

# Kyungjae Myung

## List of Publications by Year in descending order

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94  
papers

5,504  
citations

109264

35  
h-index

85498

71  
g-index

95  
all docs

95  
docs citations

95  
times ranked

6400  
citing authors

#	ARTICLE	IF	CITATIONS
1	Maintenance of Genome Stability in <i>Saccharomyces cerevisiae</i> . <i>Science</i> , 2002, 297, 552-557.	6.0	442
2	Multiple pathways cooperate in the suppression of genome instability in <i>Saccharomyces cerevisiae</i> . <i>Nature</i> , 2001, 411, 1073-1076.	13.7	336
3	SGS1, the <i>Saccharomyces cerevisiae</i> homologue of BLM and WRN, suppresses genome instability and homeologous recombination. <i>Nature Genetics</i> , 2001, 27, 113-116.	9.4	309
4	Suppression of Spontaneous Chromosomal Rearrangements by S Phase Checkpoint Functions in <i>Saccharomyces cerevisiae</i> . <i>Cell</i> , 2001, 104, 397-408.	13.5	301
5	Polyubiquitination of proliferating cell nuclear antigen by HLF and SHPRH prevents genomic instability from stalled replication forks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 12411-12416.	3.3	237
6	A Histone-Fold Complex and FANCM Form a Conserved DNA-Remodeling Complex to Maintain Genome Stability. <i>Molecular Cell</i> , 2010, 37, 865-878.	4.5	204
7	Evidence Suggesting that Pif1 Helicase Functions in DNA Replication with the Dna2 Helicase/Nuclease and DNA Polymerase $\delta$ . <i>Molecular and Cellular Biology</i> , 2006, 26, 2490-2500.	1.1	184
8	Smc5 and Smc6 mediate DNA double-strand-break repair by promoting sister-chromatid recombination. <i>Nature Cell Biology</i> , 2006, 8, 1032-1034.	4.6	170
9	Human SHPRH suppresses genomic instability through proliferating cell nuclear antigen polyubiquitination. <i>Journal of Cell Biology</i> , 2006, 175, 703-708.	2.3	170
10	The exon junction complex component Magoh controls brain size by regulating neural stem cell division. <i>Nature Neuroscience</i> , 2010, 13, 551-558.	7.1	156
11	The Complete Spectrum of Yeast Chromosome Instability Genes Identifies Candidate CIN Cancer Genes and Functional Roles for ASTRA Complex Components. <i>PLoS Genetics</i> , 2011, 7, e1002057.	1.5	156
12	Suppression of genome instability by redundant S-phase checkpoint pathways in <i>Saccharomyces cerevisiae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 4500-4507.	3.3	135
13	PCNA modifications for regulation of post-replication repair pathways. <i>Molecules and Cells</i> , 2008, 26, 5-11.	1.0	127
14	PCNA Ubiquitination Is Important, But Not Essential for Translesion DNA Synthesis in Mammalian Cells. <i>PLoS Genetics</i> , 2011, 7, e1002262.	1.5	113
15	Functional Analyses of Glycyl-tRNA Synthetase Mutations Suggest a Key Role for tRNA-Charging Enzymes in Peripheral Axons. <i>Journal of Neuroscience</i> , 2006, 26, 10397-10406.	1.7	112
16	Human ELG1 Regulates the Level of Ubiquitinated Proliferating Cell Nuclear Antigen (PCNA) through Its Interactions with PCNA and USP1. <i>Journal of Biological Chemistry</i> , 2010, 285, 10362-10369.	1.6	110
17	ATAD5 regulates the lifespan of DNA replication factories by modulating PCNA level on the chromatin. <i>Journal of Cell Biology</i> , 2013, 200, 31-44.	2.3	105
18	High-throughput genotoxicity assay identifies antioxidants as inducers of DNA damage response and cell death. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 5423-5428.	3.3	104

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19	Myelodysplasia in autosomal dominant and sporadic monocytopenia immunodeficiency syndrome: diagnostic features and clinical implications. <i>Haematologica</i> , 2011, 96, 1221-1225.	1.7	97
20	Checkpoint-Dependent Activation of Mutagenic Repair in <i>Saccharomyces cerevisiae</i> pol3-01 Mutants. <i>Molecular Cell</i> , 2000, 6, 593-603.	4.5	94
21	Regulation of Telomere Length and Suppression of Genomic Instability in Human Somatic Cells by Ku86. <i>Molecular and Cellular Biology</i> , 2004, 24, 5050-5059.	1.1	91
22	Induction of genome instability by DNA damage in <i>Saccharomyces cerevisiae</i> . <i>DNA Repair</i> , 2003, 2, 243-258.	1.3	74
23	Predisposition to Cancer Caused by Genetic and Functional Defects of Mammalian Atad5. <i>PLoS Genetics</i> , 2011, 7, e1002245.	1.5	73
24	Regulation of PCNA cycling on replicating DNA by RFC and RFC-like complexes. <i>Nature Communications</i> , 2019, 10, 2420.	5.8	72
25	Identification of Two Domains of the p70 Ku Protein Mediating Dimerization with p80 and DNA Binding. <i>Journal of Biological Chemistry</i> , 1998, 273, 842-848.	1.6	69
26	Regulation of Gross Chromosomal Rearrangements by Ubiquitin and SUMO Ligases in <i>Saccharomyces cerevisiae</i> . <i>Molecular and Cellular Biology</i> , 2006, 26, 1424-1433.	1.1	65
27	DNA-PK-Dependent RPA2 Hyperphosphorylation Facilitates DNA Repair and Suppresses Sister Chromatid Exchange. <i>PLoS ONE</i> , 2011, 6, e21424.	1.1	62
28	An Annulative Synthetic Strategy for Building Triphenylene Frameworks by Multiple C-H Bond Activations. <i>Angewandte Chemie - International Edition</i> , 2017, 56, 5007-5011.	7.2	61
29	GlcNAcylation regulates dopamine neuron function, survival and degeneration in Parkinson disease. <i>Brain</i> , 2020, 143, 3699-3716.	3.7	52
30	Direct diversification of unmasked quinazolin-4(3H)-ones through orthogonal reactivity modulation. <i>Chemical Communications</i> , 2017, 53, 10394-10397.	2.2	51
31	A novel role for the mono-ADP-ribosyltransferase PARP14/ARTD8 in promoting homologous recombination and protecting against replication stress. <i>Nucleic Acids Research</i> , 2015, 43, 3143-3153.	6.5	48
32	Increased Genome Instability and Telomere Length in the <i>elg1</i> -Deficient <i>Saccharomyces cerevisiae</i> Mutant Are Regulated by S-Phase Checkpoints. <i>Eukaryotic Cell</i> , 2004, 3, 1557-1566.	3.4	44
33	Mph1p promotes gross chromosomal rearrangement through partial inhibition of homologous recombination. <i>Journal of Cell Biology</i> , 2008, 181, 1083-1093.	2.3	42
34	TRAIPI/RNF206 is required for recruitment of RAP80 to sites of DNA damage. <i>Nature Communications</i> , 2016, 7, 10463.	5.8	42
35	TonEBP recognizes R-loops and initiates m6A RNA methylation for R-loop resolution. <i>Nucleic Acids Research</i> , 2021, 49, 269-284.	6.5	41
36	Tonicity-responsive enhancer-binding protein promotes hepatocellular carcinogenesis, recurrence and metastasis. <i>Gut</i> , 2019, 68, 347-358.	6.1	39

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37	Is PCNA unloading the central function of the Elg1/ATAD5 replication factor C-like complex?. <i>Cell Cycle</i> , 2013, 12, 2570-2579.	1.3	37
38	ATAD5 promotes replication restart by regulating RAD51 and PCNA in response to replication stress. <i>Nature Communications</i> , 2019, 10, 5718.	5.8	35
39	Suppression of gross chromosomal rearrangements by the multiple functions of the Mre11-Rad50-Xrs2 complex in <i>Saccharomyces cerevisiae</i> . <i>DNA Repair</i> , 2005, 4, 606-617.	1.3	34
40	Hyper-Acetylation of Histone H3K56 Limits Break-Induced Replication by Inhibiting Extensive Repair Synthesis. <i>PLoS Genetics</i> , 2015, 11, e1004990.	1.5	33
41	GCA links TRAF6-ULK1-dependent autophagy activation in resistant chronic myeloid leukemia. <i>Autophagy</i> , 2019, 15, 2076-2090.	4.3	33
42	Rad5-dependent DNA Repair Functions of the <i>Saccharomyces cerevisiae</i> FANCM Protein Homolog Mph1. <i>Journal of Biological Chemistry</i> , 2012, 287, 26563-26575.	1.6	31
43	Microhomology-mediated end joining induces hypermutagenesis at breakpoint junctions. <i>PLoS Genetics</i> , 2017, 13, e1006714.	1.5	31
44	ATAD5 restricts R-loop formation through PCNA unloading and RNA helicase maintenance at the replication fork. <i>Nucleic Acids Research</i> , 2020, 48, 7218-7238.	6.5	30
45	The structure of human EXD2 reveals a chimeric 3' to 5' exonuclease domain that discriminates substrates via metal coordination. <i>Nucleic Acids Research</i> , 2019, 47, 7078-7093.	6.5	29
46	Smc5-Smc6 complex suppresses gross chromosomal rearrangements mediated by break-induced replications. <i>DNA Repair</i> , 2008, 7, 1426-1436.	1.3	27
47	Copper-Catalyzed Direct Synthesis of 1,2,4-Oxadiazoles from Amides and Organic Nitriles by Oxidative N-O Bond Formation. <i>European Journal of Organic Chemistry</i> , 2016, 2016, 438-442.	1.2	27
48	The Rad1-Rad10 Complex Promotes the Production of Gross Chromosomal Rearrangements From Spontaneous DNA Damage in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2005, 169, 1927-1937.	1.2	26
49	Chemoselective Trifluoroethylation Reactions of Quinazolinones and Identification of Photostability. <i>Journal of Organic Chemistry</i> , 2019, 84, 6737-6751.	1.7	26
50	SHPRH regulates rRNA transcription by recognizing the histone code in an mTOR-dependent manner. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E3424-E3433.	3.3	25
51	PCNA Unloading Is Negatively Regulated by BET Proteins. <i>Cell Reports</i> , 2019, 29, 4632-4645.e5.	2.9	25
52	CTCF cooperates with CtIP to drive homologous recombination repair of double-strand breaks. <i>Nucleic Acids Research</i> , 2019, 47, 9160-9179.	6.5	23
53	Genetic analysis of ionizing radiation-induced mutagenesis in <i>Saccharomyces cerevisiae</i> reveals TransLesion Synthesis (TLS) independent of PCNA K164 SUMOylation and ubiquitination. <i>DNA Repair</i> , 2006, 5, 1475-1488.	1.3	21
54	Unligated Okazaki Fragments Induce PCNA Ubiquitination and a Requirement for Rad59-Dependent Replication Fork Progression. <i>PLoS ONE</i> , 2013, 8, e66379.	1.1	21

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55	A Novel Chemotherapeutic Agent to Treat Tumors with DNA Mismatch Repair Deficiencies. <i>Cancer Research</i> , 2016, 76, 4183-4191.	0.4	21
56	Eukaryotic DNA replication: Orchestrated action of multi-subunit protein complexes. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2018, 809, 58-69.	0.4	21
57	Differential expression of the rhp51+ gene, a recA and RAD51 homolog from the fission yeast <i>Schizosaccharomyces pombe</i> . <i>Gene</i> , 1996, 169, 125-130.	1.0	19
58	Spt2p Defines a New Transcription-Dependent Gross Chromosomal Rearrangement Pathway. <i>PLoS Genetics</i> , 2008, 4, e1000290.	1.5	19
59	Crosstalk between different DNA repair pathways for DNA double strand break repairs. <i>Mutation Research - Genetic Toxicology and Environmental Mutagenesis</i> , 2022, 873, 503438.	0.9	18
60	Histone Deacetylase Inhibitors Selectively Target Homology Dependent DNA Repair Defective Cells and Elevate Non-Homologous Endjoining Activity. <i>PLoS ONE</i> , 2014, 9, e87203.	1.1	17
61	Thrap3 promotes R-loop resolution via interaction with methylated DDX5. <i>Experimental and Molecular Medicine</i> , 2021, 53, 1602-1611.	3.2	17
62	Hypomorphic Mutations in TONSL Cause SPONASTRIME Dysplasia. <i>American Journal of Human Genetics</i> , 2019, 104, 439-453.	2.6	16
63	Ewing sarcoma protein promotes dissociation of poly(ADP-ribose) polymerase 1 from chromatin. <i>EMBO Reports</i> , 2020, 21, e48676.	2.0	16
64	Precision targeting tumor cells using cancer-specific InDel mutations with CRISPR-Cas9. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	15
65	An Annulative Synthetic Strategy for Building Triphenylene Frameworks by Multiple C-H Bond Activations. <i>Angewandte Chemie</i> , 2017, 129, 5089-5093.	1.6	14
66	Suppression of gross chromosomal rearrangements by a new alternative replication factor C complex. <i>Biochemical and Biophysical Research Communications</i> , 2007, 362, 546-549.	1.0	13
67	TonEBP Regulates PCNA Polyubiquitination in Response to DNA Damage through Interaction with SHPRH and USP1. <i>iScience</i> , 2019, 19, 177-190.	1.9	13
68	Large-scale generation and phenotypic characterization of zebrafish CRISPR mutants of DNA repair genes. <i>DNA Repair</i> , 2021, 107, 103173.	1.3	13
69	Timely termination of repair DNA synthesis by ATAD5 is important in oxidative DNA damage-induced single-strand break repair. <i>Nucleic Acids Research</i> , 2021, 49, 11746-11764.	6.5	13
70	Suppression of gross chromosomal rearrangements by yKu70-yKu80 heterodimer through DNA damage checkpoints. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 1816-1821.	3.3	12
71	Ring finger protein 126 (RNF126) suppresses ionizing radiation-induced p53-binding protein 1 (53BP1) focus formation. <i>Journal of Biological Chemistry</i> , 2018, 293, 588-598.	1.6	12
72	Background-suppressed live visualization of genomic loci with an improved CRISPR system based on a split fluorophore. <i>Genome Research</i> , 2020, 30, 1306-1316.	2.4	12

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73	Faithful after break-up: suppression of chromosomal translocations. <i>Cellular and Molecular Life Sciences</i> , 2009, 66, 3149-3160.	2.4	11
74	Dynamic Regulation of Single-Stranded Telomeres in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2008, 178, 693-701.	1.2	10
75	ATAD5 Deficiency Decreases B Cell Division and <i>Igh</i> Recombination. <i>Journal of Immunology</i> , 2015, 194, 35-42.	0.4	10
76	Flightless-1 inhibits ER stress-induced apoptosis in colorectal cancer cells by regulating Ca <sup>2+</sup> homeostasis. <i>Experimental and Molecular Medicine</i> , 2020, 52, 940-950.	3.2	10
77	<i>FAM213A</i> is linked to prognostic significance in acute myeloid leukemia through regulation of oxidative stress and myelopoiesis. <i>Hematological Oncology</i> , 2020, 38, 381-389.	0.8	10
78	ATAD5 suppresses centrosome over-duplication by regulating UAF1 and ID1. <i>Cell Cycle</i> , 2020, 19, 1952-1968.	1.3	10
79	Cell-based high-throughput screens for the discovery of chemotherapeutic agents. <i>Oncotarget</i> , 2012, 3, 581-585.	0.8	10
80	Haematopoietic stem cell-dependent Notch transcription is mediated by p53 through the Histone chaperone Supt16h. <i>Nature Cell Biology</i> , 2020, 22, 1411-1422.	4.6	9
81	Loss of adipose TET proteins enhances $\beta$ -adrenergic responses and protects against obesity by epigenetic regulation of $\beta$ 3-AR expression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	7
82	SHPRH as a new player in ribosomal RNA transcription and its potential role in homeostasis of ribosomal DNA repeats. <i>Transcription</i> , 2018, 9, 190-195.	1.7	6
83	AML poor prognosis factor, TPD52, is associated with the maintenance of haematopoietic stem cells through regulation of cell proliferation. <i>Journal of Cellular Biochemistry</i> , 2021, 122, 403-412.	1.2	6
84	NSMF promotes the replication stress-induced DNA damage response for genome maintenance. <i>Nucleic Acids Research</i> , 2021, 49, 5605-5622.	6.5	6
85	Neuropeptide Y: a potential theranostic biomarker for diabetic peripheral neuropathy in patients with type-2 diabetes. <i>Therapeutic Advances in Chronic Disease</i> , 2021, 12, 204062232110419.	1.1	4
86	PWWP2B promotes DNA end resection and homologous recombination. <i>EMBO Reports</i> , 2022, , e53492.	2.0	4
87	Tissue-specific DNA damage response in Mouse Whole-body irradiation. <i>Molecular and Cellular Toxicology</i> , 2022, 18, 131-139.	0.8	3
88	Reciprocal interactions among Cobll1, PACSIN2, and SH3BP1 regulate drug resistance in chronic myeloid leukemia. <i>Cancer Medicine</i> , 2022, , .	1.3	2
89	Distinct Motifs in ATAD5 C-Terminal Domain Modulate PCNA Unloading Process. <i>Cells</i> , 2022, 11, 1832.	1.8	2
90	Reply to Kojo: Mechanisms of antioxidant-induced DNA damage. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E2029-E2029.	3.3	1

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91	Targeting the cancer cell state. <i>Cell Cycle</i> , 2015, 14, 2385-2386.	1.3	0
92	Eukaryotic 4Rs: DNA replication, repair, recombination, and damage response. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2018, 809, 56-57.	0.4	0
93	A novel mechanism of regulation of SHPRH by circular RNA, circ-SHPRH in glioblastoma. <i>Non-coding RNA Investigation</i> , 0, 2, 31-31.	0.6	0
94	Cobll1: A new player in CML. <i>Oncotarget</i> , 2017, 8, 90626-90627.	0.8	0