

Stephen Philip Jackson

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284
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67,179
ext. citations

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L-index

#	Paper	IF	Citations
284	Targeting the DNA repair defect in BRCA mutant cells as a therapeutic strategy. <i>Nature</i> , 2005 , 434, 917-21	31.4	4468
283	The DNA-damage response in human biology and disease. <i>Nature</i> , 2009 , 461, 1071-8	50.4	3641
282	A DNA damage checkpoint response in telomere-initiated senescence. <i>Nature</i> , 2003 , 426, 194-8	50.4	2025
281	DNA double-strand breaks: signaling, repair and the cancer connection. <i>Nature Genetics</i> , 2001 , 27, 247-54	36.3	1832
280	The DNA-dependent protein kinase: requirement for DNA ends and association with Ku antigen. <i>Cell</i> , 1993 , 72, 131-42	56.2	1018
279	Human CtIP promotes DNA end resection. <i>Nature</i> , 2007 , 450, 509-14	50.4	1000
278	Identification and characterization of a novel and specific inhibitor of the ataxia-telangiectasia mutated kinase ATM. <i>Cancer Research</i> , 2004 , 64, 9152-9	10.1	978
277	Conserved modes of recruitment of ATM, ATR and DNA-PKcs to sites of DNA damage. <i>Nature</i> , 2005 , 434, 605-11	50.4	975
276	ATM- and cell cycle-dependent regulation of ATR in response to DNA double-strand breaks. <i>Nature Cell Biology</i> , 2006 , 8, 37-45	23.4	859
275	O-glycosylation of eukaryotic transcription factors: implications for mechanisms of transcriptional regulation. <i>Cell</i> , 1988 , 55, 125-33	56.2	831
274	MDC1 directly binds phosphorylated histone H2AX to regulate cellular responses to DNA double-strand breaks. <i>Cell</i> , 2005 , 123, 1213-26	56.2	816
273	Sensing and repairing DNA double-strand breaks. <i>Carcinogenesis</i> , 2002 , 23, 687-96	4.6	802
272	ATM, ATR, and DNA-PK: The Trinity at the Heart of the DNA Damage Response. <i>Molecular Cell</i> , 2017 , 66, 801-817	17.6	800
271	Dynamics of DNA damage response proteins at DNA breaks: a focus on protein modifications. <i>Genes and Development</i> , 2011 , 25, 409-33	12.6	797
270	Regulation of p53 in response to DNA damage. <i>Oncogene</i> , 1999 , 18, 7644-55	9.2	742
269	Defective DNA-dependent protein kinase activity is linked to V(D)J recombination and DNA repair defects associated with the murine scid mutation. <i>Cell</i> , 1995 , 80, 813-23	56.2	727
268	The Mre11 complex: at the crossroads of dna repair and checkpoint signalling. <i>Nature Reviews Molecular Cell Biology</i> , 2002 , 3, 317-27	48.7	725

267	Orchestration of the DNA-damage response by the RNF8 ubiquitin ligase. <i>Science</i> , 2007 , 318, 1637-40	33.3	709
266	A pathway of double-strand break rejoining dependent upon ATM, Artemis, and proteins locating to gamma-H2AX foci. <i>Molecular Cell</i> , 2004 , 16, 715-24	17.6	706
265	The DNA-dependent protein kinase. <i>Genes and Development</i> , 1999 , 13, 916-34	12.6	673
264	DNA-dependent protein kinase catalytic subunit: a relative of phosphatidylinositol 3-kinase and the ataxia telangiectasia gene product. <i>Cell</i> , 1995 , 82, 849-56	56.2	648
263	GC box binding induces phosphorylation of Sp1 by a DNA-dependent protein kinase. <i>Cell</i> , 1990 , 63, 155-65	56.2	621
262	XLF interacts with the XRCC4-DNA ligase IV complex to promote DNA nonhomologous end-joining. <i>Cell</i> , 2006 , 124, 301-13	56.2	587
261	Ku80: product of the XRCC5 gene and its role in DNA repair and V(D)J recombination. <i>Science</i> , 1994 , 265, 1442-5	33.3	569
260	Interfaces between the detection, signaling, and repair of DNA damage. <i>Science</i> , 2002 , 297, 547-51	33.3	566
259	A role for <i>Saccharomyces cerevisiae</i> histone H2A in DNA repair. <i>Nature</i> , 2000 , 408, 1001-4	50.4	526
258	Components of the Ku-dependent non-homologous end-joining pathway are involved in telomeric length maintenance and telomeric silencing. <i>EMBO Journal</i> , 1998 , 17, 1819-28	13	518
257	Synergistic activation by the glutamine-rich domains of human transcription factor Sp1. <i>Cell</i> , 1989 , 59, 827-36	56.2	516
256	DNA end-joining: from yeast to man. <i>Trends in Biochemical Sciences</i> , 1998 , 23, 394-8	10.3	482
255	Small-molecule-induced DNA damage identifies alternative DNA structures in human genes. <i>Nature Chemical Biology</i> , 2012 , 8, 301-10	11.7	467
254	Human HDAC1 and HDAC2 function in the DNA-damage response to promote DNA nonhomologous end-joining. <i>Nature Structural and Molecular Biology</i> , 2010 , 17, 1144-51	17.6	459
253	Binding of chromatin-modifying activities to phosphorylated histone H2A at DNA damage sites. <i>Molecular Cell</i> , 2004 , 16, 979-90	17.6	459
252	Regulation of DNA damage responses by ubiquitin and SUMO. <i>Molecular Cell</i> , 2013 , 49, 795-807	17.6	447
251	MDC1 is required for the intra-S-phase DNA damage checkpoint. <i>Nature</i> , 2003 , 421, 952-6	50.4	438
250	DNA helicases Sgs1 and BLM promote DNA double-strand break resection. <i>Genes and Development</i> , 2008 , 22, 2767-72	12.6	432

249	DNA-PK, ATM and ATR as sensors of DNA damage: variations on a theme?. <i>Current Opinion in Cell Biology</i> , 2001 , 13, 225-31	9	424
248	Poly(ADP-ribose)-dependent regulation of DNA repair by the chromatin remodeling enzyme ALC1. <i>Science</i> , 2009 , 325, 1240-3	33.3	416
247	Mammalian SUMO E3-ligases PIAS1 and PIAS4 promote responses to DNA double-strand breaks. <i>Nature</i> , 2009 , 462, 935-9	50.4	403
246	Transcriptionally active chromatin recruits homologous recombination at DNA double-strand breaks. <i>Nature Structural and Molecular Biology</i> , 2014 , 21, 366-74	17.6	386
245	Mammalian DNA double-strand break repair protein XRCC4 interacts with DNA ligase IV. <i>Current Biology</i> , 1997 , 7, 588-98	6.3	385
244	Genome-wide reprogramming in the mouse germ line entails the base excision repair pathway. <i>Science</i> , 2010 , 329, 78-82	33.3	380
243	Identification of a <i>Saccharomyces cerevisiae</i> Ku80 homologue: roles in DNA double strand break rejoining and in telomeric maintenance. <i>Nucleic Acids Research</i> , 1996 , 24, 4639-48	20.1	372
242	CDK targets Sae2 to control DNA-end resection and homologous recombination. <i>Nature</i> , 2008 , 455, 689-92	32.4	359
241	The molecular basis of FHA domain:phosphopeptide binding specificity and implications for phospho-dependent signaling mechanisms. <i>Molecular Cell</i> , 2000 , 6, 1169-82	17.6	357
240	Human CtIP mediates cell cycle control of DNA end resection and double strand break repair. <i>Journal of Biological Chemistry</i> , 2009 , 284, 9558-65	5.4	351
239	Yeast Rtt109 promotes genome stability by acetylating histone H3 on lysine 56. <i>Science</i> , 2007 , 315, 649-53	33.3	343
238	Human cell senescence as a DNA damage response. <i>Mechanisms of Ageing and Development</i> , 2005 , 126, 111-7	5.6	332
237	The FHA domain is a modular phosphopeptide recognition motif. <i>Molecular Cell</i> , 1999 , 4, 387-94	17.6	332
236	Mdc1 couples DNA double-strand break recognition by Nbs1 with its H2AX-dependent chromatin retention. <i>EMBO Journal</i> , 2004 , 23, 2674-83	13	326
235	Targeting DNA Repair in Cancer: Beyond PARP Inhibitors. <i>Cancer Discovery</i> , 2017 , 7, 20-37	24.4	320
234	gammaH2AX and MDC1: anchoring the DNA-damage-response machinery to broken chromosomes. <i>DNA Repair</i> , 2006 , 5, 534-43	4.3	319
233	Identification of a defect in DNA ligase IV in a radiosensitive leukaemia patient. <i>Current Biology</i> , 1999 , 9, 699-702	6.3	319
232	Deubiquitylating enzymes and drug discovery: emerging opportunities. <i>Nature Reviews Drug Discovery</i> , 2018 , 17, 57-78	64.1	312

231	DNA double-strand break repair and V(D)J recombination: involvement of DNA-PK. <i>Trends in Biochemical Sciences</i> , 1995 , 20, 412-5	10.3	312
230	The FHA domain. <i>FEBS Letters</i> , 2002 , 513, 58-66	3.8	308
229	Human SIRT6 promotes DNA end resection through CtIP deacetylation. <i>Science</i> , 2010 , 329, 1348-53	33.3	305
228	Direct interaction between Sp1 and the BPV enhancer E2 protein mediates synergistic activation of transcription. <i>Cell</i> , 1991 , 65, 493-505	56.2	304
227	A means to a DNA end: the many roles of Ku. <i>Nature Reviews Molecular Cell Biology</i> , 2004 , 5, 367-78	48.7	300
226	DNA-dependent protein kinase activity is absent in xrs-6 cells: implications for site-specific recombination and DNA double-strand break repair. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1995 , 92, 320-4	11.5	298
225	Identification of a nonsense mutation in the carboxyl-terminal region of DNA-dependent protein kinase catalytic subunit in the scid mouse. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1996 , 93, 10285-90	11.5	293
224	DNA looping between sites for transcriptional activation: self-association of DNA-bound Sp1. <i>Genes and Development</i> , 1991 , 5, 820-6	12.6	289
223	Targeted disruption of the catalytic subunit of the DNA-PK gene in mice confers severe combined immunodeficiency and radiosensitivity. <i>Immunity</i> , 1998 , 9, 355-66	32.3	274
222	Chromothripsis and cancer: causes and consequences of chromosome shattering. <i>Nature Reviews Cancer</i> , 2012 , 12, 663-70	31.3	268
221	hnRNP K: an HDM2 target and transcriptional coactivator of p53 in response to DNA damage. <i>Cell</i> , 2005 , 123, 1065-78	56.2	261
220	Regulation of DNA-damage responses and cell-cycle progression by the chromatin remodelling factor CHD4. <i>EMBO Journal</i> , 2010 , 29, 3130-9	13	253
219	Identification of a DNA nonhomologous end-joining complex in bacteria. <i>Science</i> , 2002 , 297, 1686-9	33.3	251
218	The interaction of Alba, a conserved archaeal chromatin protein, with Sir2 and its regulation by acetylation. <i>Science</i> , 2002 , 296, 148-51	33.3	244
217	Screen for DNA-damage-responsive histone modifications identifies H3K9Ac and H3K56Ac in human cells. <i>EMBO Journal</i> , 2009 , 28, 1878-89	13	242
216	Proteomic investigations reveal a role for RNA processing factor THRAP3 in the DNA damage response. <i>Molecular Cell</i> , 2012 , 46, 212-25	17.6	239
215	Replication stress induces 53BP1-containing OPT domains in G1 cells. <i>Journal of Cell Biology</i> , 2011 , 193, 97-108	7.3	234
214	Effects of DNA nonhomologous end-joining factors on telomere length and chromosomal stability in mammalian cells. <i>Current Biology</i> , 2001 , 11, 1192-6	6.3	233

213	DNA damage signaling in response to double-strand breaks during mitosis. <i>Journal of Cell Biology</i> , 2010 , 190, 197-207	7.3	230
212	RNF4, a SUMO-targeted ubiquitin E3 ligase, promotes DNA double-strand break repair. <i>Genes and Development</i> , 2012 , 26, 1179-95	12.6	225
211	DNA looping and Sp1 multimer links: a mechanism for transcriptional synergism and enhancement. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1991 , 88, 5670-4	11.5	222
210	A Compendium of Mutational Signatures of Environmental Agents. <i>Cell</i> , 2019 , 177, 821-836.e16	56.2	220
209	BRCA1-associated exclusion of 53BP1 from DNA damage sites underlies temporal control of DNA repair. <i>Journal of Cell Science</i> , 2012 , 125, 3529-34	5.3	218
208	Predicting the mutations generated by repair of Cas9-induced double-strand breaks. <i>Nature Biotechnology</i> , 2018 ,	44.5	215
207	Phospho-dependent interactions between NBS1 and MDC1 mediate chromatin retention of the MRN complex at sites of DNA damage. <i>EMBO Reports</i> , 2008 , 9, 795-801	6.5	214
206	Functional links between telomeres and proteins of the DNA-damage response. <i>Genes and Development</i> , 2004 , 18, 1781-99	12.6	213
205	Ku, a DNA repair protein with multiple cellular functions?. <i>Mutation Research DNA Repair</i> , 1999 , 434, 3-15		209
204	Identification of <i>Saccharomyces cerevisiae</i> DNA ligase IV: involvement in DNA double-strand break repair. <i>EMBO Journal</i> , 1997 , 16, 4788-95	13	208
203	DNA repair. PAXX, a paralog of XRCC4 and XLF, interacts with Ku to promote DNA double-strand break repair. <i>Science</i> , 2015 , 347, 185-188	33.3	202
202	Crystal structure of an Xrcc4-DNA ligase IV complex. <i>Nature Structural Biology</i> , 2001 , 8, 1015-9		200
201	Menage à trois: double strand break repair, V(D)J recombination and DNA-PK. <i>BioEssays</i> , 1995 , 17, 949-57.1		198
200	A heterotrimeric PCNA in the hyperthermophilic archaeon <i>Sulfolobus solfataricus</i> . <i>Molecular Cell</i> , 2003 , 11, 275-82	17.6	195
199	ATM, a central controller of cellular responses to DNA damage. <i>Cell Death and Differentiation</i> , 2001 , 8, 1052-65	12.7	187
198	Functions of poly(ADP-ribose) polymerase in controlling telomere length and chromosomal stability. <i>Nature Genetics</i> , 1999 , 23, 76-80	36.3	186
197	Repression of RNA polymerase III transcription by the retinoblastoma protein. <i>Nature</i> , 1996 , 382, 88-90	50.4	186
196	Distinct roles of chromatin-associated proteins MDC1 and 53BP1 in mammalian double-strand break repair. <i>Molecular Cell</i> , 2007 , 28, 1045-57	17.6	184

195	Structural and functional versatility of the FHA domain in DNA-damage signaling by the tumor suppressor kinase Chk2. <i>Molecular Cell</i> , 2002 , 9, 1045-54	17.6	179
194	Shieldin complex promotes DNA end-joining and counters homologous recombination in BRCA1-null cells. <i>Nature Cell Biology</i> , 2018 , 20, 954-965	23.4	178
193	Chemical inhibition of NAT10 corrects defects of laminopathic cells. <i>Science</i> , 2014 , 344, 527-32	33.3	174
192	Mechanism and regulation of transcription in archaea. <i>Current Opinion in Microbiology</i> , 2001 , 4, 208-13	7.9	173
191	Purification and analysis of RNA polymerase II transcription factors by using wheat germ agglutinin affinity chromatography. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1989 , 86, 1781-5	11.5	170
190	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> , 2013 , 202, 579-95	7.3	169
189	Transcription and translation in Archaea: a mosaic of eukaryal and bacterial features. <i>Trends in Microbiology</i> , 1998 , 6, 222-8	12.4	169
188	The yeast Xrs2 complex functions in S phase checkpoint regulation. <i>Genes and Development</i> , 2001 , 15, 2238-49	12.6	169
187	Genetic interaction between PARP and DNA-PK in V(D)J recombination and tumorigenesis. <i>Nature Genetics</i> , 1997 , 17, 479-82	36.3	165
186	The TATA-binding protein: a general transcription factor in eukaryotes and archaeobacteria. <i>Science</i> , 1994 , 264, 1326-9	33.3	164
185	Molecular and biochemical characterization of xrs mutants defective in Ku80. <i>Molecular and Cellular Biology</i> , 1997 , 17, 1264-73	4.8	160
184	Lcd1p recruits Mec1p to DNA lesions in vitro and in vivo. <i>Molecular Cell</i> , 2002 , 9, 857-69	17.6	159
183	The crystal structure of a hyperthermophilic archaeal TATA-box binding protein. <i>Journal of Molecular Biology</i> , 1996 , 264, 1072-84	6.5	153
182	Rapid PIKK-dependent release of Chk1 from chromatin promotes the DNA-damage checkpoint response. <i>Current Biology</i> , 2006 , 16, 150-9	6.3	151
181	Purification and DNA binding properties of the ataxia-telangiectasia gene product ATM. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1999 , 96, 11134-9	11.5	148
180	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> , 2005 , 70, 139-48	3.9	145
179	Suppression of homologous recombination by the <i>Saccharomyces cerevisiae</i> linker histone. <i>Molecular Cell</i> , 2003 , 11, 1685-92	17.6	140
178	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> , 2009 , 15, 171-83	24.3	138

177	KAT5 tyrosine phosphorylation couples chromatin sensing to ATM signalling. <i>Nature</i> , 2013 , 498, 70-4	50.4	137
176	Orientation of the transcription preinitiation complex in archaea. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1999 , 96, 13662-7	11.5	134
175	Targeting BRCA1 and BRCA2 Deficiencies with G-Quadruplex-Interacting Compounds. <i>Molecular Cell</i> , 2016 , 61, 449-460	17.6	133
174	A role for the TATA-box-binding protein component of the transcription factor IID complex as a general RNA polymerase III transcription factor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1992 , 89, 1949-53	11.5	132
173	A supramodular FHA/BRCT-repeat architecture mediates Nbs1 adaptor function in response to DNA damage. <i>Cell</i> , 2009 , 139, 100-11	56.2	131
172	Mechanism of TATA-binding protein recruitment to a TATA-less class III promoter. <i>Cell</i> , 1992 , 71, 1041-53	36.2	131
171	Regulation of DNA-end resection by hnRNPU-like proteins promotes DNA double-strand break signaling and repair. <i>Molecular Cell</i> , 2012 , 45, 505-16	17.6	130
170	<i>Saccharomyces cerevisiae</i> Sin3p facilitates DNA double-strand break repair. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 1644-9	11.5	125
169	Suppression of HIV-1 infection by a small molecule inhibitor of the ATM kinase. <i>Nature Cell Biology</i> , 2005 , 7, 493-500	23.4	122
168	Sequence-specific DNA binding by the <i>S. shibatae</i> TFIIB homolog, TFB, and its effect on promoter strength. <i>Molecular Cell</i> , 1998 , 1, 389-400	17.6	116
167	Factor requirements for transcription in the Archaeon <i>Sulfolobus shibatae</i> . <i>EMBO Journal</i> , 1997 , 16, 2927-36	36	115
166	Rad9 BRCT domain interaction with phosphorylated H2AX regulates the G1 checkpoint in budding yeast. <i>EMBO Reports</i> , 2007 , 8, 851-7	6.5	115
165	DNA double-strand break repair. <i>Current Biology</i> , 1999 , 9, R759-61	6.3	115
164	Conserved functional domains of the RNA polymerase III general transcription factor BRF. <i>Genes and Development</i> , 1994 , 8, 2879-90	12.6	115
163	Regulating transcription factor activity by phosphorylation. <i>Trends in Cell Biology</i> , 1992 , 2, 104-8	18.3	114
162	SV40 stimulates expression of the transacting factor Sp1 at the mRNA level. <i>Genes and Development</i> , 1990 , 4, 659-66	12.6	114
161	LCD1: an essential gene involved in checkpoint control and regulation of the MEC1 signalling pathway in <i>Saccharomyces cerevisiae</i> . <i>EMBO Journal</i> , 2000 , 19, 5801-12	13	110
160	The ataxia-telangiectasia related protein ATR mediates DNA-dependent phosphorylation of p53. <i>Oncogene</i> , 1999 , 18, 3989-95	9.2	110

159	DNA-dependent protein kinase: a potent inhibitor of transcription by RNA polymerase I. <i>Genes and Development</i> , 1995 , 9, 193-203	12.6	108
158	Disruption of Trrap causes early embryonic lethality and defects in cell cycle progression. <i>Nature Genetics</i> , 2001 , 29, 206-11	36.3	106
157	Ubiquitylation, neddylation and the DNA damage response. <i>Open Biology</i> , 2015 , 5, 150018	7	103
156	Identification of bacterial homologues of the Ku DNA repair proteins. <i>FEBS Letters</i> , 2001 , 500, 186-8	3.8	103
155	DNA damage triggers disruption of telomeric silencing and Mec1p-dependent relocation of Sir3p. <i>Current Biology</i> , 1999 , 9, 963-6	6.3	103
154	A phospho-proteomic screen identifies substrates of the checkpoint kinase Chk1. <i>Genome Biology</i> , 2011 , 12, R78	18.3	102
153	Systematic characterization of deubiquitylating enzymes for roles in maintaining genome integrity. <i>Nature Cell Biology</i> , 2014 , 16, 1016-26, 1-8	23.4	101
152	c-Jun is phosphorylated by the DNA-dependent protein kinase in vitro; definition of the minimal kinase recognition motif. <i>Nucleic Acids Research</i> , 1993 , 21, 1289-95	20.1	101
151	Mitotic regulation of a TATA-binding-protein-containing complex. <i>Molecular and Cellular Biology</i> , 1995 , 15, 1983-92	4.8	100
150	Crystal structure of human XLF/Cernunnos reveals unexpected differences from XRCC4 with implications for NHEJ. <i>EMBO Journal</i> , 2008 , 27, 290-300	13	98
149	Transcriptional regulation of an archaeal operon in vivo and in vitro. <i>Molecular Cell</i> , 1999 , 4, 971-82	17.6	98
148	The TATA-binding protein: a central role in transcription by RNA polymerases I, II and III. <i>Trends in Genetics</i> , 1992 , 8, 284-288	8.5	98
147	Characterization of the residues phosphorylated in vitro by different C-terminal domain kinases. <i>Journal of Biological Chemistry</i> , 1998 , 273, 6769-75	5.4	97
146	CtIP Mutations Cause Seckel and Jawad Syndromes. <i>PLoS Genetics</i> , 2011 , 7, e1002310	6	96
145	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> , 2007 , 26, 7414-22	9.2	95
144	MDC1/NFBD1: a key regulator of the DNA damage response in higher eukaryotes. <i>DNA Repair</i> , 2004 , 3, 953-7	4.3	94
143	Structure of Mre11-Nbs1 complex yields insights into ataxia-telangiectasia-like disease mutations and DNA damage signaling. <i>Nature Structural and Molecular Biology</i> , 2012 , 19, 693-700	17.6	91
142	Human and mouse homologs of <i>Schizosaccharomyces pombe</i> rad1(+) and <i>Saccharomyces cerevisiae</i> RAD17: linkage to checkpoint control and mammalian meiosis. <i>Genes and Development</i> , 1998 , 12, 2560-73	12.6	91

141	Gene for the catalytic subunit of the human DNA-activated protein kinase maps to the site of the XRCC7 gene on chromosome 8. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1995 , 92, 7515-9	11.5	90
140	Lif1p targets the DNA ligase Lig4p to sites of DNA double-strand breaks. <i>Current Biology</i> , 2000 , 10, 165-8.	6.3	89
139	Validating the concept of mutational signatures with isogenic cell models. <i>Nature Communications</i> , 2018 , 9, 1744	17.4	87
138	Cleavage and inactivation of ATM during apoptosis. <i>Molecular and Cellular Biology</i> , 1999 , 19, 6076-84	4.8	86
137	CtIP-mediated resection is essential for viability and can operate independently of BRCA1. <i>Journal of Experimental Medicine</i> , 2014 , 211, 1027-36	16.6	85
136	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> , 2009 , 20, 1671-82	3.5	85
135	Cell cycle regulation of RNA polymerase III transcription. <i>Molecular and Cellular Biology</i> , 1995 , 15, 6653-62.	2.8	85
134	Structure-specific DNA endonuclease Mus81/Eme1 generates DNA damage caused by Chk1 inactivation. <i>PLoS ONE</i> , 2011 , 6, e23517	3.7	84
133	DNA repair: how Ku makes ends meet. <i>Current Biology</i> , 2001 , 11, R920-4	6.3	84
132	The association of ATR protein with mouse meiotic chromosome cores. <i>Chromosoma</i> , 1999 , 108, 95-102	2.8	83
131	Genetic predisposition to mosaic Y chromosome loss in blood. <i>Nature</i> , 2019 , 575, 652-657	50.4	83
130	Coordinated nuclease activities counteract Ku at single-ended DNA double-strand breaks. <i>Nature Communications</i> , 2016 , 7, 12889	17.4	82
129	The archaeal TFIIIEalpha homologue facilitates transcription initiation by enhancing TATA-box recognition. <i>EMBO Reports</i> , 2001 , 2, 133-8	6.5	82
128	DNA-dependent protein kinase. <i>International Journal of Biochemistry and Cell Biology</i> , 1997 , 29, 935-8	5.6	81
127	Neddylation promotes ubiquitylation and release of Ku from DNA-damage sites. <i>Cell Reports</i> , 2015 , 11, 704-14	10.6	80
126	Mechanistic analysis of RNA polymerase III regulation by the retinoblastoma protein. <i>EMBO Journal</i> , 1997 , 16, 2061-71	13	79
125	Yeast Nhp6A/B and mammalian Hmgb1 facilitate the maintenance of genome stability. <i>Current Biology</i> , 2005 , 15, 68-72	6.3	78
124	Expression of Ku70 correlates with survival in carcinoma of the cervix. <i>British Journal of Cancer</i> , 2000 , 83, 1702-6	8.7	78

123	Structural basis for the NAD-dependent deacetylase mechanism of Sir2. <i>Journal of Biological Chemistry</i> , 2002 , 277, 34489-98	5.4	77
122	CDK targeting of NBS1 promotes DNA-end resection, replication restart and homologous recombination. <i>EMBO Reports</i> , 2012 , 13, 561-8	6.5	76
121	Mechanism of autoregulation by an archaeal transcriptional repressor. <i>Journal of Biological Chemistry</i> , 2000 , 275, 31624-9	5.4	74
120	Spreading of mammalian DNA-damage response factors studied by ChIP-chip at damaged telomeres. <i>EMBO Journal</i> , 2007 , 26, 2707-18	13	73
119	ATM orchestrates the DNA-damage response to counter toxic non-homologous end-joining at broken replication forks. <i>Nature Communications</i> , 2019 , 10, 87	17.4	73
118	Deubiquitylating enzymes and DNA damage response pathways. <i>Cell Biochemistry and Biophysics</i> , 2013 , 67, 25-43	3.2	71
117	Separation-of-function mutants of yeast Ku80 reveal a Yku80p-Sir4p interaction involved in telomeric silencing. <i>Journal of Biological Chemistry</i> , 2004 , 279, 86-94	5.4	71
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