γH2AX as a Checkpoint Maintenance Signal. Cell Cycle, 2006, 5, 1376-1381.	2.6	50
105	The F-Box Protein Dia2 Overcomes Replication Impedance to Promote Genome Stability in Saccharomyces cerevisiae. Genetics, 2006, 174, 1709-1727.	2.9	53
106	Ccr4 contributes to tolerance of replication stress through control of CRT1 mRNA poly(A) tail length. Journal of Cell Science, 2006, 119, 5178-5192.	2.0	57
107	Saccharomyces cerevisiae Rad9 Acts as a Mec1 Adaptor to Allow Rad53 Activation. Current Biology, 2005, 15, 1364-1375.	3.9	207
108	The FHA Domain. , 2005, , 143-162.		0

#	Article	IF	Citations
109	Problems with Co-Funding in Canada. Science, 2005, 308, 1867b-1867b.	12.6	6
110	The Molecular Architecture of the Mammalian DNA Repair Enzyme, Polynucleotide Kinase. Molecular Cell, 2005, 17, 657-670.	9.7	191
111	Xrcc4 physically links DNA end processing by polynucleotide kinase to DNA ligation by DNA ligase IV. EMBO Journal, 2004, 23, 3874-3885.	7.8	218
112	Elg1 Forms an Alternative PCNA-Interacting RFC Complex Required to Maintain Genome Stability. Current Biology, 2003, 13, 1583-1595.	3.9	154
113	Bacterial signal transduction: a FHAscinating glimpse at the origins of phospho-dependent signal transduction. Trends in Microbiology, 2003, 11, 67-68.	7.7	6
114	The FHA domain. FEBS Letters, 2002, 513, 58-66.	2.8	358
115	Structural and Functional Versatility of the FHA Domain in DNA-Damage Signaling by the Tumor Suppressor Kinase Chk2. Molecular Cell, 2002, 9, 1045-1054.	9.7	207
116	Systematic identification of protein complexes in Saccharomyces cerevisiae by mass spectrometry. Nature, 2002, 415, 180-183.	27.8	3,445
117	DNA-PK, ATM and ATR as sensors of DNA damage: variations on a theme?. Current Opinion in Cell Biology, 2001, 13, 225-231.	5.4	457
118	The Molecular Basis of FHA Domain:Phosphopeptide Binding Specificity and Implications for Phospho-Dependent Signaling Mechanisms. Molecular Cell, 2000, 6, 1169-1182.	9.7	412
119	The FHA Domain in DNA Repair and Checkpoint Signaling. Cold Spring Harbor Symposia on Quantitative Biology, 2000, 65, 423-432.	1.1	31
120	The FHA Domain Is a Modular Phosphopeptide Recognition Motif. Molecular Cell, 1999, 4, 387-394.	9.7	368
121	Combinatorial interactions regulating cardiac transcription. , 1998, 22, 250-262.		91
122	Combinatorial interactions regulating cardiac transcription. Genesis, 1998, 22, 250-262.	2.1	4
123	The cardiac transcription factors Nkx2-5 and GATA-4 are mutual cofactors. EMBO Journal, 1997, 16, 5687-5696.	7.8	594
124	Localization of the Catf1 transcription factor gene to mouse Chromosome 19. Mammalian Genome, 1995, 6, 147-148.	2.2	13
125	RÃ©tinoÃ¯des et bases molÃ©culaires des malformations cardiaques congÃ©nitales. Medecine/Sciences, 1995, 11, 132.	0.2	0
126	Global cellular response to chemical perturbation of PLK4 activity and abnormal centrosome number. ELife, 0, 11, .	6.0	2