Kyungjae Myung

List of Publications by Year in descending order

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94 papers 5,504 citations

35 h-index 71 g-index

95 all docs 95 docs citations 95 times ranked 6400 citing authors

#	Article	IF	CITATIONS
1	Tissue-specific DNA damage response in Mouse Whole-body irradiation. Molecular and Cellular Toxicology, 2022, 18, 131-139.	1.7	3
2	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
3	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
4	Reciprocal interactions among Cobll 1, PACSIN2, and SH3BP1 regulate drug resistance in chronic myeloid leukemia. Cancer Medicine, 2022, , .	2.8	2
5	PWWP2B promotes DNA end resection and homologous recombination. EMBO Reports, 2022, , e53492.	4.5	4
6	Distinct Motifs in ATAD5 C-Terminal Domain Modulate PCNA Unloading Process. Cells, 2022, 11, 1832.	4.1	2
7	Loss of adipose TET proteins enhances \hat{l}^2 -adrenergic responses and protects against obesity by epigenetic regulation of \hat{l}^2 3-AR expression. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	7
8	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
9	TonEBP recognizes R-loops and initiates m6A RNA methylation for R-loop resolution. Nucleic Acids Research, 2021, 49, 269-284.	14.5	41
10	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
11	NSMF promotes the replication stress-induced DNA damage response for genome maintenance. Nucleic Acids Research, 2021, 49, 5605-5622.	14.5	6
12	Large-scale generation and phenotypic characterization of zebrafish CRISPR mutants of DNA repair genes. DNA Repair, 2021, 107, 103173.	2.8	13
13	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
14	Thrap3 promotes R-loop resolution via interaction with methylated DDX5. Experimental and Molecular Medicine, 2021, 53, 1602-1611.	7.7	17
15	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
16	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
17	<i>O-</i> GlcNAcylation regulates dopamine neuron function, survival and degeneration in Parkinson disease. Brain, 2020, 143, 3699-3716.	7.6	52
18	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

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19	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
20	<scp><i>FAM213A</i>is linked to prognostic significance in acute myeloid leukemia through regulation of oxidative stress and myelopoiesis. Hematological Oncology, 2020, 38, 381-389.</scp>	1.7	10
21	ATAD5 suppresses centrosome over-duplication by regulating UAF1 and ID1. Cell Cycle, 2020, 19, 1952-1968.	2.6	10
22	Ewing sarcoma protein promotes dissociation of poly(<scp>ADP</scp> â€ribose) polymerase 1 from chromatin. EMBO Reports, 2020, 21, e48676.	4.5	16
23	TonEBP Regulates PCNA Polyubiquitination in Response to DNA Damage through Interaction with SHPRH and USP1. IScience, 2019, 19, 177-190.	4.1	13
24	CTCF cooperates with CtIP to drive homologous recombination repair of double-strand breaks. Nucleic Acids Research, 2019, 47, 9160-9179.	14.5	23
25	Regulation of PCNA cycling on replicating DNA by RFC and RFC-like complexes. Nature Communications, 2019, 10, 2420.	12.8	72
26	The structure of human EXD2 reveals a chimeric $3\hat{a}\in^2$ to $5\hat{a}\in^2$ exonuclease domain that discriminates substrates via metal coordination. Nucleic Acids Research, 2019, 47, 7078-7093.	14.5	29
27	Chemoselective Trifluoroethylation Reactions of Quinazolinones and Identification of Photostability. Journal of Organic Chemistry, 2019, 84, 6737-6751.	3.2	26
28	GCA links TRAF6-ULK1-dependent autophagy activation in resistant chronic myeloid leukemia. Autophagy, 2019, 15, 2076-2090.	9.1	33
29	Hypomorphic Mutations in TONSL Cause SPONASTRIME Dysplasia. American Journal of Human Genetics, 2019, 104, 439-453.	6.2	16
30	ATAD5 promotes replication restart by regulating RAD51 and PCNA in response to replication stress. Nature Communications, 2019, 10, 5718.	12.8	35
31	PCNA Unloading Is Negatively Regulated by BET Proteins. Cell Reports, 2019, 29, 4632-4645.e5.	6.4	25
32	Tonicity-responsive enhancer-binding protein promotes hepatocellular carcinogenesis, recurrence and metastasis. Gut, 2019, 68, 347-358.	12.1	39
33	Eukaryotic 4Rs: DNA replication, repair, recombination, and damage response. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2018, 809, 56-57.	1.0	0
34	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
35	Ring finger protein 126 (RNF126) suppresses ionizing radiation–induced p53-binding protein 1 (53BP1) focus formation. Journal of Biological Chemistry, 2018, 293, 588-598.	3.4	12
36	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

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37	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
38	An Annulative Synthetic Strategy for Building Triphenylene Frameworks by Multiple Câ^'H Bond Activations. Angewandte Chemie, 2017, 129, 5089-5093.	2.0	14
39	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
40	Direct diversification of unmasked quinazolin-4(3H)-ones through orthogonal reactivity modulation. Chemical Communications, 2017, 53, 10394-10397.	4.1	51
41	Microhomology-mediated end joining induces hypermutagenesis at breakpoint junctions. PLoS Genetics, 2017, 13, e1006714.	3 . 5	31
42	Cobll1: A new player in CML. Oncotarget, 2017, 8, 90626-90627.	1.8	0
43	Copperâ€Catalyzed Direct Synthesis of 1,2,4â€Oxadiazoles from Amides and Organic Nitriles by Oxidative N–O Bond Formation. European Journal of Organic Chemistry, 2016, 2016, 438-442.	2.4	27
44	A Novel Chemotherapeutic Agent to Treat Tumors with DNA Mismatch Repair Deficiencies. Cancer Research, 2016, 76, 4183-4191.	0.9	21
45	TRAIP/RNF206 is required for recruitment of RAP80 to sites of DNA damage. Nature Communications, 2016, 7, 10463.	12.8	42
46	ATAD5 Deficiency Decreases B Cell Division and <i>lgh</i> Recombination. Journal of Immunology, 2015, 194, 35-42.	0.8	10
47	Hyper-Acetylation of Histone H3K56 Limits Break-Induced Replication by Inhibiting Extensive Repair Synthesis. PLoS Genetics, 2015, 11, e1004990.	3.5	33
48	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
49	Targeting the cancer cell state. Cell Cycle, 2015, 14, 2385-2386.	2.6	0
50	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
51	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
52	Is PCNA unloading the central function of the Elg1/ATAD5 replication factor C-like complex?. Cell Cycle, 2013, 12, 2570-2579.	2.6	37
53	Unligated Okazaki Fragments Induce PCNA Ubiquitination and a Requirement for Rad59-Dependent Replication Fork Progression. PLoS ONE, 2013, 8, e66379.	2.5	21
54	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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55	Rad5-dependent DNA Repair Functions of the Saccharomyces cerevisiae FANCM Protein Homolog Mph1. Journal of Biological Chemistry, 2012, 287, 26563-26575.	3.4	31
56	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
57	Cell-based high-throughput screens for the discovery of chemotherapeutic agents. Oncotarget, 2012, 3, 581-585.	1.8	10
58	DNA-PK-Dependent RPA2 Hyperphosphorylation Facilitates DNA Repair and Suppresses Sister Chromatid Exchange. PLoS ONE, 2011, 6, e21424.	2.5	62
59	Myelodysplasia in autosomal dominant and sporadic monocytopenia immunodeficiency syndrome: diagnostic features and clinical implications. Haematologica, 2011, 96, 1221-1225.	3.5	97
60	PCNA Ubiquitination Is Important, But Not Essential for Translesion DNA Synthesis in Mammalian Cells. PLoS Genetics, 2011, 7, e1002262.	3.5	113
61	Predisposition to Cancer Caused by Genetic and Functional Defects of Mammalian Atad5. PLoS Genetics, 2011, 7, e1002245.	3.5	73
62	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
63	The exon junction complex component Magoh controls brain size by regulating neural stem cell division. Nature Neuroscience, 2010, 13, 551-558.	14.8	156
64	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
65	A Histone-Fold Complex and FANCM FormÂa Conserved DNA-Remodeling Complex to Maintain Genome Stability. Molecular Cell, 2010, 37, 865-878.	9.7	204
66	Faithful after break-up: suppression of chromosomal translocations. Cellular and Molecular Life Sciences, 2009, 66, 3149-3160.	5.4	11
67	Smc5–Smc6 complex suppresses gross chromosomal rearrangements mediated by break-induced replications. DNA Repair, 2008, 7, 1426-1436.	2.8	27
68	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
69	Dynamic Regulation of Single-Stranded Telomeres in <i>Saccharomyces cerevisiae</i> . Genetics, 2008, 178, 693-701.	2.9	10
70	Spt2p Defines a New Transcription-Dependent Gross Chromosomal Rearrangement Pathway. PLoS Genetics, 2008, 4, e1000290.	3.5	19
71	Mph1p promotes gross chromosomal rearrangement through partial inhibition of homologous recombination. Journal of Cell Biology, 2008, 181, 1083-1093.	5.2	42
72	PCNA modifications for regulation of post-replication repair pathways. Molecules and Cells, 2008, 26, 5-11.	2.6	127

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73	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
74	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
75	Smc5–Smc6 mediate DNA double-strand-break repair by promoting sister-chromatid recombination. Nature Cell Biology, 2006, 8, 1032-1034.	10.3	170
76	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
77	Regulation of Gross Chromosomal Rearrangements by Ubiquitin and SUMO Ligases in Saccharomyces cerevisiae. Molecular and Cellular Biology, 2006, 26, 1424-1433.	2.3	65
78	Evidence Suggesting that Pif1 Helicase Functions in DNA Replication with the Dna2 Helicase/Nuclease and DNA Polymerase δ. Molecular and Cellular Biology, 2006, 26, 2490-2500.	2.3	184
79	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
80	Human SHPRH suppresses genomic instability through proliferating cell nuclear antigen polyubiquitination. Journal of Cell Biology, 2006, 175, 703-708.	5.2	170
81	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
82	Suppression of gross chromosomal rearrangements by the multiple functions of the Mre11–Rad50–Xrs2 complex in Saccharomyces cerevisiae. DNA Repair, 2005, 4, 606-617.	2.8	34
83	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
84	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
85	Induction of genome instability by DNA damage in Saccharomyces cerevisiae. DNA Repair, 2003, 2, 243-258.	2.8	74
86	Maintenance of Genome Stability in Saccharomyces cerevisiae. Science, 2002, 297, 552-557.	12.6	442
87	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
88	Suppression of Spontaneous Chromosomal Rearrangements by S Phase Checkpoint Functions in Saccharomyces cerevisiae. Cell, 2001, 104, 397-408.	28.9	301
89	SGS1, the Saccharomyces cerevisiae homologue of BLM and WRN, suppresses genome instability and homeologous recombination. Nature Genetics, 2001, 27, 113-116.	21.4	309
90	Multiple pathways cooperate in the suppression of genome instability in Saccharomyces cerevisiae. Nature, 2001, 411, 1073-1076.	27.8	336

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91	Checkpoint-Dependent Activation of Mutagenic Repair in Saccharomyces cerevisiae pol3-01 Mutants. Molecular Cell, 2000, 6, 593-603.	9.7	94
92	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
93	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
94	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