## Wei Xiao

## List of Publications by Year in descending order

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		71102	102487
185	5,849	41	66
papers	citations	h-index	g-index
189	189	189	5092
all docs	docs citations	times ranked	citing authors

#	Article	IF	CITATIONS
1	Bcl10 activates the NF-κB pathway through ubiquitination of NEMO. Nature, 2004, 427, 167-171.	27.8	495
2	DNA postreplication repair and mutagenesis in Saccharomyces cerevisiae. Mutation Research DNA Repair, 2001, 486, 167-184.	3.7	208
3	Eukaryotic DNA damage tolerance and translesion synthesis through covalent modifications of PCNA. Cell Research, 2008, 18, 162-173.	12.0	174
4	Distinct regulation of Ubc13 functions by the two ubiquitin-conjugating enzyme variants Mms2 and Uev1A. Journal of Cell Biology, 2005, 170, 745-755.	5.2	151
5	UBC13, a DNA-damage-inducible gene, is a member of the error-free postreplication repair pathway in Saccharomyces cerevisiae. Current Genetics, 2000, 37, 168-174.	1.7	140
6	The <i>Saccharomyces cerevisiae RAD6</i> Group Is Composed of an Error-Prone and Two Error-Free Postreplication Repair Pathways. Genetics, 2000, 155, 1633-1641.	2.9	139
7	Crystal structure of the human ubiquitin conjugating enzyme complex, hMms2-hUbc13. Nature Structural Biology, 2001, 8, 669-673.	9.7	138
8	Noncovalent Interaction between Ubiquitin and the Human DNA Repair Protein Mms2 Is Required for Ubc13-mediated Polyubiquitination. Journal of Biological Chemistry, 2001, 276, 40120-40126.	3.4	121
9	<i>Arabidopsis</i> cryptochrome 1 functions in nitrogen regulation of flowering. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 7661-7666.	7.1	107
10	Arabidopsis thaliana UBC13: Implication of Error-free DNA Damage Tolerance and Lys63-linked Polyubiquitylation in Plants. Plant Molecular Biology, 2006, 61, 241-253.	3.9	105
11	Regulation of alternative replication bypass pathways at stalled replication forks and its effects on genome stability: a yeast model. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2003, 532, 137-155.	1.0	102
12	The repair of DNA methylation damage in Saccharomyces cerevisiae. Current Genetics, 1996, 30, 461-468.	1.7	98
13	The yeast Shu complex couples errorâ€free postâ€freplication repair to homologous recombination. Molecular Microbiology, 2009, 73, 89-102.	2.5	88
14	An NMR-based Model of the Ubiquitin-bound Human Ubiquitin Conjugation Complex Mms2·Ubc13. Journal of Biological Chemistry, 2003, 278, 13151-13158.	3.4	86
15	<i>Arabidopsis UEV1D</i> Promotes Lysine-63–Linked Polyubiquitination and Is Involved in DNA Damage Response. Plant Cell, 2008, 20, 213-227.	6.6	79
16	Rev3, the catalytic subunit of Poll $\P$ , is required for maintaining fragile site stability in human cells. Nucleic Acids Research, 2013, 41, 2328-2339.	14.5	76
17	Identification of a protein essential for a major pathway used by human cells to avoid UV- induced DNA damage. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 4459-4464.	7.1	74
18	Genetic interactions between error-prone and error-free postreplication repair pathways in Saccharomyces cerevisiae. Mutation Research DNA Repair, 1999, 435, 1-11.	3.7	72

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19	Rad6-Rad18 Mediates a Eukaryotic SOS Response by Ubiquitinating the 9-1-1 Checkpoint Clamp. Cell, 2008, 133, 601-611.	28.9	72
20	Roles of sequential ubiquitination of PCNA in DNAâ€damage tolerance. FEBS Letters, 2011, 585, 2786-2794.	2.8	71
21	Involvement of budding yeast Rad5 in translesion DNA synthesis through physical interaction with Rev1. Nucleic Acids Research, 2016, 44, 5231-5245.	14.5	71
22	A CONVENIENT DOMINANT SELECTION MARKER FOR GENE TRANSFER IN INDUSTRIAL STRAINS OFSACCHAROMYCESYEAST:SMRIENCODED RESISTANCE TO THE HERBICIDE SULFOMETURON METHYL. Journal of the Institute of Brewing, 1988, 94, 93-97.	2.3	69
23	Synergism between yeast nucleotide and base excision repair pathways in the protection against DNA methylation damage. Current Genetics, 1998, 33, 92-99.	1.7	64
24	<scp>UBC</scp> 13, an E2 enzyme for <scp>L</scp> ys63â€linked ubiquitination, functions in root development by affecting auxin signaling and Aux/ <scp>IAA</scp> protein stability. Plant Journal, 2014, 80, 424-436.	5.7	60
25	Suppression of genetic defects within the RAD6 pathway by srs2 is specific for error-free post-replication repair but not for damage-induced mutagenesis. Nucleic Acids Research, 2002, 30, 732-739.	14.5	57
26	Error-free DNA-damage tolerance in Saccharomyces cerevisiae. Mutation Research - Reviews in Mutation Research, 2015, 764, 43-50.	5.5	57
27	Arabidopsis <i> <scp>UBC </scp>13 </i> differentially regulates two programmed cell death pathways in responses to pathogen and lowâ€temperature stress. New Phytologist, 2019, 221, 919-934.	7.3	56
28	The TRAF6 RING finger domain mediates physical interaction with Ubc13. FEBS Letters, 2004, 566, 229-233.	2.8	53
29	DNA damage-induced gene expression in <i>Saccharomyces cerevisiae</i> . FEMS Microbiology Reviews, 2008, 32, 908-926.	8.6	52
30	Formation of the yeast Mre11-Rad50-Xrs2 complex is correlated with DNA repair and telomere maintenance. Nucleic Acids Research, 1999, 27, 2072-2079.	14.5	51
31	Identification, chromosomal mapping and tissue-specific expression of hREV3 encoding a putative human DNA polymerase zeta. Carcinogenesis, 1998, 19, 945-949.	2.8	49
32	<i>Arabidopsis thaliana</i> Yâ€family DNA polymerase η catalyses translesion synthesis and interacts functionally with PCNA2. Plant Journal, 2008, 55, 895-908.	5.7	46
33	APPLICATION OF PULSED FIELD CHROMOSOME ELECTROPHORESIS IN THE STUDY OF CHROMOSOME <i>XIII  </i>	2.3	45
34	Bidirectional regulation of two DNAâ€damageâ€inducible genes, MAG1 and DDI1 , from Saccharomyces cerevisiae. Molecular Microbiology, 1997, 23, 777-789.	2.5	45
35	Structural Basis for Non-Covalent Interaction Between Ubiquitin and the Ubiquitin Conjugating Enzyme Variant Human MMS2. Journal of Biomolecular NMR, 2006, 34, 89-100.	2.8	45
36	Ube2s regulates Sox2 stability and mouse ES cell maintenance. Cell Death and Differentiation, 2016, 23, 393-404.	11.2	45

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37	TheSaccharomyces cerevisiae MGT1DNA repair methyltransferease gene: its promoter and entire coding sequence, regulation andin vivobiological functions. Nucleic Acids Research, 1992, 20, 3599-3606.	14.5	44
38	Deletion of the MAG1 DNA glycosylase gene suppresses alkylation-induced killing and mutagenesis in yeast cells lacking AP endonucleases. Mutation Research DNA Repair, 2001, 487, 137-147.	3.7	44
39	Molecular basis of ataxia telangiectasia and related diseases. Acta Pharmacologica Sinica, 2005, 26, 897-907.	6.1	44
40	A Single Mms2 "Key―Residue Insertion into a Ubc13 Pocket Determines the Interface Specificity of a Human Lys63 Ubiquitin Conjugation Complex*. Journal of Biological Chemistry, 2005, 280, 17891-17900.	3.4	44
41	The <i>Saccharomyces cerevisiae mre11(ts)</i> Allele Confers a Separation of DNA Repair and Telomere Maintenance Functions. Genetics, 2000, 155, 569-576.	2.9	44
42	Noncanonical E2 Variant-Independent Function of UBC13 in Promoting Checkpoint Protein Assembly. Molecular and Cellular Biology, 2008, 28, 6104-6112.	2.3	43
43	Ube2s stabilizes $\hat{l}^2$ -Catenin through K11-linked polyubiquitination to promote mesendoderm specification and colorectal cancer development. Cell Death and Disease, 2018, 9, 456.	6.3	43
44	Energetics and Specificity of Interactions within Ub·Uev·Ubc13 Human Ubiquitin Conjugation Complexes. Biochemistry, 2003, 42, 7922-7930.	2.5	42
45	A stable and sensitive genotoxic testing system based on DNA damage induced gene expression in Saccharomyces cerevisiae. Mutation Research - Genetic Toxicology and Environmental Mutagenesis, 2002, 519, 83-92.	1.7	41
46	DNA Postreplication Repair Modulated by Ubiquitination and Sumoylation. Advances in Protein Chemistry, 2004, 69, 279-306.	4.4	40
47	Involvement of two endonuclease III homologs in the base excision repair pathway for the processing of DNA alkylation damage in Saccharomyces cerevisiae. DNA Repair, 2004, 3, 51-59.	2.8	39
48	Ubiquitin-conjugating enzyme complex Uev1A-Ubc13 promotes breast cancer metastasis through nuclear factor-D <sup>o</sup> B mediated matrix metalloproteinase-1 gene regulation. Breast Cancer Research, 2014, 16, R75.	5.0	39
49	Two-stage transcriptional reprogramming in Saccharomyces cerevisiae for optimizing ethanol production from xylose. Metabolic Engineering, 2014, 24, 150-159.	7.0	39
50	Uev1A, a ubiquitin conjugating enzyme variant, inhibits stress-induced apoptosis through NF-κB activation. Apoptosis: an International Journal on Programmed Cell Death, 2006, 11, 2147-2157.	4.9	36
51	Deletion of Yeast CWP Genes Enhances Cell Permeability to Genotoxic Agents. Toxicological Sciences, 2008, 103, 68-76.	3.1	36
52	DNA Damage Checkpoints Are Involved in Postreplication Repair. Genetics, 2006, 174, 1789-1800.	2.9	34
53	Construction and evaluation of two biosensors based on yeast transcriptional response to genotoxic chemicals. Biosensors and Bioelectronics, 2013, 44, 138-145.	10.1	33
54	Roles of mouse UBC13 in DNA postreplication repair and Lys63-linked ubiquitination. Gene, 2002, 285, 183-191.	2.2	32

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55	MMS1 protects against replication-dependent DNA damage in Saccharomyces cerevisiae. Molecular Genetics and Genomics, 2002, 266, 848-857.	2.1	32
56	Sequential assembly of translesion DNA polymerases at UV-induced DNA damage sites. Molecular Biology of the Cell, 2011, 22, 2373-2383.	2.1	32
57	Up-regulation of CIR1/CROC1 expression upon cell immortalization and in tumor-derived human cell lines. Oncogene, 1998, 17, 1321-1326.	5.9	31
58	Rev7/Mad2B plays a critical role in the assembly of a functional mitotic spindle. Cell Cycle, 2015, 14, 3929-3938.	2.6	30
59	Mechanism for Recognition of Polyubiquitin Chains: Balancing Affinity through Interplay between Multivalent Binding and Dynamics. Journal of the American Chemical Society, 2010, 132, 11247-11258.	13.7	29
60	RAD5a and REV3 function in two alternative pathways of DNA-damage tolerance in Arabidopsis. DNA Repair, 2011, 10, 620-628.	2.8	29
61	Cdk1 interplays with Oct4 to repress differentiation of embryonic stem cells into trophectoderm. FEBS Letters, 2012, 586, 4100-4107.	2.8	28
62	The Yeast Shu Complex Utilizes Homologous Recombination Machinery for Error-free Lesion Bypass via Physical Interaction with a Rad51 Paralogue. PLoS ONE, 2013, 8, e81371.	2.5	28
63	The construction of recombinant industrial yeasts free of bacterial sequences by directed gene replacement into a nonessential region of the genome. Gene, 1989, 76, 99-107.	2.2	27
64	Pdr3 is required for DNA damage induction of MAG1 and DDI1 via a bi-directional promoter element. Nucleic Acids Research, 2004, 32, 5066-5075.	14.5	27
65	Pol32 is required for Poll¶-dependent translesion synthesis and prevents double-strand breaks at the replication fork. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2007, 625, 164-176.	1.0	26
66	Structure, interactions, and dynamics of the RING domain from human TRAF6. Protein Science, 2007, 16, 602-614.	7.6	26
67	The Rad5 helicase activity is dispensable for error-free DNA post-replication repair. DNA Repair, 2014, 16, 74-83.	2.8	26
68	CSN6, a subunit of the COP9 signalosome, is involved in early response to iron deficiency in Oryza sativa. Scientific Reports, 2016, 6, 25485.	3.3	26
69	Rad5 coordinates translesion DNA synthesis pathway by recognizing specific DNA structures in saccharomyces cerevisiae. Current Genetics, 2018, 64, 889-899.	1.7	26
70	DNA mismatch repair mutants do not increase N-methyl-N'-nitro- N-nitrosoguanidine tolerance in O6-methylguanine DNA methyltransferase-deficient yeast cells. Carcinogenesis, 1995, 16, 1933-1939.	2.8	25
71	Catalytic Proficiency of Ubiquitin Conjugation Enzymes: Balancing p <i>K</i> <sub>a</sub> Suppression, Entropy, and Electrostatics. Journal of the American Chemical Society, 2010, 132, 17775-17786.	13.7	25
72	DNA-damage tolerance mediated by PCNA•Ub fusions in human cells is dependent on Rev1 but not Poll·. Nucleic Acids Research, 2013, 41, 7356-7369.	14.5	25

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73	Overexpression of SFA1 in engineered Saccharomyces cerevisiae to increase xylose utilization and ethanol production from different lignocellulose hydrolysates. Bioresource Technology, 2020, 313, 123724.	9.6	24
74	Yeast Survival and Growth Assays. Methods in Molecular Biology, 2014, 1163, 183-191.	0.9	24
75	Functional domains required for the Saccharomyces cerevisiae Mus81-Mms4 endonuclease complex formation and nuclear localization. DNA Repair, 2003, 2, 1435-1447.	2.8	23
76	Cdk1 is required for the selfâ€renewal of mouse embryonic stem cells. Journal of Cellular Biochemistry, 2011, 112, 942-948.	2.6	23
77	DNA-damage tolerance through PCNA ubiquitination and sumoylation. Biochemical Journal, 2020, 477, 2655-2677.	3.7	23
78	Creation of a Hyperpermeable Yeast Strain to Genotoxic Agents through Combined Inactivation of PDR and CWP Genes. Toxicological Sciences, 2010, 113, 401-411.	3.1	22
79	Rice UBC13, a candidate housekeeping gene, is required for K63-linked polyubiquitination and tolerance to DNA damage. Rice, 2012, 5, 24.	4.0	22
80	Uev1A facilitates osteosarcoma differentiation by promoting Smurf1-mediated Smad1 ubiquitination and degradation. Cell Death and Disease, 2017, 8, e2974-e2974.	6.3	22
81	Xeroderma Pigmentosum: A Glimpse into Nucleotide Excision Repair, Genetic Instability, and Cancer. Critical Reviews in Oncogenesis, 2007, 13, 159-177.	0.4	22
82	<i>POPCORN</i> Functions in the Auxin Pathway to Regulate Embryonic Body Plan and Meristem Organization in <i>Arabidopsis</i> ÂÂ. Plant Cell, 2011, 23, 4348-4367.	6.6	21
83	Structural and functional conservation of error-free DNA postreplication repair in Schizosaccharomyces pombe. DNA Repair, 2002, 1, 869-880.	2.8	20
84	Compromised DNA Repair Enhances Sensitivity of the Yeast RNR3-lacZ Genotoxicity Testing System. Toxicological Sciences, 2003, 75, 82-88.	3.1	20
85	Constitutive fusion of ubiquitin to PCNA provides DNA damage tolerance independent of translesion polymerase activities. Nucleic Acids Research, 2010, 38, 5047-5058.	14.5	20
86	Two alternative cell cycle checkpoint pathways differentially control DNA damage-dependent induction of MAG1 and DDI1 expression in yeast. Molecular Genetics and Genomics, 2001, 266, 436-444.	2.1	19
87	A Homologue of CROC-1 in a Ciliated Protist (Sterkiella histriomuscorum) Testifies to the Ancient Origin of the Ubiquitin-conjugating Enzyme Variant Family. Molecular Biology and Evolution, 2002, 19, 39-48.	8.9	19
88	Isolation of Nucleic Acids. , 2006, 313, 015-020.		19
89	Two Mms2 residues cooperatively interact with ubiquitin and are critical for Lys63 polyubiquitination in vitro and in vivo. FEBS Letters, 2007, 581, 5343-5348.	2.8	19
90	Stochastic Gate Dynamics Regulate the Catalytic Activity of Ubiquitination Enzymes. Journal of the American Chemical Society, 2014, 136, 17446-17458.	13.7	19

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91	A Role for the Respiratory Chain in Regulating Meiosis Initiation in <i>Saccharomyces cerevisiae</i> Genetics, 2018, 208, 1181-1194.	2.9	19
92	In-Depth Two-Stage Transcriptional Reprogramming and Evolutionary Engineering of <i>Saccharomyces cerevisiae</i> for Efficient Bioethanol Production from Xylose with Acetate. Journal of Agricultural and Food Chemistry, 2019, 67, 12002-12012.	5.2	19
93	Evidence for Cis- and Trans-acting element coevolution of the $2-\hat{1}\frac{1}{4}$ m circle genome in Saccharomyces cerevisiae. Journal of Molecular Evolution, 1991, 32, 145-152.	1.8	18
94	Gene transfer in industrialSaccharomycesyeasts. Food Biotechnology, 1988, 2, 1-41.	1.5	17
95	Uev1A-Ubc13 promotes colorectal cancer metastasis through regulating <i>CXCL1 </i> expression via NF-DB activation. Oncotarget, 2018, 9, 15952-15967.	1.8	17
96	Molecular cloning and functional characterization of two murine cDNAs which encode Ubc variants involved in DNA repair and mutagenesis. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 2001, 1519, 70-77.	2.4	16
97	hMMS2 serves a redundant role in human PCNA polyubiquitination. BMC Molecular Biology, 2008, 9, 24.	3.0	16
98	Three Brachypodium distachyon Uev1s Promote Ubc13-Mediated Lys63-Linked Polyubiquitination and Confer Different Functions. Frontiers in Plant Science, 2016, 7, 1551.	3.6	16
99	Uev1A-Ubc13 catalyzes K63-linked ubiquitination of RHBDF2 to promote TACE maturation. Cellular Signalling, 2018, 42, 155-164.	3.6	16
100	Arabidopsis <scp>OTU</scp> 1, a linkageâ€specific deubiquitinase, is required for <scp>endoplasmic reticulum</scp> â€associated protein degradation. Plant Journal, 2020, 101, 141-155.	5.7	16
101	Yeast chromatin remodeling complexes and their roles in transcription. Current Genetics, 2020, 66, 657-670.	1.7	16
102	MicroRNA regulation of cancer stem cells in the pathogenesis of breast cancer. Cancer Cell International, 2021, 21, 31.	4.1	16
103	Identification and characterization of CRT10 as a novel regulator of Saccharomyces cerevisiae ribonucleotide reductase genes. Nucleic Acids Research, 2006, 34, 1876-1883.	14.5	15
104	Two Duplicated Genes DDI2 and DDI3 in Budding Yeast Encode a Cyanamide Hydratase and Are Induced by Cyanamide. Journal of Biological Chemistry, 2015, 290, 12664-12675.	3.4	15
105	OsSEC24, a functional SEC24-like protein in rice, improves tolerance to iron deficiency and high pH by enhancing H + secretion mediated by PM-H + -ATPase. Plant Science, 2015, 233, 61-71.	3.6	15
106	Construction of α-Galactosidase-Positive Strains of Industrial Baker's (Saccharomyces) Tj ETQq0 0 0 rgBT /Overl	ock.10 Tf	50 142 Td (C
107	A single amino acid substitution in MSH5 results in DNA alkylation tolerance. Gene, 2003, 315, 177-182.	2.2	14
108	Structure and Interactions of the Ubiquitin-Conjugating Enzyme Variant Human Uev1a: Implications for Enzymatic Synthesis of Polyubiquitin Chainsâ€,â€−. Biochemistry, 2006, 45, 9866-9877.	2.5	14

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109	Inactivation of YAP1 Enhances Sensitivity of the Yeast RNR3-lacZ Genotoxicity Testing System to a Broad Range of DNA-Damaging Agents. Toxicological Sciences, 2011, 120, 310-321.	3.1	14
110	Zebrafish Mms2 promotes K63-linked polyubiquitination and is involved in p53-mediated DNA-damage response. DNA Repair, 2012, 11, 157-166.	2.8	14
111	Overexpressing CCW12 in Saccharomyces cerevisiae enables highly efficient ethanol production from lignocellulose hydrolysates. Bioresource Technology, 2021, 337, 125487.	9.6	14
112	Generation of an ilv bradytrophic phenocopy in yeast by antisense RNA. Current Genetics, 1988, 13, 283-289.	1.7	13
113	Sequence diversity of yeast 2 $\hat{l}$ /4m RAF gene and its co-evolution with STB and REP1. Gene, 1991, 101, 75-80.	2.2	13
114	Isolation of hMRE11B: failure to complement yeast mre11 defects due to species-specific protein interactions. Gene, 1998, 225, 107-116.	2.2	13
115	Study of Transcriptional Regulation Using a Reporter Gene Assay. , 2006, 313, 257-264.		13
116	Active Site Gate Dynamics Modulate the Catalytic Activity of the Ubiquitination Enzyme E2-25K. Scientific Reports, 2018, 8, 7002.	3.3	13
117	Cloning of industrial Saccharomyces 2-μm plasmid variants by in vivo site-specific recombination. Plasmid, 1990, 23, 67-70.	1.4	12
118	Characterization of four rice UEV1 genes required for Lys63-linked polyubiquitination and distinct functions. BMC Plant Biology, 2017, 17, 126.	3.6	12
119	Mating type regulation of cellular tolerance to DNA damage is specific to the DNA post-replication repair and mutagenesis pathway. Molecular Microbiology, 2006, 59, 637-650.	2.5	11
120	Zebrafish Ubc13 is required for Lys63-linked polyubiquitination and DNA damage tolerance. Molecular and Cellular Biochemistry, 2010, 343, 173-182.	3.1	11
121	Regulation of nucleotide excision repair through ubiquitination. Acta Biochimica Et Biophysica Sinica, 2011, 43, 919-929.	2.0	11
122	Uev1A promotes breast cancer cell survival and chemoresistance through the AKT-FOXO1-BIM pathway. Cancer Cell International, 2019, 19, 331.	4.1	11
123	Expression of the human MGMT O6-methylguanine DNA methyltransferase gene in a yeast alkylation-sensitive mutant: its effects on both exogenous and endogenous DNA alkylation damage. Mutation Research DNA Repair, 1995, 336, 133-142.	3.7	10
124	Selective tumor killing based on specific DNA-damage response deficiencies. Cancer Biology and Therapy, 2012, 13, 239-246.	3.4	10
125	Novel Method for Genomic Promoter Shuffling by Using Recyclable Cassettes. Applied and Environmental Microbiology, 2013, 79, 7042-7047.	3.1	10
126	Molecular Cloning and Functional Characterization of Two Brachypodium distachyon UBC13 Genes Whose Products Promote K63-Linked Polyubiquitination. Frontiers in Plant Science, 2015, 6, 1222.	3.6	10

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127	A method for labeling proteins with tags at the native genomic loci in budding yeast. PLoS ONE, 2017, 12, e0176184.	2.5	10
128	Sgs1 helicase is required for efficient PCNA monoubiquitination and translesion DNA synthesis in Saccharomyces cerevisiae. Current Genetics, 2018, 64, 459-468.	1.7	10
129	REV3 is required for spontaneous but not methylation damage-induced mutagenesis of Saccharomyces cerevisiae cells lacking O6-methylguanine DNA methyltransferase. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 1999, 431, 155-165.	1.0	9
130	The Mre11-Rad50-Xrs2 Complex Is Required for Yeast DNA Postreplication Repair. PLoS ONE, 2014, 9, e109292.	2.5	9
131	Utilization of a Strongly Inducible DDI2 Promoter to Control Gene Expression in Saccharomyces cerevisiae. Frontiers in Microbiology, 2018, 9, 2736.	3.5	9
132	Rev1 plays central roles in mammalian DNAâ€damage tolerance in response to UV irradiation. FEBS Journal, 2019, 286, 2711-2725.	4.7	9
133	The C-terminal extension of Arabidopsis Uev1A/B with putative prenylation site plays critical roles in protein interaction, subcellular distribution and membrane association. Plant Science, 2020, 291, 110324.	3.6	9
134	REV7 is required for processing AID initiated DNA lesions in activated B cells. Nature Communications, 2020, 11, 2812.	12.8	9
135	Minimize the Xylitol Production in Saccharomyces cerevisiae by Balancing the Xylose Redox Metabolic Pathway. Frontiers in Bioengineering and Biotechnology, 2021, 9, 639595.	4.1	9
136	An improved method for yeast 2μm plasmid curing. Gene, 1990, 88, 241-245.	2.2	8
137	Polymorphism of 2-νm plasmids in industrial strains of Saccharomyces cerevisiae. Applied Microbiology and Biotechnology, 1993, 39, 80-86.	3.6	8
138	Improving synthetic lethal screens by regulating the yeast centromere sequence. Genome, 2000, 43, 910-917.	2.0	8
139	Expression of <i>Malus xiaojinensis </i> IRT1 (MxIRT1) protein in transgenic yeast cells leads to degradation through autophagy in the presence of excessive iron. Yeast, 2015, 32, 499-517.	1.7	8
140	Transcriptomic profiling of chemical exposure reveals roles of Yap1 in protecting yeast cells from oxidative and other types of stresses. Yeast, 2016, 33, 5-19.	1.7	8
141	Drosophila bendless catalyzes K63-linked polyubiquitination and is involved in the response to DNA damage. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2018, 808, 39-47.	1.0	8
142	Biological significance of structural differences between two highly conserved Ubc variants. Biochemical and Biophysical Research Communications, 2009, 378, 563-568.	2.1	7
143	Similarities and differences between Arabidopsis PCNA1 and PCNA2 in complementing the yeast DNA damage tolerance defect. DNA Repair, 2015, 28, 28-36.	2.8	7
144	PCNA-Ub polyubiquitination inhibits cell proliferation and induces cell-cycle checkpoints. Cell Cycle, 2016, 15, 3390-3401.	2.6	7

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145	Rev7, the regulatory subunit of Polζ, undergoes UV â€induced and Cul4â€dependent degradation. FEBS Journal, 2017, 284, 1790-1803.	4.7	7
146	TMD1 domain and CRAC motif determine the association and disassociation of MxIRT1 with detergentâ€resistant membranes. Traffic, 2018, 19, 122-137.	2.7	7
147	Global reprogramming of xylose metabolism in Saccharomyces cerevisiae efficiently produces ethanol from lignocellulose hydrolysates. Industrial Crops and Products, 2022, 179, 114666.	<b>5.</b> 2	7
148	V. Yeast sequencing reports.UBP5 encodes a putative yeast ubiquitin-specific protease that is related to the human Tre-2 oncogene product. Yeast, 1994, 10, 1497-1502.	1.7	6
149	Defects in base excision repair combined with elevated intracellular dCTP levels dramatically reduce mutation induction in yeast by ethyl methanesulfonate and N-methyl-Nâ $\in$ 2-nitro-N-nitrosoguanidine., 1998, 32, 173-178.		6
150	Methionine reduces spontaneous and alkylation-induced mutagenesis in Saccharomyces cerevisiae cells deficient in O6-methylguanine-DNA methyltransferase. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 1999, 430, 99-107.	1.0	6
151	Optimizing the coordinated transcription of central xylose-metabolism genes in Saccharomyces cerevisiae. Applied Microbiology and Biotechnology, 2018, 102, 7207-7217.	3.6	6
152	Structure of Ddi2, a highly inducible detoxifying metalloenzyme from Saccharomyces cerevisiae. Journal of Biological Chemistry, 2019, 294, 10674-10685.	3.4	6
153	Distinct requirements for budding yeast Rev1 and Poll· in translesion DNA synthesis across different types of DNA damage. Current Genetics, 2020, 66, 1019-1028.	1.7	6
154	Isolation by phage display and characterization of a single-chain antibody specific for O6-methyldeoxyguanosine. Science Bulletin, 2001, 46, 1024-1029.	1.7	5
155	Uev1A promotes breast cancer cell migration by up-regulating CT45A expression via the AKT pathway. BMC Cancer, 2021, 21, 1012.	2.6	5
156	Metabolic and Evolutionary Engineering of Diploid Yeast for the Production of First- and Second-Generation Ethanol. Frontiers in Bioengineering and Biotechnology, 2021, 9, 835928.	4.1	5
157	V. Yeast mapping reports. TheMAG1 3-methladenine DNA glycosylase gene is closely linked to theSPT15 TATA-binding TFIID gene on chromosome V-R inSaccharomyces cerevisiae. Yeast, 1994, 10, 687-691.	1.7	4
158	Role of the virulence plasmid in acid resistance of Shigella flexneri. Scientific Reports, 2017, 7, 46465.	3.3	4
159	Drosophila Uev1a is dually required for Ben-dependent DNA-damage response and fly mobility. Cellular Signalling, 2020, 74, 109719.	3.6	4
160	Molecular cloning and functional characterization of Physcomitrella patens UBC13-UEV1 genes required for Lys63-linked polyubiquitination. Plant Science, 2020, 297, 110518.	3.6	4
161	Site-specific proteolytic cleavage prevents ubiquitination and degradation of human REV3L, the catalytic subunit of DNA polymerase ζ. Nucleic Acids Research, 2020, 48, 3619-3637.	14.5	4
162	Functions and mechanisms of the Ubc13-UEV complex and lysine 63-linked polyubiquitination in plants. Journal of Experimental Botany, 2022, 73, 5372-5387.	4.8	4

#	Article	lF	CITATIONS
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