

# Stephen Philip Jackson

## 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.

284  
papers

60,824  
citations

116  
h-index

245  
g-index

305  
ext. papers

67,179  
ext. citations

17.1  
avg, IF

8.01  
L-index

#	Paper	IF	Citations
284	Combinatorial CRISPR screen identifies fitness effects of gene paralogues. <i>Nature Communications</i> , <b>2021</b> , 12, 1302	17.4	16
283	Mutagenic mechanisms of cancer-associated DNA polymerase $\gamma$ alleles. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, 3919-3931	20.1	2
282	Interfaces between cellular responses to DNA damage and cancer immunotherapy. <i>Genes and Development</i> , <b>2021</b> , 35, 602-618	12.6	16
281	The ELOF(1)ant in the room of TCR. <i>Nature Cell Biology</i> , <b>2021</b> , 23, 584-586	23.4	0
280	Loss of Cyclin C or CDK8 provides ATR inhibitor resistance by suppressing transcription-associated replication stress. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, 8665-8683	20.1	6
279	CCDC61/VFL3 Is a Paralog of SAS6 and Promotes Ciliary Functions. <i>Structure</i> , <b>2020</b> , 28, 674-689.e11	5.2	12
278	Chronic irradiation of human cells reduces histone levels and deregulates gene expression. <i>Scientific Reports</i> , <b>2020</b> , 10, 2200	4.9	8
277	Parallel CRISPR-Cas9 screens clarify impacts of p53 on screen performance. <i>ELife</i> , <b>2020</b> , 9,	8.9	16
276	PALB2 chromatin recruitment restores homologous recombination in BRCA1-deficient cells depleted of 53BP1. <i>Nature Communications</i> , <b>2020</b> , 11, 819	17.4	26
275	Trajectory and uniqueness of mutational signatures in yeast mutators. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2020</b> , 117, 24947-24956	11.5	13
274	The phosphoinositide 3-kinase inhibitor alpelisib restores actin organization and improves proximal tubule dysfunction in vitro and in a mouse model of Lowe syndrome and Dent disease. <i>Kidney International</i> , <b>2020</b> , 98, 883-896	9.9	5
273	Myocardial Fibrosis in Heart Failure: Anti-Fibrotic Therapies and the Role of Cardiovascular Magnetic Resonance in Drug Trials. <i>Cardiology and Therapy</i> , <b>2020</b> , 9, 363-376	2.8	19
272	Genome architecture and stability in the <i>Saccharomyces cerevisiae</i> knockout collection. <i>Nature</i> , <b>2019</b> , 573, 416-420	50.4	24
271	Small-Molecule Inhibition of UBE2T/FANCL-Mediated Ubiquitylation in the Fanconi Anemia Pathway. <i>ACS Chemical Biology</i> , <b>2019</b> , 14, 2148-2154	4.9	12
270	Derivation and maintenance of mouse haploid embryonic stem cells. <i>Nature Protocols</i> , <b>2019</b> , 14, 1991-2018	18.8	4
269	A Compendium of Mutational Signatures of Environmental Agents. <i>Cell</i> , <b>2019</b> , 177, 821-836.e16	56.2	220
268	MDC1 PST-repeat region promotes histone H2AX-independent chromatin association and DNA damage tolerance. <i>Nature Communications</i> , <b>2019</b> , 10, 5191	17.4	11

267	Genetic predisposition to mosaic Y chromosome loss in blood. <i>Nature</i> , <b>2019</b> , 575, 652-657	50.4	83
266	Microtubules Deform the Nuclear Membrane and Disrupt Nucleocytoplasmic Transport in Tau-Mediated Frontotemporal Dementia. <i>Cell Reports</i> , <b>2019</b> , 26, 582-593.e5	10.6	64
265	ATM orchestrates the DNA-damage response to counter toxic non-homologous end-joining at broken replication forks. <i>Nature Communications</i> , <b>2019</b> , 10, 87	17.4	73
264	Detection of functional protein domains by unbiased genome-wide forward genetic screening. <i>Scientific Reports</i> , <b>2018</b> , 8, 6161	4.9	7
263	Validating the concept of mutational signatures with isogenic cell models. <i>Nature Communications</i> , <b>2018</b> , 9, 1744	17.4	87
262	Targeting of NAT10 enhances healthspan in a mouse model of human accelerated aging syndrome. <i>Nature Communications</i> , <b>2018</b> , 9, 1700	17.4	48
261	Deubiquitylating enzymes and drug discovery: emerging opportunities. <i>Nature Reviews Drug Discovery</i> , <b>2018</b> , 17, 57-78	64.1	312
260	Shieldin complex promotes DNA end-joining and counters homologous recombination in BRCA1-null cells. <i>Nature Cell Biology</i> , <b>2018</b> , 20, 954-965	23.4	178
259	Map of synthetic rescue interactions for the Fanconi anemia DNA repair pathway identifies USP48. <i>Nature Communications</i> , <b>2018</b> , 9, 2280	17.4	19
258	Predicting the mutations generated by repair of Cas9-induced double-strand breaks. <i>Nature Biotechnology</i> , <b>2018</b> ,	44.5	215
257	Phosphorylation of Histone H4T80 Triggers DNA Damage Checkpoint Recovery. <i>Molecular Cell</i> , <b>2018</b> , 72, 625-635.e4	17.6	15
256	Inhibition of the acetyltransferase NAT10 normalizes progeric and aging cells by rebalancing the Transportin-1 nuclear import pathway. <i>Science Signaling</i> , <b>2018</b> , 11,	8.8	28
255	A novel somatic mutation achieves partial rescue in a child with Hutchinson-Gilford progeria syndrome. <i>Journal of Medical Genetics</i> , <b>2017</b> , 54, 212-216	5.8	14
254	Chromatin determinants impart camptothecin sensitivity. <i>EMBO Reports</i> , <b>2017</b> , 18, 1000-1012	6.5	10
253	PGBD5 promotes site-specific oncogenic mutations in human tumors. <i>Nature Genetics</i> , <b>2017</b> , 49, 1005-1014	36.3	40
252	ATM, ATR, and DNA-PK: The Trinity at the Heart of the DNA Damage Response. <i>Molecular Cell</i> , <b>2017</b> , 66, 801-817	17.6	800
251	Genetic variants associated with mosaic Y chromosome loss highlight cell cycle genes and overlap with cancer susceptibility. <i>Nature Genetics</i> , <b>2017</b> , 49, 674-679	36.3	70
250	Targeting DNA Repair in Cancer: Beyond PARP Inhibitors. <i>Cancer Discovery</i> , <b>2017</b> , 7, 20-37	24.4	320

249	Parallel genome-wide screens identify synthetic viable interactions between the BLM helicase complex and Fanconi anemia. <i>Nature Communications</i> , <b>2017</b> , 8, 1238	17.4	16
248	Genome-wide genetic screening with chemically mutagenized haploid embryonic stem cells. <i>Nature Chemical Biology</i> , <b>2017</b> , 13, 12-14	11.7	29
247	Global genome nucleotide excision repair is organized into domains that promote efficient DNA repair in chromatin. <i>Genome Research</i> , <b>2016</b> , 26, 1376-1387	9.7	20
246	Synthetic lethality between PAXX and XLF in mammalian development. <i>Genes and Development</i> , <b>2016</b> , 30, 2152-2157	12.6	51
245	Different DNA End Configurations Dictate Which NHEJ Components Are Most Important for Joining Efficiency. <i>Journal of Biological Chemistry</i> , <b>2016</b> , 291, 24377-24389	5.4	60
244	Coordinated nuclease activities counteract Ku at single-ended DNA double-strand breaks. <i>Nature Communications</i> , <b>2016</b> , 7, 12889	17.4	82
243	Molecular Insights into Division of Single Human Cancer Cells in On-Chip Transparent Microtubes. <i>ACS Nano</i> , <b>2016</b> , 10, 5835-46	16.7	24
242	DNA REPAIR. Drugging DNA repair. <i>Science</i> , <b>2016</b> , 352, 1178-9	33.3	56
241	Targeting BRCA1 and BRCA2 Deficiencies with G-Quadruplex-Interacting Compounds. <i>Molecular Cell</i> , <b>2016</b> , 61, 449-460	17.6	133
240	The N-terminal Region of Chromodomain Helicase DNA-binding Protein 4 (CHD4) Is Essential for Activity and Contains a High Mobility Group (HMG) Box-like-domain That Can Bind Poly(ADP-ribose). <i>Journal of Biological Chemistry</i> , <b>2016</b> , 291, 924-38	5.4	32
239	TRAP1 promotes DNA damage response during genome replication and is mutated in primordial dwarfism. <i>Nature Genetics</i> , <b>2016</b> , 48, 36-43	36.3	53
238	CRISPR-Cas9(D10A) nickase-based genotypic and phenotypic screening to enhance genome editing. <i>Scientific Reports</i> , <b>2016</b> , 6, 24356	4.9	62
237	Specific Roles of XRCC4 Paralogs PAXX and XLF during V(D)J Recombination. <i>Cell Reports</i> , <b>2016</b> , 16, 2967-2979	16.2	52
236	G9a inhibition potentiates the anti-tumour activity of DNA double-strand break inducing agents by impairing DNA repair independent of p53 status. <i>Cancer Letters</i> , <b>2016</b> , 380, 467-475	9.9	28
235	Prelamin A impairs 53BP1 nuclear entry by mislocalizing NUP153 and disrupting the Ran gradient. <i>Aging Cell</i> , <b>2016</b> , 15, 1039-1050	9.9	37
234	A flow cytometry-based method to simplify the analysis and quantification of protein association to chromatin in mammalian cells. <i>Nature Protocols</i> , <b>2015</b> , 10, 1297-307	18.8	43
233	TopBP1 interacts with BLM to maintain genome stability but is dispensable for preventing BLM degradation. <i>Molecular Cell</i> , <b>2015</b> , 57, 1133-1141	17.6	42
232	Neddylation promotes ubiquitylation and release of Ku from DNA-damage sites. <i>Cell Reports</i> , <b>2015</b> , 11, 704-14	10.6	80

231	Single-stranded DNA oligomers stimulate error-prone alternative repair of DNA double-strand breaks through hijacking Ku protein. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, 10264-76	20.1	13
230	Systematic E2 screening reveals a UBE2D-RNF138-CtIP axis promoting DNA repair. <i>Nature Cell Biology</i> , <b>2015</b> , 17, 1458-1470	23.4	67
229	When two is not enough: a CtIP tetramer is required for DNA repair by Homologous Recombination. <i>Nucleus</i> , <b>2015</b> , 6, 344-8	3.9	5
228	USP4 Auto-Deubiquitylation Promotes Homologous Recombination. <i>Molecular Cell</i> , <b>2015</b> , 60, 362-73	17.6	51
227	Combinations of PARP Inhibitors with Temozolomide Drive PARP1 Trapping and Apoptosis in Ewing's Sarcoma. <i>PLoS ONE</i> , <b>2015</b> , 10, e0140988	3.7	50
226	Synthetic viability genomic screening defines Sae2 function in DNA repair. <i>EMBO Journal</i> , <b>2015</b> , 34, 1509-1522	13.2	35
225	Ubiquitylation, neddylation and the DNA damage response. <i>Open Biology</i> , <b>2015</b> , 5, 150018	7	103
224	A high-throughput in vivo micronucleus assay for genome instability screening in mice. <i>Nature Protocols</i> , <b>2015</b> , 10, 205-15	18.8	37
223	DNA repair. PAXX, a paralog of XRCC4 and XLF, interacts with Ku to promote DNA double-strand break repair. <i>Science</i> , <b>2015</b> , 347, 185-188	33.3	202
222	CtIP tetramer assembly is required for DNA-end resection and repair. <i>Nature Structural and Molecular Biology</i> , <b>2015</b> , 22, 150-157	17.6	53
221	Transcriptionally active chromatin recruits homologous recombination at DNA double-strand breaks. <i>Nature Structural and Molecular Biology</i> , <b>2014</b> , 21, 366-74	17.6	386
220	Chemical inhibition of NAT10 corrects defects of laminopathic cells. <i>Science</i> , <b>2014</b> , 344, 527-32	33.3	174
219	Rolled-up functionalized nanomembranes as three-dimensional cavities for single cell studies. <i>Nano Letters</i> , <b>2014</b> , 14, 4197-204	11.5	59
218	Confinement and deformation of single cells and their nuclei inside size-adapted microtubes. <i>Advanced Healthcare Materials</i> , <b>2014</b> , 3, 1753-8	10.1	18
217	Systematic characterization of deubiquitylating enzymes for roles in maintaining genome integrity. <i>Nature Cell Biology</i> , <b>2014</b> , 16, 1016-26, 1-8	23.4	101
216	CtIP-mediated resection is essential for viability and can operate independently of BRCA1. <i>Journal of Experimental Medicine</i> , <b>2014</b> , 211, 1027-36	16.6	85
215	Cell Microenvironment: Confinement and Deformation of Single Cells and Their Nuclei Inside Size-Adapted Microtubes (Adv. Healthcare Mater. 11/2014). <i>Advanced Healthcare Materials</i> , <b>2014</b> , 3, 1932-1932 <sup>1</sup>	10.1	1932 <sup>1</sup>
214	A quantitative 14-3-3 interaction screen connects the nuclear exosome targeting complex to the DNA damage response. <i>Genes and Development</i> , <b>2014</b> , 28, 1977-82	12.6	36

213	Keeping 53BP1 out of focus in mitosis. <i>Cell Research</i> , <b>2014</b> , 24, 781-2	24.7	1
212	USP28 is recruited to sites of DNA damage by the tandem BRCT domains of 53BP1 but plays a minor role in double-strand break metabolism. <i>Molecular and Cellular Biology</i> , <b>2014</b> , 34, 2062-74	4.8	34
211	Deubiquitylating enzymes and DNA damage response pathways. <i>Cell Biochemistry and Biophysics</i> , <b>2013</b> , 67, 25-43	3.2	71
210	Regulation of DNA damage responses by ubiquitin and SUMO. <i>Molecular Cell</i> , <b>2013</b> , 49, 795-807	17.6	447
209	On your mark, get SET(D2), go! H3K36me3 primes DNA mismatch repair. <i>Cell</i> , <b>2013</b> , 153, 513-5	56.2	14
208	KAT5 tyrosine phosphorylation couples chromatin sensing to ATM signalling. <i>Nature</i> , <b>2013</b> , 498, 70-4	50.4	137
207	ATM-dependent phosphorylation of heterogeneous nuclear ribonucleoprotein K promotes p53 transcriptional activation in response to DNA damage. <i>Cell Cycle</i> , <b>2013</b> , 12, 698-704	4.7	48
206	Dma/RNF8 proteins are evolutionarily conserved E3 ubiquitin ligases that target septins. <i>Cell Cycle</i> , <b>2013</b> , 12, 1000-8	4.7	23
205	Competing roles of DNA end resection and non-homologous end joining functions in the repair of replication-born double-strand breaks by sister-chromatid recombination. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, 1669-83	20.1	13
204	A new method for high-resolution imaging of Ku foci to decipher mechanisms of DNA double-strand break repair. <i>Journal of Cell Biology</i> , <b>2013</b> , 202, 579-95	7.3	169
203	Systematic identification of functional residues in mammalian histone H2AX. <i>Molecular and Cellular Biology</i> , <b>2013</b> , 33, 111-26	4.8	48
202	RNF8 links nucleosomal and cytoskeletal ubiquitylation of higher order protein structures. <i>Cell Cycle</i> , <b>2013</b> , 12, 1161-2	4.7	2
201	Chromothripsis and cancer: causes and consequences of chromosome shattering. <i>Nature Reviews Cancer</i> , <b>2012</b> , 12, 663-70	31.3	268
200	Regulation of DNA-end resection by hRNPU-like proteins promotes DNA double-strand break signaling and repair. <i>Molecular Cell</i> , <b>2012</b> , 45, 505-16	17.6	130
199	Proteomic investigations reveal a role for RNA processing factor THRAP3 in the DNA damage response. <i>Molecular Cell</i> , <b>2012</b> , 46, 212-25	17.6	239
198	A high-throughput, flow cytometry-based method to quantify DNA-end resection in mammalian cells. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , <b>2012</b> , 81, 922-8	4.6	47
197	Structure of Mre11-Nbs1 complex yields insights into ataxia-telangiectasia-like disease mutations and DNA damage signaling. <i>Nature Structural and Molecular Biology</i> , <b>2012</b> , 19, 693-700	17.6	91
196	BRCA1-associated exclusion of 53BP1 from DNA damage sites underlies temporal control of DNA repair. <i>Journal of Cell Science</i> , <b>2012</b> , 125, 3529-34	5.3	218

195	Small-molecule-induced DNA damage identifies alternative DNA structures in human genes. <i>Nature Chemical Biology</i> , <b>2012</b> , 8, 301-10	11.7	467
194	RNF4, a SUMO-targeted ubiquitin E3 ligase, promotes DNA double-strand break repair. <i>Genes and Development</i> , <b>2012</b> , 26, 1179-95	12.6	225
193	CDK targeting of NBS1 promotes DNA-end resection, replication restart and homologous recombination. <i>EMBO Reports</i> , <b>2012</b> , 13, 561-8	6.5	76
192	Histone marks: repairing DNA breaks within the context of chromatin. <i>Biochemical Society Transactions</i> , <b>2012</b> , 40, 370-6	5.1	67
191	Disruption of mouse Cenpj, a regulator of centriole biogenesis, phenocopies Seckel syndrome. <i>PLoS Genetics</i> , <b>2012</b> , 8, e1003022	6	67
190	A phospho-proteomic screen identifies substrates of the checkpoint kinase Chk1. <i>Genome Biology</i> , <b>2011</b> , 12, R78	18.3	102
189	Regulation of Rad51 function by phosphorylation. <i>EMBO Reports</i> , <b>2011</b> , 12, 833-9	6.5	38
188	Structure-specific DNA endonuclease Mus81/Eme1 generates DNA damage caused by Chk1 inactivation. <i>PLoS ONE</i> , <b>2011</b> , 6, e23517	3.7	84
187	Give me a break, but not in mitosis: the mitotic DNA damage response marks DNA double-strand breaks with early signaling events. <i>Cell Cycle</i> , <b>2011</b> , 10, 1215-21	4.7	46
186	Replication stress induces 53BP1-containing OPT domains in G1 cells. <i>Journal of Cell Biology</i> , <b>2011</b> , 193, 97-108	7.3	234
185	Dynamics of DNA damage response proteins at DNA breaks: a focus on protein modifications. <i>Genes and Development</i> , <b>2011</b> , 25, 409-33	12.6	797
184	CtIP Mutations Cause Seckel and Jawad Syndromes. <i>PLoS Genetics</i> , <b>2011</b> , 7, e1002310	6	96
183	Human HDAC1 and HDAC2 function in the DNA-damage response to promote DNA nonhomologous end-joining. <i>Nature Structural and Molecular Biology</i> , <b>2010</b> , 17, 1144-51	17.6	459
182	Regulation of DNA-damage responses and cell-cycle progression by the chromatin remodelling factor CHD4. <i>EMBO Journal</i> , <b>2010</b> , 29, 3130-9	13	253
181	DNA damage signaling in response to double-strand breaks during mitosis. <i>Journal of Cell Biology</i> , <b>2010</b> , 190, 197-207	7.3	230
180	Human SIRT6 promotes DNA end resection through CtIP deacetylation. <i>Science</i> , <b>2010</b> , 329, 1348-53	33.3	305
179	The PIKK Family of Protein Kinases <b>2010</b> , 575-580		2
178	Genome-wide reprogramming in the mouse germ line entails the base excision repair pathway. <i>Science</i> , <b>2010</b> , 329, 78-82	33.3	380

177	Human CtIP mediates cell cycle control of DNA end resection and double strand break repair. <i>Journal of Biological Chemistry</i> , <b>2009</b> , 284, 9558-65	5.4	351
176	The <i>Saccharomyces cerevisiae</i> Esc2 and Smc5-6 proteins promote sister chromatid junction-mediated intra-S repair. <i>Molecular Biology of the Cell</i> , <b>2009</b> , 20, 1671-82	3.5	85
175	MDM2-dependent downregulation of p21 and hnRNP K provides a switch between apoptosis and growth arrest induced by pharmacologically activated p53. <i>Cancer Cell</i> , <b>2009</b> , 15, 171-83	24.3	138
174	Screen for DNA-damage-responsive histone modifications identifies H3K9Ac and H3K56Ac in human cells. <i>EMBO Journal</i> , <b>2009</b> , 28, 1878-89	13	242
173	The DNA-damage response in human biology and disease. <i>Nature</i> , <b>2009</b> , 461, 1071-8	50.4	3641
172	Mammalian SUMO E3-ligases PIAS1 and PIAS4 promote responses to DNA double-strand breaks. <i>Nature</i> , <b>2009</b> , 462, 935-9	50.4	403
171	A supramodular FHA/BRCT-repeat architecture mediates Nbs1 adaptor function in response to DNA damage. <i>Cell</i> , <b>2009</b> , 139, 100-11	56.2	131
170	Poly(ADP-ribose)-dependent regulation of DNA repair by the chromatin remodeling enzyme ALC1. <i>Science</i> , <b>2009</b> , 325, 1240-3	33.3	416
169	The DNA-damage response: new molecular insights and new approaches to cancer therapy. <i>Biochemical Society Transactions</i> , <b>2009</b> , 37, 483-94	5.1	41
168	Phospho-dependent interactions between NBS1 and MDC1 mediate chromatin retention of the MRN complex at sites of DNA damage. <i>EMBO Reports</i> , <b>2008</b> , 9, 795-801	6.5	214
167	CDK targets Sae2 to control DNA-end resection and homologous recombination. <i>Nature</i> , <b>2008</b> , 455, 689-92	32.4	359
166	Crystal structure of human XLF/Cernunnos reveals unexpected differences from XRCC4 with implications for NHEJ. <i>EMBO Journal</i> , <b>2008</b> , 27, 290-300	13	98
165	DNA helicases Sgs1 and BLM promote DNA double-strand break resection. <i>Genes and Development</i> , <b>2008</b> , 22, 2767-72	12.6	432
164	Orchestration of the DNA-damage response by the RNF8 ubiquitin ligase. <i>Science</i> , <b>2007</b> , 318, 1637-40	33.3	709
163	DNA damage response mediators MDC1 and 53BP1: constitutive activation and aberrant loss in breast and lung cancer, but not in testicular germ cell tumours. <i>Oncogene</i> , <b>2007</b> , 26, 7414-22	9.2	95
162	Spreading of mammalian DNA-damage response factors studied by CHIP-chip at damaged telomeres. <i>EMBO Journal</i> , <b>2007</b> , 26, 2707-18	13	73
161	Rad9 BRCT domain interaction with phosphorylated H2AX regulates the G1 checkpoint in budding yeast. <i>EMBO Reports</i> , <b>2007</b> , 8, 851-7	6.5	115
160	Human CtIP promotes DNA end resection. <i>Nature</i> , <b>2007</b> , 450, 509-14	50.4	1000

159	The non-homologous end-joining protein Nej1p is a target of the DNA damage checkpoint. <i>DNA Repair</i> , <b>2007</b> , 6, 190-201	4.3	27
158	Regulation of histone H3 lysine 56 acetylation in <i>Schizosaccharomyces pombe</i> . <i>Journal of Biological Chemistry</i> , <b>2007</b> , 282, 15040-7	5.4	55
157	Distinct domains in Nbs1 regulate irradiation-induced checkpoints and apoptosis. <i>Journal of Experimental Medicine</i> , <b>2007</b> , 204, 1003-11	16.6	67
156	Yeast Rtt109 promotes genome stability by acetylating histone H3 on lysine 56. <i>Science</i> , <b>2007</b> , 315, 649-53	33.3	343
155	Distinct roles of chromatin-associated proteins MDC1 and 53BP1 in mammalian double-strand break repair. <i>Molecular Cell</i> , <b>2007</b> , 28, 1045-57	17.6	184
154	Distinct domains in Nbs1 regulate irradiation-induced checkpoints and apoptosis. <i>Journal of Cell Biology</i> , <b>2007</b> , 177, i8-i8	7.3	
153	Rapid PIKK-dependent release of Chk1 from chromatin promotes the DNA-damage checkpoint response. <i>Current Biology</i> , <b>2006</b> , 16, 150-9	6.3	151
152	Evolutionary and functional conservation of the DNA non-homologous end-joining protein, XLF/Cernunnos. <i>Journal of Biological Chemistry</i> , <b>2006</b> , 281, 37517-26	5.4	66
151	EDD mediates DNA damage-induced activation of CHK2. <i>Journal of Biological Chemistry</i> , <b>2006</b> , 281, 39994-40006	9.4	1006
150	XLF interacts with the XRCC4-DNA ligase IV complex to promote DNA nonhomologous end-joining. <i>Cell</i> , <b>2006</b> , 124, 301-13	56.2	587
149	Structure of an Xrcc4-DNA ligase IV yeast ortholog complex reveals a novel BRCT interaction mode. <i>DNA Repair</i> , <b>2006</b> , 5, 362-8	4.3	55
148	gammaH2AX and MDC1: anchoring the DNA-damage-response machinery to broken chromosomes. <i>DNA Repair</i> , <b>2006</b> , 5, 534-43	4.3	319
147	Double-strand breaks trigger MRX- and Mec1-dependent, but Tel1-independent, checkpoint activation. <i>FEMS Yeast Research</i> , <b>2006</b> , 6, 836-47	3.1	14
146	ATM- and cell cycle-dependent regulation of ATR in response to DNA double-strand breaks. <i>Nature Cell Biology</i> , <b>2006</b> , 8, 37-45	23.4	859
145	hnRNP K: an HDM2 target and transcriptional coactivator of p53 in response to DNA damage. <i>Cell</i> , <b>2005</b> , 123, 1065-78	56.2	261
144	MDC1 directly binds phosphorylated histone H2AX to regulate cellular responses to DNA double-strand breaks. <i>Cell</i> , <b>2005</b> , 123, 1213-26	56.2	816
143	Exploiting the DNA repair defect in BRCA mutant cells in the design of new therapeutic strategies for cancer. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , <b>2005</b> , 70, 139-48	3.9	145
142	Suppression of HIV-1 infection by a small molecule inhibitor of the ATM kinase. <i>Nature Cell Biology</i> , <b>2005</b> , 7, 493-500	23.4	122

141	Conserved modes of recruitment of ATM, ATR and DNA-PKcs to sites of DNA damage. <i>Nature</i> , <b>2005</b> , 434, 605-11	50.4	975
140	Targeting the DNA repair defect in BRCA mutant cells as a therapeutic strategy. <i>Nature</i> , <b>2005</b> , 434, 917-21	50.4	4468
139	Yeast Nhp6A/B and mammalian Hmgb1 facilitate the maintenance of genome stability. <i>Current Biology</i> , <b>2005</b> , 15, 68-72	6.3	78
138	Human cell senescence as a DNA damage response. <i>Mechanisms of Ageing and Development</i> , <b>2005</b> , 126, 111-7	5.6	332
137	<i>Saccharomyces cerevisiae</i> histone H2A Ser122 facilitates DNA repair. <i>Genetics</i> , <b>2005</b> , 170, 543-53	4	38
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