

Stephen Philip Jackson

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2068338/publications.pdf>

Version: 2024-02-01

290
papers

72,620
citations

867

120
h-index

691

261
g-index

305
all docs

305
docs citations

305
times ranked

56357
citing authors

#	ARTICLE	IF	CITATIONS
1	Microarray screening reveals two non-conventional SUMO-binding modules linked to DNA repair by non-homologous end-joining. <i>Nucleic Acids Research</i> , 2022, 50, 4732-4754.	6.5	4
2	SHLD1 is dispensable for 53BP1-dependent V(D)J recombination but critical for productive class switch recombination. <i>Nature Communications</i> , 2022, 13, .	5.8	7
3	Mutagenic mechanisms of cancer-associated DNA polymerase δ alleles. <i>Nucleic Acids Research</i> , 2021, 49, 3919-3931.	6.5	12
4	Interfaces between cellular responses to DNA damage and cancer immunotherapy. <i>Genes and Development</i> , 2021, 35, 602-618.	2.7	61
5	The ELOF(1)ant in the room of TCR. <i>Nature Cell Biology</i> , 2021, 23, 584-586.	4.6	2
6	Loss of Cyclin C or CDK8 provides ATR inhibitor resistance by suppressing transcription-associated replication stress. <i>Nucleic Acids Research</i> , 2021, 49, 8665-8683.	6.5	25
7	Combinatorial CRISPR screen identifies fitness effects of gene paralogues. <i>Nature Communications</i> , 2021, 12, 1302.	5.8	59
8	Trajectory and uniqueness of mutational signatures in yeast mutators. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 24947-24956.	3.3	29
9	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> , 2020, 98, 883-896.	2.6	14
10	Myocardial Fibrosis in Heart Failure: Anti-Fibrotic Therapies and the Role of Cardiovascular Magnetic Resonance in Drug Trials. <i>Cardiology and Therapy</i> , 2020, 9, 363-376.	1.1	35
11	CCDC61/VFL3 Is a Paralog of SAS6 and Promotes Ciliary Functions. <i>Structure</i> , 2020, 28, 674-689.e11.	1.6	16
12	Chronic irradiation of human cells reduces histone levels and deregulates gene expression. <i>Scientific Reports</i> , 2020, 10, 2200.	1.6	18
13	PALB2 chromatin recruitment restores homologous recombination in BRCA1-deficient cells depleted of 53BP1. <i>Nature Communications</i> , 2020, 11, 819.	5.8	43
14	Parallel CRISPR-Cas9 screens clarify impacts of p53 on screen performance. <i>ELife</i> , 2020, 9, .	2.8	36
15	MDC1 PST-repeat region promotes histone H2AX-independent chromatin association and DNA damage tolerance. <i>Nature Communications</i> , 2019, 10, 5191.	5.8	35
16	Genome architecture and stability in the <i>Saccharomyces cerevisiae</i> knockout collection. <i>Nature</i> , 2019, 573, 416-420.	13.7	72
17	Small-Molecule Inhibition of UBE2T/FANCL-Mediated Ubiquitylation in the Fanconi Anemia Pathway. <i>ACS Chemical Biology</i> , 2019, 14, 2148-2154.	1.6	17
18	Derivation and maintenance of mouse haploid embryonic stem cells. <i>Nature Protocols</i> , 2019, 14, 1991-2014.	5.5	12

#	ARTICLE	IF	CITATIONS
19	A Compendium of Mutational Signatures of Environmental Agents. <i>Cell</i> , 2019, 177, 821-836.e16.	13.5	437
20	Genetic predisposition to mosaic Y chromosome loss in blood. <i>Nature</i> , 2019, 575, 652-657.	13.7	198
21	Predicting the mutations generated by repair of Cas9-induced double-strand breaks. <i>Nature Biotechnology</i> , 2019, 37, 64-72.	9.4	359
22	Microtubules Deform the Nuclear Membrane and Disrupt Nucleocytoplasmic Transport in Tau-Mediated Frontotemporal Dementia. <i>Cell Reports</i> , 2019, 26, 582-593.e5.	2.9	119
23	ATM orchestrates the DNA-damage response to counter toxic non-homologous end-joining at broken replication forks. <i>Nature Communications</i> , 2019, 10, 87.	5.8	133
24	Detection of functional protein domains by unbiased genome-wide forward genetic screening. <i>Scientific Reports</i> , 2018, 8, 6161.	1.6	14
25	Validating the concept of mutational signatures with isogenic cell models. <i>Nature Communications</i> , 2018, 9, 1744.	5.8	128
26	Targeting of NAT10 enhances healthspan in a mouse model of human accelerated aging syndrome. <i>Nature Communications</i> , 2018, 9, 1700.	5.8	103
27	Deubiquitylating enzymes and drug discovery: emerging opportunities. <i>Nature Reviews Drug Discovery</i> , 2018, 17, 57-78.	21.5	555
28	Phosphorylation of Histone H4T80 Triggers DNA Damage Checkpoint Recovery. <i>Molecular Cell</i> , 2018, 72, 625-635.e4.	4.5	21
29	Inhibition of the acetyltransferase NAT10 normalizes progeric and aging cells by rebalancing the Transportin-1 nuclear import pathway. <i>Science Signaling</i> , 2018, 11, .	1.6	57
30	Shieldin complex promotes DNA end-joining and counters homologous recombination in BRCA1-null cells. <i>Nature Cell Biology</i> , 2018, 20, 954-965.	4.6	291
31	Map of synthetic rescue interactions for the Fanconi anemia DNA repair pathway identifies USP48. <i>Nature Communications</i> , 2018, 9, 2280.	5.8	34
32	A novel somatic mutation achieves partial rescue in a child with Hutchinson-Gilford progeria syndrome. <i>Journal of Medical Genetics</i> , 2017, 54, 212-216.	1.5	28
33	Chromatin determinants impart camptothecin sensitivity. <i>EMBO Reports</i> , 2017, 18, 1000-1012.	2.0	18
34	PGBD5 promotes site-specific oncogenic mutations in human tumors. <i>Nature Genetics</i> , 2017, 49, 1005-1014.	9.4	69
35	ATM, ATR, and DNA-PK: The Trinity at the Heart of the DNA Damage Response. <i>Molecular Cell</i> , 2017, 66, 801-817.	4.5	1,319
36	Genetic variants associated with mosaic Y chromosome loss highlight cell cycle genes and overlap with cancer susceptibility. <i>Nature Genetics</i> , 2017, 49, 674-679.	9.4	117

#	ARTICLE	IF	CITATIONS
37	Targeting DNA Repair in Cancer: Beyond PARP Inhibitors. <i>Cancer Discovery</i> , 2017, 7, 20-37.	7.7	488
38	Parallel genome-wide screens identify synthetic viable interactions between the BLM helicase complex and Fanconi anemia. <i>Nature Communications</i> , 2017, 8, 1238.	5.8	25
39	Genome-wide genetic screening with chemically mutagenized haploid embryonic stem cells. <i>Nature Chemical Biology</i> , 2017, 13, 12-14.	3.9	36
40	CRISPR-Cas9D10A nickase-based genotypic and phenotypic screening to enhance genome editing. <i>Scientific Reports</i> , 2016, 6, 24356.	1.6	111
41	Specific Roles of XRCC4 Paralogs PAXX and XLF during V(D)J Recombination. <i>Cell Reports</i> , 2016, 16, 2967-2979.	2.9	70
42	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> , 2016, 380, 467-475.	3.2	37
43	Prelamin A impairs 53BP1 nuclear entry by mislocalizing NUP153 and disrupting the Ran gradient. <i>Aging Cell</i> , 2016, 15, 1039-1050.	3.0	48
44	Global genome nucleotide excision repair is organized into domains that promote efficient DNA repair in chromatin. <i>Genome Research</i> , 2016, 26, 1376-1387.	2.4	32
45	Synthetic lethality between PAXX and XLF in mammalian development. <i>Genes and Development</i> , 2016, 30, 2152-2157.	2.7	68
46	Different DNA End Configurations Dictate Which NHEJ Components Are Most Important for Joining Efficiency. <i>Journal of Biological Chemistry</i> , 2016, 291, 24377-24389.	1.6	83
47	Coordinated nuclease activities counteract Ku at single-ended DNA double-strand breaks. <i>Nature Communications</i> , 2016, 7, 12889.	5.8	113
48	Molecular Insights into Division of Single Human Cancer Cells in On-Chip Transparent Microtubes. <i>ACS Nano</i> , 2016, 10, 5835-5846.	7.3	31
49	Drugging DNA repair. <i>Science</i> , 2016, 352, 1178-1179.	6.0	71
50	Targeting BRCA1 and BRCA2 Deficiencies with G-Quadruplex-Interacting Compounds. <i>Molecular Cell</i> , 2016, 61, 449-460.	4.5	185
51	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> , 2016, 291, 924-938.	1.6	49
52	TRAP1 promotes DNA damage response during genome replication and is mutated in primordial dwarfism. <i>Nature Genetics</i> , 2016, 48, 36-43.	9.4	74
53	USP4 Auto-Deubiquitylation Promotes Homologous Recombination. <i>Molecular Cell</i> , 2015, 60, 362-373.	4.5	67
54	Combinations of PARP Inhibitors with Temozolomide Drive PARP1 Trapping and Apoptosis in Ewing's Sarcoma. <i>PLoS ONE</i> , 2015, 10, e0140988.	1.1	72

#	ARTICLE	IF	CITATIONS
55	Synthetic viability genomic screening defines Sae2 function in DNA repair. <i>EMBO Journal</i> , 2015, 34, 1509-1522.	3.5	37
56	Ubiquitylation, neddylation and the DNA damage response. <i>Open Biology</i> , 2015, 5, 150018.	1.5	117
57	A high-throughput in vivo micronucleus assay for genome instability screening in mice. <i>Nature Protocols</i> , 2015, 10, 205-215.	5.5	61
58	PAXX, a paralog of XRCC4 and XLF, interacts with Ku to promote DNA double-strand break repair. <i>Science</i> , 2015, 347, 185-188.	6.0	252
59	CtIP tetramer assembly is required for DNA-end resection and repair. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 150-157.	3.6	63
60	A flow cytometry-based method to simplify the analysis and quantification of protein association to chromatin in mammalian cells. <i>Nature Protocols</i> , 2015, 10, 1297-1307.	5.5	62
61	TopBP1 Interacts with BLM to Maintain Genome Stability but Is Dispensable for Preventing BLM Degradation. <i>Molecular Cell</i> , 2015, 57, 1133-1141.	4.5	59
62	Neddylation Promotes Ubiquitylation and Release of Ku from DNA-Damage Sites. <i>Cell Reports</i> , 2015, 11, 704-714.	2.9	107
63	Single-stranded DNA oligomers stimulate error-prone alternative repair of DNA double-strand breaks through hijacking Ku protein. <i>Nucleic Acids Research</i> , 2015, 43, gkv894.	6.5	14
64	Systematic E2 screening reveals a UBE2D-RNF138-CtIP axis promoting DNA repair. <i>Nature Cell Biology</i> , 2015, 17, 1458-1470.	4.6	90
65	When two is not enough: a CtIP tetramer is required for DNA repair by Homologous Recombination. <i>Nucleus</i> , 2015, 6, 344-348.	0.6	7
66	Ubiquitin regulates dissociation of DNA repair factors from chromatin. <i>Oncotarget</i> , 2015, 6, 14727-14728.	0.8	5
67	A quantitative 14-3-3 interaction screen connects the nuclear exosome targeting complex to the DNA damage response. <i>Genes and Development</i> , 2014, 28, 1977-1982.	2.7	50
68	Keeping 53BP1 out of focus in mitosis. <i>Cell Research</i> , 2014, 24, 781-782.	5.7	4
69	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> , 2014, 34, 2062-2074.	1.1	46
70	Transcriptionally active chromatin recruits homologous recombination at DNA double-strand breaks. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 366-374.	3.6	536
71	Chemical Inhibition of NAT10 Corrects Defects of Laminopathic Cells. <i>Science</i> , 2014, 344, 527-532.	6.0	265
72	Rolled-up Functionalized Nanomembranes as Three-Dimensional Cavities for Single Cell Studies. <i>Nano Letters</i> , 2014, 14, 4197-4204.	4.5	65

#	ARTICLE	IF	CITATIONS
73	Confinement and Deformation of Single Cells and Their Nuclei Inside Size-Adapted Microtubes. <i>Advanced Healthcare Materials</i> , 2014, 3, 1753-1758.	3.9	26
74	Systematic characterization of deubiquitylating enzymes for roles in maintaining genome integrity. <i>Nature Cell Biology</i> , 2014, 16, 1016-1026.	4.6	134
75	CtIP-mediated resection is essential for viability and can operate independently of BRCA1. <i>Journal of Experimental Medicine</i> , 2014, 211, 1027-1036.	4.2	108
76	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> , 2014, 3, 1932-1932.	3.9	1
77	Deubiquitylating Enzymes and DNA Damage Response Pathways. <i>Cell Biochemistry and Biophysics</i> , 2013, 67, 25-43.	0.9	77
78	Regulation of DNA Damage Responses by Ubiquitin and SUMO. <i>Molecular Cell</i> , 2013, 49, 795-807.	4.5	522
79	On Your MARK, Get SET(D2), Go! H3K36me3 Primes DNA Mismatch Repair. <i>Cell</i> , 2013, 153, 513-515.	13.5	15
80	KAT5 tyrosine phosphorylation couples chromatin sensing to ATM signalling. <i>Nature</i> , 2013, 498, 70-74.	13.7	149
81	ATM-dependent phosphorylation of heterogeneous nuclear ribonucleoprotein K promotes p53 transcriptional activation in response to DNA damage. <i>Cell Cycle</i> , 2013, 12, 698-704.	1.3	53
82	Dma/RNF8 proteins are evolutionarily conserved E3 ubiquitin ligases that target septins. <i>Cell Cycle</i> , 2013, 12, 1000-1008.	1.3	29
83	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> , 2013, 41, 1669-1683.	6.5	14
84	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, 579-595.	2.3	218
85	Systematic Identification of Functional Residues in Mammalian Histone H2AX. <i>Molecular and Cellular Biology</i> , 2013, 33, 111-126.	1.1	54
86	RNF8 links nucleosomal and cytoskeletal ubiquitylation of higher order protein structures. <i>Cell Cycle</i> , 2013, 12, 1161-1161.	1.3	2
87	Disruption of Mouse Cenpj, a Regulator of Centriole Biogenesis, Phenocopies Seckel Syndrome. <i>PLoS Genetics</i> , 2012, 8, e1003022.	1.5	84
88	Chromothripsis and cancer: causes and consequences of chromosome shattering. <i>Nature Reviews Cancer</i> , 2012, 12, 663-670.	12.8	333
89	Regulation of DNA-End Resection by hnRNPU-like Proteins Promotes DNA Double-Strand Break Signaling and Repair. <i>Molecular Cell</i> , 2012, 45, 505-516.	4.5	160
90	Proteomic Investigations Reveal a Role for RNA Processing Factor THRAP3 in the DNA Damage Response. <i>Molecular Cell</i> , 2012, 46, 212-225.	4.5	298

#	ARTICLE	IF	CITATIONS
91	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> , 2012, 81A, 922-928.	1.1	67
92	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.	3.6	108
93	BRCA1-associated exclusion of 53BP1 from DNA damage sites underlies temporal control of DNA repair. <i>Journal of Cell Science</i> , 2012, 125, 3529-3534.	1.2	280
94	Small-molecule-induced DNA damage identifies alternative DNA structures in human genes. <i>Nature Chemical Biology</i> , 2012, 8, 301-310.	3.9	576
95	RNF4, a SUMO-targeted ubiquitin E3 ligase, promotes DNA double-strand break repair. <i>Genes and Development</i> , 2012, 26, 1179-1195.	2.7	273
96	CDK targeting of NBS1 promotes DNA end resection, replication restart and homologous recombination. <i>EMBO Reports</i> , 2012, 13, 561-568.	2.0	86
97	Histone marks: repairing DNA breaks within the context of chromatin. <i>Biochemical Society Transactions</i> , 2012, 40, 370-376.	1.6	74
98	A phospho-proteomic screen identifies substrates of the checkpoint kinase Chk1. <i>Genome Biology</i> , 2011, 12, R78.	13.9	123
99	Regulation of Rad51 function by phosphorylation. <i>EMBO Reports</i> , 2011, 12, 833-839.	2.0	53
100	Structure-Specific DNA Endonuclease Mus81/Eme1 Generates DNA Damage Caused by Chk1 Inactivation. <i>PLoS ONE</i> , 2011, 6, e23517.	1.1	97
101	Give me a break, but not in mitosis. <i>Cell Cycle</i> , 2011, 10, 1215-1221.	1.3	51
102	Replication stress induces 53BP1-containing OPT domains in G1 cells. <i>Journal of Cell Biology</i> , 2011, 193, 97-108.	2.3	284
103	Dynamics of DNA damage response proteins at DNA breaks: a focus on protein modifications. <i>Genes and Development</i> , 2011, 25, 409-433.	2.7	927
104	CtIP Mutations Cause Seckel and Jawad Syndromes. <i>PLoS Genetics</i> , 2011, 7, e1002310.	1.5	109
105	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, 1144-1151.	3.6	542
106	Regulation of DNA-damage responses and cell-cycle progression by the chromatin remodelling factor CHD4. <i>EMBO Journal</i> , 2010, 29, 3130-3139.	3.5	300
107	DNA damage signaling in response to double-strand breaks during mitosis. <i>Journal of Cell Biology</i> , 2010, 190, 197-207.	2.3	271
108	The PIKK Family of Protein Kinases. , 2010, , 575-580.		3

#	ARTICLE	IF	CITATIONS
109	Genome-Wide Reprogramming in the Mouse Germ Line Entails the Base Excision Repair Pathway. <i>Science</i> , 2010, 329, 78-82.	6.0	420
110	Human CtIP Mediates Cell Cycle Control of DNA End Resection and Double Strand Break Repair. <i>Journal of Biological Chemistry</i> , 2009, 284, 9558-9565.	1.6	420
111	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, 1671-1682.	0.9	92
112	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, 171-183.	7.7	159
113	Screen for DNA-damage-responsive histone modifications identifies H3K9Ac and H3K56Ac in human cells. <i>EMBO Journal</i> , 2009, 28, 1878-1889.	3.5	288
114	The DNA-damage response in human biology and disease. <i>Nature</i> , 2009, 461, 1071-1078.	13.7	4,718
115	Mammalian SUMO E3-ligases PIAS1 and PIAS4 promote responses to DNA double-strand breaks. <i>Nature</i> , 2009, 462, 935-939.	13.7	461
116	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
117	Poly(ADP-ribose)-Dependent Regulation of DNA Repair by the Chromatin Remodeling Enzyme ALC1. <i>Science</i> , 2009, 325, 1240-1243.	6.0	504
118	The DNA-damage response: new molecular insights and new approaches to cancer therapy. <i>Biochemical Society Transactions</i> , 2009, 37, 483-494.	1.6	48
119	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.	2.0	248
120	CDK targets Sae2 to control DNA-end resection and homologous recombination. <i>Nature</i> , 2008, 455, 689-692.	13.7	402
121	Crystal structure of human XLF/Cernunnos reveals unexpected differences from XRCC4 with implications for NHEJ. <i>EMBO Journal</i> , 2008, 27, 290-300.	3.5	106
122	DNA helicases Sgs1 and BLM promote DNA double-strand break resection. <i>Genes and Development</i> , 2008, 22, 2767-2772.	2.7	498
123	Regulation of Histone H3 Lysine 56 Acetylation in <i>Schizosaccharomyces pombe</i> . <i>Journal of Biological Chemistry</i> , 2007, 282, 15040-15047.	1.6	70
124	Distinct domains in Nbs1 regulate irradiation-induced checkpoints and apoptosis. <i>Journal of Experimental Medicine</i> , 2007, 204, 1003-1011.	4.2	71
125	Yeast Rtt109 Promotes Genome Stability by Acetylating Histone H3 on Lysine 56. <i>Science</i> , 2007, 315, 649-652.	6.0	397
126	Distinct Roles of Chromatin-Associated Proteins MDC1 and 53BP1 in Mammalian Double-Strand Break Repair. <i>Molecular Cell</i> , 2007, 28, 1045-1057.	4.5	195

#	ARTICLE	IF	CITATIONS
127	Orchestration of the DNA-Damage Response by the RNF8 Ubiquitin Ligase. <i>Science</i> , 2007, 318, 1637-1640.	6.0	800
128	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, 7414-7422.	2.6	105
129	Spreading of mammalian DNA-damage response factors studied by ChIP-chip at damaged telomeres. <i>EMBO Journal</i> , 2007, 26, 2707-2718.	3.5	84
130	Rad9 BRCT domain interaction with phosphorylated H2AX regulates the G1 checkpoint in budding yeast. <i>EMBO Reports</i> , 2007, 8, 851-857.	2.0	131
131	Human CtIP promotes DNA end resection. <i>Nature</i> , 2007, 450, 509-514.	13.7	1,158
132	The non-homologous end-joining protein Nej1p is a target of the DNA damage checkpoint. <i>DNA Repair</i> , 2007, 6, 190-201.	1.3	34
133	Distinct domains in Nbs1 regulate irradiation-induced checkpoints and apoptosis. <i>Journal of Cell Biology</i> , 2007, 177, i8-i8.	2.3	0
134	XLF Interacts with the XRCC4-DNA Ligase IV Complex to Promote DNA Nonhomologous End-Joining. <i>Cell</i> , 2006, 124, 301-313.	13.5	666
135	Structure of an Xrcc4-DNA ligase IV yeast ortholog complex reveals a novel BRCT interaction mode. <i>DNA Repair</i> , 2006, 5, 362-368.	1.3	60
136	γH2AX and MDC1: Anchoring the DNA-damage-response machinery to broken chromosomes. <i>DNA Repair</i> , 2006, 5, 534-543.	1.3	371
137	Double-strand breaks trigger MRX- and Mec1-dependent, but Tel1-independent, checkpoint activation. <i>FEMS Yeast Research</i> , 2006, 6, 836-847.	1.1	17
138	ATM- and cell cycle-dependent regulation of ATR in response to DNA double-strand breaks. <i>Nature Cell Biology</i> , 2006, 8, 37-45.	4.6	942
139	Rapid PIKK-Dependent Release of Chk1 from Chromatin Promotes the DNA-Damage Checkpoint Response. <i>Current Biology</i> , 2006, 16, 150-159.	1.8	166
140	Evolutionary and Functional Conservation of the DNA Non-homologous End-joining Protein, XLF/Cernunnos*. <i>Journal of Biological Chemistry</i> , 2006, 281, 37517-37526.	1.6	74
141	EDD Mediates DNA Damage-induced Activation of CHK2. <i>Journal of Biological Chemistry</i> , 2006, 281, 39990-40000.	1.6	51
142	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, 139-148.	2.0	172
143	Suppression of HIV-1 infection by a small molecule inhibitor of the ATM kinase. <i>Nature Cell Biology</i> , 2005, 7, 493-500.	4.6	135
144	Conserved modes of recruitment of ATM, ATR and DNA-PKcs to sites of DNA damage. <i>Nature</i> , 2005, 434, 605-611.	13.7	1,099

#	ARTICLE	IF	CITATIONS
145	Targeting the DNA repair defect in BRCA mutant cells as a therapeutic strategy. <i>Nature</i> , 2005, 434, 917-921.	13.7	5,595
146	Yeast Nhp6A/B and Mammalian Hmgb1 Facilitate the Maintenance of Genome Stability. <i>Current Biology</i> , 2005, 15, 68-72.	1.8	84
147	Human cell senescence as a DNA damage response. <i>Mechanisms of Ageing and Development</i> , 2005, 126, 111-117.	2.2	383
148	<i>Saccharomyces cerevisiae</i> Histone H2A Ser122 Facilitates DNA Repair. <i>Genetics</i> , 2005, 170, 543-553.	1.2	49
149	Specific Association of Mouse MDC1/NFBD1 with NBS1 at Sites of DNA-Damage. <i>Cell Cycle</i> , 2005, 4, 177-182.	1.3	31
150	hnRNP K: An HDM2 Target and Transcriptional Coactivator of p53 in Response to DNA Damage. <i>Cell</i> , 2005, 123, 1065-1078.	13.5	305
151	MDC1 Directly Binds Phosphorylated Histone H2AX to Regulate Cellular Responses to DNA Double-Strand Breaks. <i>Cell</i> , 2005, 123, 1213-1226.	13.5	957
152	Functional links between telomeres and proteins of the DNA-damage response. <i>Genes and Development</i> , 2004, 18, 1781-1799.	2.7	244
153	Identification and Characterization of a Novel and Specific Inhibitor of the Ataxia-Telangiectasia Mutated Kinase ATM. <i>Cancer Research</i> , 2004, 64, 9152-9159.	0.4	1,089
154	p53 Prevents the Accumulation of Double-Strand DNA Breaks at Stalled-Replication Forks Induced by UV in Human Cells. <i>Cell Cycle</i> , 2004, 3, 1543-1557.	1.3	37
155	<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, 1644-1649.	3.3	137
156	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.	1.6	84
157	Activation of the DNA Damage Response by Telomere Attrition: A Passage to Cellular Senescence. <i>Cell Cycle</i> , 2004, 3, 541-544.	1.3	61
158	Tudor domains track down DNA breaks. <i>Nature Cell Biology</i> , 2004, 6, 1150-1152.	4.6	15
159	A means to a DNA end: the many roles of Ku. <i>Nature Reviews Molecular Cell Biology</i> , 2004, 5, 367-378.	16.1	334
160	Mdc1 couples DNA double-strand break recognition by Nbs1 with its H2AX-dependent chromatin retention. <i>EMBO Journal</i> , 2004, 23, 2674-2683.	3.5	356
161	Suppression of retroviral infection by the RAD52 DNA repair protein. <i>EMBO Journal</i> , 2004, 23, 3421-3429.	3.5	67
162	MDC1/NFBD1: a key regulator of the DNA damage response in higher eukaryotes. <i>DNA Repair</i> , 2004, 3, 953-957.	1.3	99

#	ARTICLE	IF	CITATIONS
163	A Pathway of Double-Strand Break Rejoining Dependent upon ATM, Artemis, and Proteins Locating to γ -H2AX Foci. <i>Molecular Cell</i> , 2004, 16, 715-724.	4.5	790
164	Binding of Chromatin-Modifying Activities to Phosphorylated Histone H2A at DNA Damage Sites. <i>Molecular Cell</i> , 2004, 16, 979-990.	4.5	513
165	ATM and ATR. <i>Current Biology</i> , 2003, 13, R468.	1.8	22
166	MDC1 is required for the intra-S-phase DNA damage checkpoint. <i>Nature</i> , 2003, 421, 952-956.	13.7	472
167	A DNA damage checkpoint response in telomere-initiated senescence. <i>Nature</i> , 2003, 426, 194-198.	13.7	2,381
168	The Gam protein of bacteriophage Mu is an orthologue of eukaryotic Ku. <i>EMBO Reports</i> , 2003, 4, 47-52.	2.0	76
169	Protective packaging for DNA. <i>Nature</i> , 2003, 424, 732-734.	13.7	21
170	Increased Genome Instability in Aging Yeast. <i>Cell</i> , 2003, 115, 1-2.	13.5	13
171	A Heterotrimeric PCNA in the Hyperthermophilic Archaeon <i>Sulfolobus solfataricus</i> . <i>Molecular Cell</i> , 2003, 11, 275-282.	4.5	215
172	Suppression of Homologous Recombination by the <i>Saccharomyces cerevisiae</i> Linker Histone. <i>Molecular Cell</i> , 2003, 11, 1685-1692.	4.5	153
173	Double-Strand Break Recognition and Its Repair by Nonhomologous End Joining. , 2003, , 219-224.		0
174	The PIKK Family of Protein Kinases. , 2003, , 557-561.		7
175	Structural Basis for the NAD-dependent Deacetylase Mechanism of Sir2. <i>Journal of Biological Chemistry</i> , 2002, 277, 34489-34498.	1.6	84
176	Sensing and repairing DNA double-strand breaks. <i>Carcinogenesis</i> , 2002, 23, 687-696.	1.3	927
177	Screening the yeast genome for new DNA-repair genes. <i>Genome Biology</i> , 2002, 3, reviews1009.1.	13.9	13
178	The Interaction of Alba, a Conserved Archaeal Chromatin Protein, with Sir2 and Its Regulation by Acetylation. <i>Science</i> , 2002, 296, 148-151.	6.0	271
179	The FHA domain. <i>FEBS Letters</i> , 2002, 513, 58-66.	1.3	358
180	Lcd1p Recruits Mec1p to DNA Lesions In Vitro and In Vivo. <i>Molecular Cell</i> , 2002, 9, 857-869.	4.5	169

#	ARTICLE	IF	CITATIONS
181	Structural and Functional Versatility of the FHA Domain in DNA-Damage Signaling by the Tumor Suppressor Kinase Chk2. <i>Molecular Cell</i> , 2002, 9, 1045-1054.	4.5	207
182	Identification of a DNA Nonhomologous End-Joining Complex in Bacteria. <i>Science</i> , 2002, 297, 1686-1689.	6.0	284
183	The MRE11 complex: at the crossroads of DNA repair and checkpoint signalling. <i>Nature Reviews Molecular Cell Biology</i> , 2002, 3, 317-327.	16.1	778
184	Interfaces Between the Detection, Signaling, and Repair of DNA Damage. <i>Science</i> , 2002, 297, 547-551.	6.0	650
185	The archaeal TFIIE \pm homologue facilitates transcription initiation by enhancing TATA $\hat{=}$ box recognition. <i>EMBO Reports</i> , 2001, 2, 133-138.	2.0	86
186	Crystal structure of an Xrcc4-DNA ligase IV complex. <i>Nature Structural Biology</i> , 2001, 8, 1015-1019.	9.7	229
187	Mechanism and regulation of transcription in archaea. <i>Current Opinion in Microbiology</i> , 2001, 4, 208-213.	2.3	191
188	Identification of bacterial homologues of the Ku DNA repair proteins. <i>FEBS Letters</i> , 2001, 500, 186-188.	1.3	124
189	Basal and regulated transcription in Archaea. <i>Biochemical Society Transactions</i> , 2001, 29, 392-395.	1.6	61
190	Telomerase subunit overexpression suppresses telomere $\hat{=}$ specific checkpoint activation in the yeast yku80 mutant. <i>EMBO Reports</i> , 2001, 2, 197-202.	2.0	49
191	DNA double-strand breaks: signaling, repair and the cancer connection. <i>Nature Genetics</i> , 2001, 27, 247-254.	9.4	2,116
192	Disruption of Ttrap causes early embryonic lethality and defects in cell cycle progression. <i>Nature Genetics</i> , 2001, 29, 206-211.	9.4	122
193	ATM, a central controller of cellular responses to DNA damage. <i>Cell Death and Differentiation</i> , 2001, 8, 1052-1065.	5.0	220
194	Effects of DNA nonhomologous end-joining factors on telomere length and chromosomal stability in mammalian cells. <i>Current Biology</i> , 2001, 11, 1192-1196.	1.8	260
195	DNA repair: How Ku makes ends meet. <i>Current Biology</i> , 2001, 11, R920-R924.	1.8	95
196	DNA-PK, ATM and ATR as sensors of DNA damage: variations on a theme?. <i>Current Opinion in Cell Biology</i> , 2001, 13, 225-231.	2.6	457
197	Identification of a Conserved Archaeal RNA Polymerase Subunit Contacted by the Basal Transcription Factor TFB. <i>Journal of Biological Chemistry</i> , 2001, 276, 46693-46696.	1.6	35
198	The yeast Xrs2 complex functions in S phase checkpoint regulation. <i>Genes and Development</i> , 2001, 15, 2238-2249.	2.7	194

#	ARTICLE	IF	CITATIONS
199	A Role for TAF3B2 in the Repression of Human RNA Polymerase III Transcription in Nonproliferating Cells. <i>Journal of Biological Chemistry</i> , 2001, 276, 21158-21165.	1.6	11
200	Detecting, signalling and repairing DNA double-strand breaks. <i>Biochemical Society Transactions</i> , 2001, 29, 655-61.	1.6	56
201	Comparison of DNA repair protein expression and activities between human fibroblast cell lines with different radiosensitivities. , 2000, 85, 845-849.		34
202	Charting a course through RNA polymerase. , 2000, 7, 703-705.		123
203	A role for <i>Saccharomyces cerevisiae</i> histone H2A in DNA repair. <i>Nature</i> , 2000, 408, 1001-1004.	13.7	598
204	Lif1p targets the DNA ligase Lig4p to sites of DNA double-strand breaks. <i>Current Biology</i> , 2000, 10, 165-168.	1.8	96
205	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, 5801-5812.	3.5	123
206	Mechanism of Autoregulation by an Archaeal Transcriptional Repressor. <i>Journal of Biological Chemistry</i> , 2000, 275, 31624-31629.	1.6	83
207	Expression of Ku70 correlates with survival in carcinoma of the cervix. <i>British Journal of Cancer</i> , 2000, 83, 1702-1706.	2.9	92
208	The Role of Transcription Factor B in Transcription Initiation and Promoter Clearance in the Archaeon <i>Sulfolobus acidocaldarius</i> . <i>Journal of Biological Chemistry</i> , 2000, 275, 12934-12940.	1.6	63
209	The Molecular Basis of FHA Domain:Phosphopeptide Binding Specificity and Implications for Phospho-Dependent Signaling Mechanisms. <i>Molecular Cell</i> , 2000, 6, 1169-1182.	4.5	412
210	Comparison of DNA repair protein expression and activities between human fibroblast cell lines with different radiosensitivities. <i>International Journal of Cancer</i> , 2000, 85, 845.	2.3	1
211	Expression and nuclear localization of BLM, a chromosome stability protein mutated in Bloom's syndrome, suggest a role in recombination during meiotic prophase. <i>Journal of Cell Science</i> , 2000, 113, 663-672.	1.2	83
212	7 DNA-dependent protein kinase and related proteins. , 1999, , 91-104.		23
213	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, 11134-11139.	3.3	157
214	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, 13662-13667.	3.3	149
215	Functions of poly(ADP-ribose) polymerase in controlling telomere length and chromosomal stability. <i>Nature Genetics</i> , 1999, 23, 76-80.	9.4	218
216	Regulation of p53 in response to DNA damage. <i>Oncogene</i> , 1999, 18, 7644-7655.	2.6	873

#	ARTICLE	IF	CITATIONS
217	The association of ATR protein with mouse meiotic chromosome cores. <i>Chromosoma</i> , 1999, 108, 95-102.	1.0	89
218	DNA double-strand break repair. <i>Current Biology</i> , 1999, 9, R759-R761.	1.8	154
219	Identification of a defect in DNA ligase IV in a radiosensitive leukaemia patient. <i>Current Biology</i> , 1999, 9, 699-S2.	1.8	361
220	DNA damage triggers disruption of telomeric silencing and Mec1p-dependent relocation of Sir3p. <i>Current Biology</i> , 1999, 9, 963-S1.	1.8	113
221	Transcriptional Regulation of an Archaeal Operon In Vivo and In Vitro. <i>Molecular Cell</i> , 1999, 4, 971-982.	4.5	105
222	The FHA Domain Is a Modular Phosphopeptide Recognition Motif. <i>Molecular Cell</i> , 1999, 4, 387-394.	4.5	368
223	Ku, a DNA repair protein with multiple cellular functions?. <i>Mutation Research DNA Repair</i> , 1999, 434, 3-15.	3.8	242
224	The ataxia-telangiectasia related protein ATR mediates DNA-dependent phosphorylation of p53. <i>Oncogene</i> , 1999, 18, 3989-3995.	2.6	120
225	Cleavage and Inactivation of ATM during Apoptosis. <i>Molecular and Cellular Biology</i> , 1999, 19, 6076-6084.	1.1	95
226	Involvement of DNA End-Binding Protein Ku in Ty Element Retrotransposition. <i>Molecular and Cellular Biology</i> , 1999, 19, 6260-6268.	1.1	68
227	The DNA-dependent protein kinase. <i>Genes and Development</i> , 1999, 13, 916-934.	2.7	760
228	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, 1819-1828.	3.5	590
229	DNA repair: The Nijmegen breakage syndrome protein. <i>Current Biology</i> , 1998, 8, R622-R625.	1.8	49
230	DNA end-joining: from yeast to man. <i>Trends in Biochemical Sciences</i> , 1998, 23, 394-398.	3.7	541
231	Transcription and translation in Archaea: a mosaic of eukaryal and bacterial features. <i>Trends in Microbiology</i> , 1998, 6, 222-228.	3.5	182
232	Targeted Disruption of the Catalytic Subunit of the DNA-PK Gene in Mice Confers Severe Combined Immunodeficiency and Radiosensitivity. <i>Immunity</i> , 1998, 9, 355-366.	6.6	301
233	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.	4.5	125
234	Fanconi anemia C gene product plays a role in the fidelity of blunt DNA end-joining. <i>Journal of Molecular Biology</i> , 1998, 279, 375-385.	2.0	75

#	ARTICLE	IF	CITATIONS
235	Characterization of the Residues Phosphorylated in Vitro by Different C-terminal Domain Kinases. <i>Journal of Biological Chemistry</i> , 1998, 273, 6769-6775.	1.6	106
236	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, 2560-2573.	2.7	100
237	DNA end-independent activation of DNA-PK mediated via association with the DNA-binding protein hCtIP. <i>Genes and Development</i> , 1998, 12, 2188-2199.	2.7	71
238	Molecular and biochemical characterisation of DNA-dependent protein kinase-defective rodent mutant irs-20. <i>Nucleic Acids Research</i> , 1998, 26, 1965-1973.	6.5	74
239	Temperature, template topology, and factor requirements of archaeal transcription. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1998, 95, 15218-15222.	3.3	72
240	Molecular and Biochemical Characterization of <i>Xrs</i> Mutants Defective in Ku80. <i>Molecular and Cellular Biology</i> , 1997, 17, 1264-1273.	1.1	171
241	Chromosomes and expression mechanisms. <i>Current Opinion in Genetics and Development</i> , 1997, 7, 149-151.	1.5	3
242	DNA-dependent protein kinase. <i>International Journal of Biochemistry and Cell Biology</i> , 1997, 29, 935-938.	1.2	103
243	Genetic interaction between PARP and DNA-PK in V(D)J recombination and tumorigenesis. <i>Nature Genetics</i> , 1997, 17, 479-482.	9.4	173
244	Silencing and DNA repair connect. <i>Nature</i> , 1997, 388, 829-830.	13.7	22
245	Mammalian DNA double-strand break repair protein XRCC4 interacts with DNA ligase IV. <i>Current Biology</i> , 1997, 7, 588-598.	1.8	422
246	Factor requirements for transcription in the Archaeon <i>Sulfolobus shibatae</i> . <i>EMBO Journal</i> , 1997, 16, 2927-2936.	3.5	129
247	Identification of <i>Saccharomyces cerevisiae</i> DNA ligase IV: involvement in DNA double-strand break repair. <i>EMBO Journal</i> , 1997, 16, 4788-4795.	3.5	236
248	Mechanistic analysis of RNA polymerase III regulation by the retinoblastoma protein. <i>EMBO Journal</i> , 1997, 16, 2061-2071.	3.5	93
249	The Crystal Structure of a Hyperthermophilic Archaeal TATA-box Binding Protein. <i>Journal of Molecular Biology</i> , 1996, 264, 1072-1084.	2.0	159
250	The recognition of DNA damage. <i>Current Opinion in Genetics and Development</i> , 1996, 6, 19-25.	1.5	77
251	An archaeobacterial homologue of the essential eubacterial cell division protein FtsZ. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1996, 93, 6726-6730.	3.3	69
252	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, 10285-10290.	3.3	322

#	ARTICLE	IF	CITATIONS
253	Expression of DNA-Dependent Protein Kinase Holoenzyme Upon Induction of Lymphocyte Differentiation and V(D)J Recombination. <i>FEBS Journal</i> , 1996, 241, 931-940.	0.2	49
254	Lack of detectable defect in DNA double-strand break repair and DNA-dependent protein kinase activity in radiosensitive human severe combined immunodeficiency fibroblasts. <i>European Journal of Immunology</i> , 1996, 26, 1118-1122.	1.6	49
255	Repression of RNA polymerase III transcription by the retinoblastoma protein. <i>Nature</i> , 1996, 382, 88-90.	13.7	204
256	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, 4639-4648.	6.5	431
257	Identification of the Catalytic Subunit of DNA Dependent Protein Kinase as the Product of the Mouse <i>scid</i> Gene. <i>Current Topics in Microbiology and Immunology</i> , 1996, 217, 79-89.	0.7	13
258	Gene for the catalytic subunit of the human DNA-activated protein kinase maps to the site of the <i>XRCC7</i> gene on chromosome 8.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1995, 92, 7515-7519.	3.3	98
259	DNA-dependent protein kinase activity is absent in <i>xrs-6</i> 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, 320-324.	3.3	324
260	Mitotic Regulation of a TATA-Binding-Protein-Containing Complex. <i>Molecular and Cellular Biology</i> , 1995, 15, 1983-1992.	1.1	105
261	Cell Cycle Regulation of RNA Polymerase III Transcription. <i>Molecular and Cellular Biology</i> , 1995, 15, 6653-6662.	1.1	95
262	Cancer Predisposition: Ataxia-telangiectasia at the crossroads. <i>Current Biology</i> , 1995, 5, 1210-1212.	1.8	56
263	DNA double-strand break repair and V(D)J recombination: involvement of DNA-PK. <i>Trends in Biochemical Sciences</i> , 1995, 20, 412-415.	3.7	343
264	Menage à trois: Double strand break repair, V(D)J recombination and DNA-PK. <i>BioEssays</i> , 1995, 17, 949-957.	1.2	237
265	Extraordinary sequence conservation of the PRP8 splicing factor. <i>Yeast</i> , 1995, 11, 337-342.	0.8	62
266	DNA-dependent protein kinase: a potent inhibitor of transcription by RNA polymerase I.. <i>Genes and Development</i> , 1995, 9, 193-203.	2.7	121
267	Defective DNA-dependent protein kinase activity is linked to V(D)J recombination and DNA repair defects associated with the murine <i>scid</i> mutation. <i>Cell</i> , 1995, 80, 813-823.	13.5	809
268	DNA-dependent protein kinase catalytic subunit: A relative of phosphatidylinositol 3-kinase and the ataxia telangiectasia gene product. <i>Cell</i> , 1995, 82, 849-856.	13.5	712
269	A YAC Contig Encompassing the <i>XRCC5</i> (Ku80) DNA Repair Gene and Complementation of Defective Cells by YAC Protoplast Fusion. <i>Genomics</i> , 1995, 30, 320-328.	1.3	13
270	The TATA-binding protein: a general transcription factor in eukaryotes and archaeobacteria. <i>Science</i> , 1994, 264, 1326-1329.	6.0	190

#	ARTICLE	IF	CITATIONS
271	Ku80: product of the XRCC5 gene and its role in DNA repair and V(D)J recombination. <i>Science</i> , 1994, 265, 1442-1445.	6.0	624
272	Conserved functional domains of the RNA polymerase III general transcription factor BRF.. <i>Genes and Development</i> , 1994, 8, 2879-2890.	2.7	121
273	MPSA short communications. <i>The Protein Journal</i> , 1994, 13, 431-512.	1.1	0
274	Protein kinases and DNA damage. <i>Trends in Biochemical Sciences</i> , 1994, 19, 500-503.	3.7	53
275	The DNA-dependent protein kinase: Requirement for DNA ends and association with Ku antigen. <i>Cell</i> , 1993, 72, 131-142.	13.5	1,136
276	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, 1289-1295.	6.5	110
277	Transcription factor phosphorylation by the DNA-dependent protein kinase. <i>Biochemical Society Transactions</i> , 1993, 21, 930-935.	1.6	29
278	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, 1949-1953.	3.3	142
279	The TATA-binding protein is a general transcription factor for RNA polymerase III. <i>Journal of Cell Science</i> , 1992, 1992, 1-7.	1.2	17
280	Mechanism of TATA-binding protein recruitment to a TATA-less class III promoter. <i>Cell</i> , 1992, 71, 1041-1053.	13.5	138
281	Regulating transcription factor activity by phosphorylation. <i>Trends in Cell Biology</i> , 1992, 2, 104-108.	3.6	121
282	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.	2.9	104
283	Direct interaction between Sp1 and the BPV enhancer E2 protein mediates synergistic activation of transcription. <i>Cell</i> , 1991, 65, 493-505.	13.5	350
284	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, 5670-5674.	3.3	240
285	DNA looping between sites for transcriptional activation: self-association of DNA-bound Sp1.. <i>Genes and Development</i> , 1991, 5, 820-826.	2.7	354
286	SV40 stimulates expression of the transacting factor Sp1 at the mRNA level.. <i>Genes and Development</i> , 1990, 4, 659-666.	2.7	133
287	GC box binding induces phosphorylation of Sp1 by a DNA-dependent protein kinase. <i>Cell</i> , 1990, 63, 155-165.	13.5	683
288	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, 1781-1785.	3.3	184

#	ARTICLE	IF	CITATIONS
289	Synergistic activation by the glutamine-rich domains of human transcription factor Sp1. <i>Cell</i> , 1989, 59, 827-836.	13.5	560
290	O-glycosylation of eukaryotic transcription factors: Implications for mechanisms of transcriptional regulation. <i>Cell</i> , 1988, 55, 125-133.	13.5	899