Kyungjae Myung

List of Publications by Year
in descending order

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94 papers	5,504 citations	109321 35 h-index	85541 71 g-index
95 all docs	95 docs citations	95 times ranked	6400 citing authors

#	Article	IF	Citations
1	Maintenance of Genome Stability in Saccharomyces cerevisiae. Science, 2002, 297, 552-557.	12.6	442
2	Multiple pathways cooperate in the suppression of genome instability in Saccharomyces cerevisiae. Nature, 2001, 411, 1073-1076.	27.8	336
3	SGS1, the Saccharomyces cerevisiae homologue of BLM and WRN, suppresses genome instability and homeologous recombination. Nature Genetics, 2001, 27, 113-116.	21.4	309
4	Suppression of Spontaneous Chromosomal Rearrangements by S Phase Checkpoint Functions in Saccharomyces cerevisiae. Cell, 2001, 104, 397-408.	28.9	301
5	Polyubiquitination of proliferating cell nuclear antigen by HLTF and SHPRH prevents genomic instability from stalled replication forks. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 12411-12416.	7.1	237
6	A Histone-Fold Complex and FANCM FormÂa Conserved DNA-Remodeling Complex to Maintain Genome Stability. Molecular Cell, 2010, 37, 865-878.	9.7	204
7	Evidence Suggesting that Pif1 Helicase Functions in DNA Replication with the Dna2 Helicase/Nuclease and DNA Polymerase Î´. Molecular and Cellular Biology, 2006, 26, 2490-2500.	2.3	184
8	Smc5â€“Smc6 mediate DNA double-strand-break repair by promoting sister-chromatid recombination. Nature Cell Biology, 2006, 8, 1032-1034.	10.3	170
9	Human SHPRH suppresses genomic instability through proliferating cell nuclear antigen polyubiquitination. Journal of Cell Biology, 2006, 175, 703-708.	5.2	170
10	The exon junction complex component Magoh controls brain size by regulating neural stem cell division. Nature Neuroscience, 2010, 13, 551-558.	14.8	156
11	The Complete Spectrum of Yeast Chromosome Instability Genes Identifies Candidate CIN Cancer Genes and Functional Roles for ASTRA Complex Components. PLoS Genetics, 2011, 7, e1002057.	3.5	156
12	Suppression of genome instability by redundant S-phase checkpoint pathways in Saccharomyces cerevisiae. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 4500-4507.	7.1	135
13	PCNA modifications for regulation of post-replication repair pathways. Molecules and Cells, 2008, 26, 5-11.	2.6	127
14	PCNA Ubiquitination Is Important, But Not Essential for Translesion DNA Synthesis in Mammalian Cells. PLoS Genetics, 2011, 7, e1002262.	3.5	113
15	Functional Analyses of Glycyl-tRNA Synthetase Mutations Suggest a Key Role for tRNA-Charging Enzymes in Peripheral Axons. Journal of Neuroscience, 2006, 26, 10397-10406.	3.6	112
16	Human ELG1 Regulates the Level of Ubiquitinated Proliferating Cell Nuclear Antigen (PCNA) through Its Interactions with PCNA and USP1. Journal of Biological Chemistry, 2010, 285, 10362-10369.	3.4	110
17	ATAD5 regulates the lifespan of DNA replication factories by modulating PCNA level on the chromatin. Journal of Cell Biology, 2013, 200, 31-44.	5.2	105
18	High-throughput genotoxicity assay identifies antioxidants as inducers of DNA damage response and cell death. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 5423-5428.	7.1	104

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19	Myelodysplasia in autosomal dominant and sporadic monocytopenia immunodeficiency syndrome: diagnostic features and clinical implications. Haematologica, 2011, 96, 1221-1225.	3.5	97
20	Checkpoint-Dependent Activation of Mutagenic Repair in Saccharomyces cerevisiae pol3-01 Mutants. Molecular Cell, 2000, 6, 593-603.	9.7	94
21	Regulation of Telomere Length and Suppression of Genomic Instability in Human Somatic Cells by Ku86. Molecular and Cellular Biology, 2004, 24, 5050-5059.	2.3	91
22	Induction of genome instability by DNA damage in Saccharomyces cerevisiae. DNA Repair, 2003, 2, 243-258.	2.8	74
23	Predisposition to Cancer Caused by Genetic and Functional Defects of Mammalian Atad5. PLoS Genetics, 2011, 7, e1002245.	3.5	73
24	Regulation of PCNA cycling on replicating DNA by RFC and RFC-like complexes. Nature Communications, 2019, 10, 2420.	12.8	72
25	Identification of Two Domains of the p70 Ku Protein Mediating Dimerization with p80 and DNA Binding. Journal of Biological Chemistry, 1998, 273, 842-848.	3.4	69
26	Regulation of Gross Chromosomal Rearrangements by Ubiquitin and SUMO Ligases in Saccharomyces cerevisiae. Molecular and Cellular Biology, 2006, 26, 1424-1433.	2.3	65
27	DNA-PK-Dependent RPA2 Hyperphosphorylation Facilitates DNA Repair and Suppresses Sister Chromatid Exchange. PLoS ONE, 2011, 6, e21424.	2.5	62
28	An Annulative Synthetic Strategy for Building Triphenylene Frameworks by Multiple Câ”H Bond Activations. Angewandte Chemie - International Edition, 2017, 56, 5007-5011.	13.8	61
29	O-GlcNAcylation regulates dopamine neuron function, survival and degeneration in Parkinson disease. Brain, 2020, 143, 3699-3716.	7.6	52
30	Direct diversification of unmasked quinazolin-4(3H)-ones through orthogonal reactivity modulation. Chemical Communications, 2017, 53, 10394-10397.	4.1	51
31	A novel role for the mono-ADP-ribosyltransferase PARP14/ARTD8 in promoting homologous recombination and protecting against replication stress. Nucleic Acids Research, 2015, 43, 3143-3153.	14.5	48
32	Increased Genome Instability and Telomere Length in the elg1 -Deficient Saccharomyces cerevisiae Mutant Are Regulated by S-Phase Checkpoints. Eukaryotic Cell, 2004, 3, 1557-1566.	3.4	44
33	Mph1p promotes gross chromosomal rearrangement through partial inhibition of homologous recombination. Journal of Cell Biology, 2008, 181, 1083-1093.	5.2	42
34	TRAIP/RNF206 is required for recruitment of RAP80 to sites of DNA damage. Nature Communications, 2016, 7, 10463.	12.8	42
35	TonEBP recognizes R-loops and initiates m6A RNA methylation for R-loop resolution. Nucleic Acids Research, 2021, 49, 269-284.	14.5	41
36	Tonicity-responsive enhancer-binding protein promotes hepatocellular carcinogenesis, recurrence and metastasis. Gut, 2019, 68, 347-358.	12.1	39

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37	Is PCNA unloading the central function of the Elg1/ATAD5 replication factor C-like complex?. Cell Cycle, 2013, 12, 2570-2579.	2.6	37
38	ATAD5 promotes replication restart by regulating RAD51 and PCNA in response to replication stress. Nature Communications, 2019, 10, 5718.	12.8	35
39	Suppression of gross chromosomal rearrangements by the multiple functions of the Mre11â€“Rad50â€“Xrs2 complex in Saccharomyces cerevisiae. DNA Repair, 2005, 4, 606-617.	2.8	34
40	Hyper-Acetylation of Histone H3K56 Limits Break-Induced Replication by Inhibiting Extensive Repair Synthesis. PLoS Genetics, 2015, 11, e1004990.	3.5	33
41	GCA links TRAF6-ULK1-dependent autophagy activation in resistant chronic myeloid leukemia. Autophagy, 2019, 15, 2076-2090.	9.1	33
42	Rad5-dependent DNA Repair Functions of the Saccharomyces cerevisiae FANCM Protein Homolog Mph1. Journal of Biological Chemistry, 2012, 287, 26563-26575.	3.4	31
43	Microhomology-mediated end joining induces hypermutagenesis at breakpoint junctions. PLoS Genetics, 2017, 13, e1006714.	3.5	31
44	ATAD5 restricts R-loop formation through PCNA unloading and RNA helicase maintenance at the replication fork. Nucleic Acids Research, 2020, 48, 7218-7238.	14.5	30
45	The structure of human EXD2 reveals a chimeric 3â€² to 5â€² exonuclease domain that discriminates substrates via metal coordination. Nucleic Acids Research, 2019, 47, 7078-7093.	14.5	29
46	Smc5â€“Smc6 complex suppresses gross chromosomal rearrangements mediated by break-induced replications. DNA Repair, 2008, 7, 1426-1436.	2.8	27
47	Copperâ€Catalyzed Direct Synthesis of 1,2,4â€Oxadiazoles from Amides and Organic Nitriles by Oxidative Nâ€“O Bond Formation. European Journal of Organic Chemistry, 2016, 2016, 438-442.	2.4	27
48	The Rad1-Rad10 Complex Promotes the Production of Gross Chromosomal Rearrangements From Spontaneous DNA Damage in Saccharomyces cerevisiae. Genetics, 2005, 169, 1927-1937.	2.9	26
49	Chemoselective Trifluoroethylation Reactions of Quinazolinones and Identification of Photostability. Journal of Organic Chemistry, 2019, 84, 6737-6751.	3.2	26
50	SHPRH regulates rRNA transcription by recognizing the histone code in an mTOR-dependent manner. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E3424-E3433.	7.1	25
51	PCNA Unloading Is Negatively Regulated by BET Proteins. Cell Reports, 2019, 29, 4632-4645.e5.	6.4	25
52	CTCF cooperates with CtIP to drive homologous recombination repair of double-strand breaks. Nucleic Acids Research, 2019, 47, 9160-9179.	14.5	23
53	Genetic analysis of ionizing radiation-induced mutagenesis in Saccharomyces cerevisiae reveals TransLesion Synthesis (TLS) independent of PCNA K164 SUMOylation and ubiquitination. DNA Repair, 2006, 5, 1475-1488.	2.8	21
54	Unligated Okazaki Fragments Induce PCNA Ubiquitination and a Requirement for Rad59-Dependent Replication Fork Progression. PLoS ONE, 2013, 8, e66379.	2.5	21

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55	A Novel Chemotherapeutic Agent to Treat Tumors with DNA Mismatch Repair Deficiencies. Cancer Research, 2016, 76, 4183-4191.	0.9	21
56	Eukaryotic DNA replication: Orchestrated action of multi-subunit protein complexes. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2018, 809, 58-69.	1.0	21
57	Differential expression of the rhp51+ gene, a recA and RAD51 homolog from the fission yeast Schizosaccharomyces pombe. Gene, 1996, 169, 125-130.	2.2	19
58	Spt2p Defines a New Transcription-Dependent Gross Chromosomal Rearrangement Pathway. PLoS Genetics, 2008, 4, e1000290.	3.5	19
59	Crosstalk between different DNA repair pathways for DNA double strand break repairs. Mutation Research - Genetic Toxicology and Environmental Mutagenesis, 2022, 873, 503438.	1.7	18
60	Histone Deacetylase Inhibitors Selectively Target Homology Dependent DNA Repair Defective Cells and Elevate Non-Homologous Endjoining Activity. PLoS ONE, 2014, 9, e87203.	2.5	17
61	Thrap3 promotes R-loop resolution via interaction with methylated DDX5. Experimental and Molecular Medicine, 2021, 53, 1602-1611.	7.7	17
62	Hypomorphic Mutations in TONSL Cause SPONASTRIME Dysplasia. American Journal of Human Genetics, 2019, 104, 439-453.	6.2	16
63	Ewing sarcoma protein promotes dissociation of poly(<scp>ADP</scp> â€ribose) polymerase 1 from chromatin. EMBO Reports, 2020, 21, e48676.	4.5	16
64	Precision targeting tumor cells using cancer-specific InDel mutations with CRISPR-Cas9. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	15
65	An Annulative Synthetic Strategy for Building Triphenylene Frameworks by Multiple Câ^'H Bond Activations. Angewandte Chemie, 2017, 129, 5089-5093.	2.0	14
66	Suppression of gross chromosomal rearrangements by a new alternative replication factor C complex. Biochemical and Biophysical Research Communications, 2007, 362, 546-549.	2.1	13
67	TonEBP Regulates PCNA Polyubiquitination in Response to DNA Damage through Interaction with SHPRH and USP1. IScience, 2019, 19, 177-190.	4.1	13
68	Large-scale generation and phenotypic characterization of zebrafish CRISPR mutants of DNA repair genes. DNA Repair, 2021, 107, 103173.	2.8	13
69	Timely termination of repair DNA synthesis by ATAD5 is important in oxidative DNA damage-induced single-strand break repair. Nucleic Acids Research, 2021, 49, 11746-11764.	14.5	13
70	Suppression of gross chromosomal rearrangements by yKu70-yKu80 heterodimer through DNA damage checkpoints. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 1816-1821.	7.1	12
71	Ring finger protein 126 (RNF126) suppresses ionizing radiationâ€"induced p53-binding protein 1 (53BP1) focus formation. Journal of Biological Chemistry, 2018, 293, 588-598.	3.4	12
72	Background-suppressed live visualization of genomic loci with an improved CRISPR system based on a split fluorophore. Genome Research, 2020, 30, 1306-1316.	5.5	12

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73	Faithful after break-up: suppression of chromosomal translocations. Cellular and Molecular Life Sciences, 2009, 66, 3149-3160.	5.4	11
74	Dynamic Regulation of Single-Stranded Telomeres in Saccharomyces cerevisiae. Genetics, 2008, 178, 693-701.	2.9	10
75	ATAD5 Deficiency Decreases B Cell Division and Igh Recombination. Journal of Immunology, 2015, 194, 35-42.	0.8	10
76	Flightless-1 inhibits ER stress-induced apoptosis in colorectal cancer cells by regulating Ca2+ homeostasis. Experimental and Molecular Medicine, 2020, 52, 940-950.	7.7	10
77	<scp>FAM213A</scp> is linked to prognostic significance in acute myeloid leukemia through regulation of oxidative stress and myelopoiesis. Hematological Oncology, 2020, 38, 381-389.	1.7	10
78	ATAD5 suppresses centrosome over-duplication by regulating UAF1 and ID1. Cell Cycle, 2020, 19, 1952-1968.	2.6	10
79	Cell-based high-throughput screens for the discovery of chemotherapeutic agents. Oncotarget, 2012, 3, 581-585.	1.8	10
80	Haematopoietic stem cell-dependent Notch transcription is mediated by p53 through the Histone chaperone Supt16h. Nature Cell Biology, 2020, 22, 1411-1422.	10.3	9
81	Loss of adipose TET proteins enhances Î²-adrenergic responses and protects against obesity by epigenetic regulation of Î²3-AR expression. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	7
82	SHPRH as a new player in ribosomal RNA transcription and its potential role in homeostasis of ribosomal DNA repeats. Transcription, 2018, 9, 190-195.	3.1	6
83	AML poor prognosis factor, TPD52, is associated with the maintenance of haematopoietic stem cells through regulation of cell proliferation. Journal of Cellular Biochemistry, 2021, 122, 403-412.	2.6	6
84	NSMF promotes the replication stress-induced DNA damage response for genome maintenance. Nucleic Acids Research, 2021, 49, 5605-5622.	14.5	6
85	Neuropeptide Y: a potential theranostic biomarker for diabetic peripheral neuropathy in patients with type-2 diabetes. Therapeutic Advances in Chronic Disease, 2021, 12, 204062232110419.	2.5	4
86	PWWP2B promotes DNA end resection and homologous recombination. EMBO Reports, 2022, , e53492.	4.5	4
87	Tissue-specific DNA damage response in Mouse Whole-body irradiation. Molecular and Cellular Toxicology, 2022, 18, 131-139.	1.7	3
88	Reciprocal interactions among Cobll1, PACSIN2, and SH3BP1 regulate drug resistance in chronic myeloid leukemia. Cancer Medicine, 2022, , .	2.8	2
89	Distinct Motifs in ATAD5 C-Terminal Domain Modulate PCNA Unloading Process. Cells, 2022, 11, 1832.	4.1	2
90	Reply to Kojo: Mechanisms of antioxidant-induced DNA damage. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E2029-E2029.	7.1	1

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91	Targeting the cancer cell state. Cell Cycle, 2015, 14, 2385-2386.	2.6	0
92	Eukaryotic 4Rs: DNA replication, repair, recombination, and damage response. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2018, 809, 56-57.	1.0	0
93	A novel mechanism of regulation of SHPRH by circular RNA, circ-SHPRH in glioblastoma. Non-coding RNA Investigation, 0, 2, 31-31.	0.6	0
94	Cobll1: A new player in CML. Oncotarget, 2017, 8, 90626-90627.	1.8	0