

# Li-Lin Du

## List of Publications by Year in descending order

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Version: 2024-02-01

63  
papers

6,765  
citations

293460

24  
h-index

162838

57  
g-index

77  
all docs

77  
docs citations

77  
times ranked

17518  
citing authors

#	ARTICLE	IF	CITATIONS
1	An improved auxin-inducible degron system for fission yeast. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	16
2	Fission Yeast Autophagy Machinery. <i>Cells</i> , 2022, 11, 1086.	1.8	10
3	Insights into the ecology of <i>Schizosaccharomyces</i> species in natural and artificial habitats. <i>Antonie Van Leeuwenhoek</i> , 2022, 115, 661-695.	0.7	10
4	Reactivation of transposable elements following hybridization in fission yeast. <i>Genome Research</i> , 2022, 32, 324-336.	2.4	13
5	Canavanine resistance mutation in is a missense mutation in the ubiquitin ligase adaptor gene .. <i>MicroPublication Biology</i> , 2022, 2022, .	0.1	3
6	Structural mechanism of protein recognition by the FW domain of autophagy receptor Nbr1. <i>Nature Communications</i> , 2022, 13, .	5.8	4
7	Atg11-mediated activation of Atg1 kinase in fission yeast. <i>Autophagy</i> , 2021, 17, 584-585.	4.3	3
8	Molecular and structural mechanisms of ZZ domain-mediated cargo selection by Nbr1. <i>EMBO Journal</i> , 2021, 40, e107497.	3.5	14
9	Perturbation of kinetochore function using GFP-binding protein in fission yeast. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	0
10	Visual detection of binary, ternary and quaternary protein interactions in fission yeast using a Pil1 co-tethering assay. <i>Journal of Cell Science</i> , 2021, 134, .	1.2	4
11	Cryo-EM structure of fission yeast tetrameric Î±-mannosidase Ams1. <i>FEBS Open Bio</i> , 2020, 10, 2437-2451.	1.0	5
12	Genetically encoded tags for direct synthesis of EM-visible gold nanoparticles in cells. <i>Nature Methods</i> , 2020, 17, 937-946.	9.0	30
13	CRL4Cdt2 ubiquitin ligase regulates Dna2 and Rad16 (XPF) nucleases by targeting Pxd1 for degradation. <i>PLoS Genetics</i> , 2020, 16, e1008933.	1.5	2
14	A UPR-Induced Soluble ER-Phagy Receptor Acts with VAPs to Confer ER Stress Resistance. <i>Molecular Cell</i> , 2020, 79, 963-977.e3.	4.5	60
15	Epr1, a UPR-upregulated soluble autophagy receptor for reticulophagy. <i>Autophagy</i> , 2020, 16, 2112-2113.	4.3	4
16	Resurrection from lethal knockouts: Bypass of gene essentiality. <i>Biochemical and Biophysical Research Communications</i> , 2020, 528, 405-412.	1.0	7
17	Atg38-Atg8 interaction in fission yeast establishes a positive feedback loop to promote autophagy. <i>Autophagy</i> , 2020, 16, 2036-2051.	4.3	19
18	Atg1 kinase in fission yeast is activated by Atg11-mediated dimerization and cis-autophosphorylation. <i>ELife</i> , 2020, 9, .	2.8	21

#	ARTICLE	IF	CITATIONS
19	Title is missing!. , 2020, 16, e1008933.		0
20	Title is missing!. , 2020, 16, e1008933.		0
21	Title is missing!. , 2020, 16, e1008933.		0
22	Title is missing!. , 2020, 16, e1008933.		0
23	Mck1 defines a key S-phase checkpoint effector in response to various degrees of replication threats. PLoS Genetics, 2019, 15, e1008136.	1.5	9
24	Intraspecific Diversity of Fission Yeast Mitochondrial Genomes. Genome Biology and Evolution, 2019, 11, 2312-2329.	1.1	24
25	Systematic analysis reveals the prevalence and principles of bypassable gene essentiality. Nature Communications, 2019, 10, 1002.	5.8	40
26	A Cloning-Free Method for CRISPR/Cas9-Mediated Genome Editing in Fission Yeast. G3: Genes, Genomes, Genetics, 2018, 8, 2067-2077.	0.8	29
27	Tdp1 processes chromate-induced single-strand DNA breaks that collapse replication forks. PLoS Genetics, 2018, 14, e1007595.	1.5	4
28	Lipidation-independent vacuolar functions of Atg8 rely on its noncanonical interaction with a vacuole membrane protein. ELife, 2018, 7, .	2.8	34
29	SUMO-Targeted DNA Translocase Rrp2 Protects the Genome from Top2-Induced DNA Damage. Molecular Cell, 2017, 66, 581-596.e6.	4.5	37
30	Conserved and unique features of the fission yeast core Atg1 complex. Autophagy, 2017, 13, 2018-2027.	4.3	21
31	A large gene family in fission yeast encodes spore killers that subvert Mendel's law. ELife, 2017, 6, .	2.8	93
32	Global Fitness Profiling Identifies Arsenic and Cadmium Tolerance Mechanisms in Fission Yeast. G3: Genes, Genomes, Genetics, 2016, 6, 3317-3333.	0.8	27
33	Preferential Protection of Genetic Fidelity within Open Chromatin by the Mismatch Repair Machinery. Journal of Biological Chemistry, 2016, 291, 17692-17705.	1.6	21
34	Atg20 and Atg24 family proteins promote organelle autophagy in fission yeast. Journal of Cell Science, 2016, 129, 4289-4304.	1.2	41
35	Guidelines for the use and interpretation of assays for monitoring autophagy (3rd edition). Autophagy, 2016, 12, 1-222.	4.3	4,701
36	Dimerization Mediated by a Divergent Forkhead-associated Domain Is Essential for the DNA Damage and Spindle Functions of Fission Yeast Mdb1. Journal of Biological Chemistry, 2015, 290, 21054-21066.	1.6	9

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37	A selective autophagy pathway takes an unconventional route. <i>Autophagy</i> , 2015, 11, 2381-2382.	4.3	10
38	Bulk Segregant Analysis Reveals the Genetic Basis of a Natural Trait Variation in Fission Yeast. <i>Genome Biology and Evolution</i> , 2015, 7, 3496-3510.	1.1	33
39	Parallel Profiling of Fission Yeast Deletion Mutants for Proliferation and for Lifespan During Long-Term Quiescence. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 145-155.	0.8	38
40	ESCRTs Cooperate with a Selective Autophagy Receptor to Mediate Vacuolar Targeting of Soluble Cargos. <i>Molecular Cell</i> , 2015, 59, 1035-1042.	4.5	91
41	Fission Yeast Pxd1 Promotes Proper DNA Repair by Activating Rad16XPF and Inhibiting Dna2. <i>PLoS Biology</i> , 2014, 12, e1001946.	2.6	19
42	A genome-wide profiling of cell response mechanisms to non-thermal plasma treatment. , 2014, , .		0
43	Regulation of spindle pole body assembly and cytokinesis by the centrin-binding protein Sfi1 in fission yeast. <i>Molecular Biology of the Cell</i> , 2014, 25, 2735-2749.	0.9	31
44	Genome-wide Screens for Sensitivity to Ionizing Radiation Identify the Fission Yeast Nonhomologous End Joining Factor Xrc4. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 1297-1306.	0.8	11
45	piggyBac Transposon-Based Insertional Mutagenesis for the Fission Yeast <i>Schizosaccharomyces pombe</i> . <i>Methods in Molecular Biology</i> , 2014, 1163, 213-222.	0.4	5
46	Mdb1, a Fission Yeast Homolog of Human MDC1, Modulates DNA Damage Response and Mitotic Spindle Function. <i>PLoS ONE</i> , 2014, 9, e97028.	1.1	23
47	Phosphorylation-Dependent Assembly and Coordination of the DNA Damage Checkpoint Apparatus by Rad4TopBP1. <i>Molecular Cell</i> , 2013, 51, 723-736.	4.5	27
48	A proteome-wide visual screen identifies fission yeast proteins localizing to DNA double-strand breaks. <i>DNA Repair</i> , 2013, 12, 433-443.	1.3	31
49	Global Analysis of Fission Yeast Mating Genes Reveals New Autophagy Factors. <i>PLoS Genetics</i> , 2013, 9, e1003715.	1.5	83
50	Mapping genomic hotspots of DNA damage by a single-strand-DNA-compatible and strand-specific ChIP-seq method. <i>Genome Research</i> , 2013, 23, 705-715.	2.4	35
51	Phosphorylation-Dependent Interactions between Crb2 and Chk1 Are Essential for DNA Damage Checkpoint. <i>PLoS Genetics</i> , 2012, 8, e1002817.	1.5	16
52	Multiple end joining mechanisms repair a chromosomal DNA break in fission yeast. <i>DNA Repair</i> , 2012, 11, 120-130.	1.3	28
53	A piggyBac transposon-based mutagenesis system for the fission yeast <i>Schizosaccharomyces pombe</i> . <i>Nucleic Acids Research</i> , 2011, 39, e40-e40.	6.5	36
54	BRCT Domain Interactions with Phospho-Histone H2A Target Crb2 to Chromatin at Double-Strand Breaks and Maintain the DNA Damage Checkpoint. <i>Molecular and Cellular Biology</i> , 2010, 30, 4732-4743.	1.1	26

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55	Global fitness profiling of fission yeast deletion strains by barcode sequencing. <i>Genome Biology</i> , 2010, 11, R60.	13.9	82
56	Protection of telomeres by a conserved Stn1-Ten1 complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 14038-14043.	3.3	95
57	Rad22Rad52-dependent Repair of Ribosomal DNA Repeats Cleaved by Slx1-Slx4 Endonuclease. <i>Molecular Biology of the Cell</i> , 2006, 17, 2081-2090.	0.9	34
58	Histone modification-dependent and -independent pathways for recruitment of checkpoint protein Crb2 to double-strand breaks. <i>Genes and Development</i> , 2006, 20, 1583-1596.	2.7	131
59	Homo-oligomerization Is the Essential Function of the Tandem BRCT Domains in the Checkpoint Protein Crb2. <i>Journal of Biological Chemistry</i> , 2004, 279, 38409-38414.	1.6	30
60	Histone H2A Phosphorylation Controls Crb2 Recruitment at DNA Breaks, Maintains Checkpoint Arrest, and Influences DNA Repair in Fission Yeast. <i>Molecular and Cellular Biology</i> , 2004, 24, 6215-6230.	1.1	180
61	Retention but Not Recruitment of Crb2 at Double-Strand Breaks Requires Rad1 and Rad3 Complexes. <i>Molecular and Cellular Biology</i> , 2003, 23, 6150-6158.	1.1	91
62	Swi1 Prevents Replication Fork Collapse and Controls Checkpoint Kinase Cds1. <i>Molecular and Cellular Biology</i> , 2003, 23, 7861-7874.	1.1	157
63	Pag1p, a Novel Protein Associated with Protein Kinase Cbk1p, Is Required for Cell Morphogenesis and Proliferation in <i>Saccharomyces cerevisiae</i> . <i>Molecular Biology of the Cell</i> , 2002, 13, 503-514.	0.9	102