Wei Xiao

List of Publications by Year
in descending order

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

#	Article	IF	Citations
1	Molecular cloning and functional characterization of UBC13 and MMS2 from Candida albicans. Gene, 2022, 816, 146163.	2.2	0
2	Identification of Nanog as a novel inhibitor of Rad51. Cell Death and Disease, 2022, 13, 193.	6.3	3
3	Global reprogramming of xylose metabolism in Saccharomyces cerevisiae efficiently produces ethanol from lignocellulose hydrolysates. Industrial Crops and Products, 2022, 179, 114666.	5.2	7
4	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
5	<i>TEB</i>/<i>POLQ</i> plays dual roles in protecting <i>Arabidopsis</i> from NO-induced DNA damage. Nucleic Acids Research, 2022, 50, 6820-6836.	14.5	2
6	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
7	Engineered Polyploid Yeast Strains Enable Efficient Xylose Utilization and Ethanol Production in Corn Hydrolysates. Frontiers in Bioengineering and Biotechnology, 2021, 9, 655272.	4.1	2
8	Uev1A promotes breast cancer cell migration by up-regulating CT45A expression via the AKT pathway. BMC Cancer, 2021, 21, 1012.	2.6	5
9	Overexpressing CCW12 in Saccharomyces cerevisiae enables highly efficient ethanol production from lignocellulose hydrolysates. Bioresource Technology, 2021, 337, 125487.	9.6	14
10	MicroRNA regulation of cancer stem cells in the pathogenesis of breast cancer. Cancer Cell International, 2021, 21, 31.	4.1	16
11	Genomic Promoter Shuffling by Using Recyclable Cassettes. Methods in Molecular Biology, 2021, 2196, 39-51.	0.9	0
12	Genetic and physical interactions between PolÎ· and Rev1 in response to UV-induced DNA damage in mammalian cells. Scientific Reports, 2021, 11, 21364.	3.3	1
13	Study Essential Gene Functions by Plasmid Shuffling. Methods in Molecular Biology, 2021, 2196, 53-62.	0.9	3
14	Scarless Genomic Protein Labeling in Saccharomyces cerevisiae. Methods in Molecular Biology, 2021, 2196, 63-75.	0.9	0
15	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
16	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
17	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
18	Uev1A amino terminus stimulates poly-ubiquitin chain assembly and is required for NF-ÎºB activation. Cellular Signalling, 2020, 74, 109712.	3.6	3

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19	Drosophila Uev1a is dually required for Ben-dependent DNA-damage response and fly mobility. Cellular Signalling, 2020, 74, 109719.	3.6	4
20	Molecular cloning and functional characterization of Physcomitrella patens UBC13-UEV1 genes required for Lys63-linked polyubiquitination. Plant Science, 2020, 297, 110518.	3.6	4
21	REV7 is required for processing AID initiated DNA lesions in activated B cells. Nature Communications, 2020, 11, 2812.	12.8	9
22	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
23	Distinct requirements for budding yeast Rev1 and PolÎ· in translesion DNA synthesis across different types of DNA damage. Current Genetics, 2020, 66, 1019-1028.	1.7	6
24	Site-specific proteolytic cleavage prevents ubiquitination and degradation of human REV3L, the catalytic subunit of DNA polymerase Î¶. Nucleic Acids Research, 2020, 48, 3619-3637.	14.5	4
25	Yeast chromatin remodeling complexes and their roles in transcription. Current Genetics, 2020, 66, 657-670.	1.7	16
26	DNA-damage tolerance through PCNA ubiquitination and sumoylation. Biochemical Journal, 2020, 477, 2655-2677.	3.7	23
27	Structure of Ddi2, a highly inducible detoxifying metalloenzyme from Saccharomyces cerevisiae. Journal of Biological Chemistry, 2019, 294, 10674-10685.	3.4	6
28	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
29	Rev1 plays central roles in mammalian DNAâ€damage tolerance in response to UV irradiation. FEBS Journal, 2019, 286, 2711-2725.	4.7	9
30	Uev1A promotes breast cancer cell survival and chemoresistance through the AKT-FOXO1-BIM pathway. Cancer Cell International, 2019, 19, 331.	4.1	11
31	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
32	Ube2s stabilizes Î²-Catenin through K11-linked polyubiquitination to promote mesendoderm specification and colorectal cancer development. Cell Death and Disease, 2018, 9, 456.	6.3	43
33	Rad5 coordinates translesion DNA synthesis pathway by recognizing specific DNA structures in saccharomyces cerevisiae. Current Genetics, 2018, 64, 889-899.	1.7	26
34	A Role for the Respiratory Chain in Regulating Meiosis Initiation in <i>Saccharomyces cerevisiae</i>. Genetics, 2018, 208, 1181-1194.	2.9	19
35	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
36	Uev1A-Ubc13 catalyzes K63-linked ubiquitination of RHBDF2 to promote TACE maturation. Cellular Signalling, 2018, 42, 155-164.	3.6	16

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37	Sgs1 helicase is required for efficient PCNA monoubiquitination and translesion DNA synthesis in Saccharomyces cerevisiae. Current Genetics, 2018, 64, 459-468.	1.7	10
38	Linear ubiquitin chain induces apoptosis and inhibits tumor growth. Apoptosis: an International Journal on Programmed Cell Death, 2018, 23, 16-26.	4.9	1
39	TMD1 domain and CRAC motif determine the association and disassociation of MxIRT1 with detergentâ€resistant membranes. Traffic, 2018, 19, 122-137.	2.7	7
40	Utilization of a Strongly Inducible DDI2 Promoter to Control Gene Expression in Saccharomyces cerevisiae. Frontiers in Microbiology, 2018, 9, 2736.	3.5	9
41	Optimizing the coordinated transcription of central xylose-metabolism genes in Saccharomyces cerevisiae. Applied Microbiology and Biotechnology, 2018, 102, 7207-7217.	3.6	6
42	Active Site Gate Dynamics Modulate the Catalytic Activity of the Ubiquitination Enzyme E2-25K. Scientific Reports, 2018, 8, 7002.	3.3	13
43	Uev1A-Ubc13 promotes colorectal cancer metastasis through regulating<i>CXCL1</i>expression via NF-ÐºB activation. Oncotarget, 2018, 9, 15952-15967.	1.8	17
44	Rev7, the regulatory subunit of PolÎ¶, undergoes UV â€induced and Cul4â€dependent degradation. FEBS Journal, 2017, 284, 1790-1803.	4.7	7
45	Role of the virulence plasmid in acid resistance of Shigella flexneri. Scientific Reports, 2017, 7, 46465.	3.3	4
46	Uev1A facilitates osteosarcoma differentiation by promoting Smurf1-mediated Smad1 ubiquitination and degradation. Cell Death and Disease, 2017, 8, e2974-e2974.	6.3	22
47	An H-NS Family Protein, Sfh, Regulates Acid Resistance by Inhibition of Glutamate Decarboxylase Expression in Shigella flexneri 2457T. Frontiers in Microbiology, 2017, 8, 1923.	3.5	1
48	A method for labeling proteins with tags at the native genomic loci in budding yeast. PLoS ONE, 2017, 12, e0176184.	2.5	10
49	Characterization of four rice UEV1 genes required for Lys63-linked polyubiquitination and distinct functions. BMC Plant Biology, 2017, 17, 126.	3.6	12
50	Three Brachypodium distachyon Uev1s Promote Ubc13-Mediated Lys63-Linked Polyubiquitination and Confer Different Functions. Frontiers in Plant Science, 2016, 7, 1551.	3.6	16
51	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
52	The Pol30-K196 residue plays a critical role in budding yeast DNA postreplication repair through interaction with Rad18. DNA Repair, 2016, 47, 42-48.	2.8	3
53	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
54	PCNA-Ub polyubiquitination inhibits cell proliferation and induces cell-cycle checkpoints. Cell Cycle, 2016, 15, 3390-3401.	2.6	7

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55	<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
56	Involvement of budding yeast Rad5 in translesion DNA synthesis through physical interaction with Rev1. Nucleic Acids Research, 2016, 44, 5231-5245.	14.5	71
57	Ube2s regulates Sox2 stability and mouse ES cell maintenance. Cell Death and Differentiation, 2016, 23, 393-404.	11.2	45
58	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
59	Rev7/Mad2B plays a critical role in the assembly of a functional mitotic spindle. Cell Cycle, 2015, 14, 3929-3938.	2.6	30
60	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
61	Error-free DNA-damage tolerance in Saccharomyces cerevisiae. Mutation Research - Reviews in Mutation Research, 2015, 764, 43-50.	5.5	57
62	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
63	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
64	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
65	The Mre11-Rad50-Xrs2 Complex Is Required for Yeast DNA Postreplication Repair. PLoS ONE, 2014, 9, e109292.	2.5	9
66	Ubiquitin-conjugating enzyme complex Uev1A-Ubc13 promotes breast cancer metastasis through nuclear factor-Ðº B mediated matrix metalloproteinase-1 gene regulation. Breast Cancer Research, 2014, 16, R75.	5.0	39
67	<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
68	Stochastic Gate Dynamics Regulate the Catalytic Activity of Ubiquitination Enzymes. Journal of the American Chemical Society, 2014, 136, 17446-17458.	13.7	19
69	The Rad5 helicase activity is dispensable for error-free DNA post-replication repair. DNA Repair, 2014, 16, 74-83.	2.8	26
70	Two-stage transcriptional reprogramming in Saccharomyces cerevisiae for optimizing ethanol production from xylose. Metabolic Engineering, 2014, 24, 150-159.	7.0	39
71	Yeast Survival and Growth Assays. Methods in Molecular Biology, 2014, 1163, 183-191.	0.9	24
72	Spontaneous Mutagenesis Assay. Methods in Molecular Biology, 2014, 1163, 193-199.	0.9	1

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73	Detection of Protein Posttranslational Modifications from Whole-Cell Extracts in Saccharomyces cerevisiae. Methods in Molecular Biology, 2014, 1163, 249-255.	0.9	2
74	Isolation of Yeast Nucleic Acids. Methods in Molecular Biology, 2014, 1163, 15-21.	0.9	3
75	Construction and evaluation of two biosensors based on yeast transcriptional response to genotoxic chemicals. Biosensors and Bioelectronics, 2013, 44, 138-145.	10.1	33
76	DNA-damage tolerance mediated by PCNAâ€¢Ub fusions in human cells is dependent on Rev1 but not PolÎ·. Nucleic Acids Research, 2013, 41, 7356-7369.	14.5	25
77	Rev3, the catalytic subunit of PolÎ¶, is required for maintaining fragile site stability in human cells. Nucleic Acids Research, 2013, 41, 2328-2339.	14.5	76
78	Novel Method for Genomic Promoter Shuffling by Using Recyclable Cassettes. Applied and Environmental Microbiology, 2013, 79, 7042-7047.	3.1	10
79	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
80	Selective tumor killing based on specific DNA-damage response deficiencies. Cancer Biology and Therapy, 2012, 13, 239-246.	3.4	10
81	Cdk1 interplays with Oct4 to repress differentiation of embryonic stem cells into trophectoderm. FEBS Letters, 2012, 586, 4100-4107.	2.8	28
82	Rice UBC13, a candidate housekeeping gene, is required for K63-linked polyubiquitination and tolerance to DNA damage. Rice, 2012, 5, 24.	4.0	22
83	Zebrafish Mms2 promotes K63-linked polyubiquitination and is involved in p53-mediated DNA-damage response. DNA Repair, 2012, 11, 157-166.	2.8	14
84	DNA damage research in China. DNA Repair, 2012, 11, 101.	2.8	1
85	RAD5a and REV3 function in two alternative pathways of DNA-damage tolerance in Arabidopsis. DNA Repair, 2011, 10, 620-628.	2.8	29
86	Roles of sequential ubiquitination of PCNA in DNAâ€damage tolerance. FEBS Letters, 2011, 585, 2786-2794.	2.8	71
87	Cdk1 is required for the selfâ€renewal of mouse embryonic stem cells. Journal of Cellular Biochemistry, 2011, 112, 942-948.	2.6	23
88	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
89	Sequential assembly of translesion DNA polymerases at UV-induced DNA damage sites. Molecular Biology of the Cell, 2011, 22, 2373-2383.	2.1	32
90	Regulation of nucleotide excision repair through ubiquitination. Acta Biochimica Et Biophysica Sinica, 2011, 43, 919-929.	2.0	11

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91	<i>POPCORN</i>Functions in the Auxin Pathway to Regulate Embryonic Body Plan and Meristem Organization in<i>Arabidopsis</i>Â Â. Plant Cell, 2011, 23, 4348-4367.	6.6	21
92	Zebrafish Ubc13 is required for Lys63-linked polyubiquitination and DNA damage tolerance. Molecular and Cellular Biochemistry, 2010, 343, 173-182.	3.1	11
93	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
94	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
95	Development of Th1 Imprints to rBCG Expressing a Foreign Protein: Implications for Vaccination against HIV-1 and Diverse Influenza Strains. Journal of Biomedicine and Biotechnology, 2010, 2010, 1-8.	3.0	1
96	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
97	Catalytic Proficiency of Ubiquitin Conjugation Enzymes: Balancing p<i>K</i>_a Suppression, Entropy, and Electrostatics. Journal of the American Chemical Society, 2010, 132, 17775-17786.	13.7	25
98	The yeast Shu complex couples errorâ€free postâ€replication repair to homologous recombination. Molecular Microbiology, 2009, 73, 89-102.	2.5	88
99	Biological significance of structural differences between two highly conserved Ubc variants. Biochemical and Biophysical Research Communications, 2009, 378, 563-568.	2.1	7
100	hMMS2 serves a redundant role in human PCNA polyubiquitination. BMC Molecular Biology, 2008, 9, 24.	3.0	16
101	DNA damage-induced gene expression in<i>Saccharomyces cerevisiae</i>. FEMS Microbiology Reviews, 2008, 32, 908-926.	8.6	52
102	Eukaryotic DNA damage tolerance and translesion synthesis through covalent modifications of PCNA. Cell Research, 2008, 18, 162-173.	12.0	174
103	<i>Arabidopsis thaliana</i> Yâ€family DNA polymerase Î· catalyses translesion synthesis and interacts functionally with PCNA2. Plant Journal, 2008, 55, 895-908.	5.7	46
104	Rad6-Rad18 Mediates a Eukaryotic SOS Response by Ubiquitinating the 9-1-1 Checkpoint Clamp. Cell, 2008, 133, 601-611.	28.9	72
105	Noncanonical E2 Variant-Independent Function of UBC13 in Promoting Checkpoint Protein Assembly. Molecular and Cellular Biology, 2008, 28, 6104-6112.	2.3	43
106	Deletion of Yeast CWP Genes Enhances Cell Permeability to Genotoxic Agents. Toxicological Sciences, 2008, 103, 68-76.	3.1	36
107	<i>Arabidopsis UEV1D</i>Promotes Lysine-63â€“Linked Polyubiquitination and Is Involved in DNA Damage Response. Plant Cell, 2008, 20, 213-227.	6.6	79
108	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

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109	Pol32 is required for PolÎ¶-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
110	Structure, interactions, and dynamics of the RING domain from human TRAF6. Protein Science, 2007, 16, 602-614.	7.6	26
111	Xeroderma Pigmentosum: A Glimpse into Nucleotide Excision Repair, Genetic Instability, and Cancer. Critical Reviews in Oncogenesis, 2007, 13, 159-177.	0.4	22
112	DNA Damage Tolerance and Translesion Synthesis. , 2007, , 233-265.		0
113	Study of Transcriptional Regulation Using a Reporter Gene Assay. , 2006, 313, 257-264.		13
114	Isolation of Nucleic Acids. , 2006, 313, 015-020.		19
115	Structure and Interactions of the Ubiquitin-Conjugating Enzyme Variant Human Uev1a:Â Implications for Enzymatic Synthesis of Polyubiquitin Chainsâ€,â€–. Biochemistry, 2006, 45, 9866-9877.	2.5	14
116	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
117	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
118	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
119	Uev1A, a ubiquitin conjugating enzyme variant, inhibits stress-induced apoptosis through NF-Î°B activation. Apoptosis: an International Journal on Programmed Cell Death, 2006, 11, 2147-2157.	4.9	36
120	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
121	DNA Damage Checkpoints Are Involved in Postreplication Repair. Genetics, 2006, 174, 1789-1800.	2.9	34
122	Molecular basis of ataxia telangiectasia and related diseases. Acta Pharmacologica Sinica, 2005, 26, 897-907.	6.1	44
123	A Single Mms2 â€œKeyâ€• 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
124	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
125	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
126	Assessing DNA Damage Using a Reporter Gene System. , 2004, , 315-323.		1

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127	Bcl10 activates the NF-Î°B pathway through ubiquitination of NEMO. Nature, 2004, 427, 167-171.	27.8	495
128	DNA Postreplication Repair Modulated by Ubiquitination and Sumoylation. Advances in Protein Chemistry, 2004, 69, 279-306.	4.4	40
129	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
130	The TRAF6 RING finger domain mediates physical interaction with Ubc13. FEBS Letters, 2004, 566, 229-233.	2.8	53
131	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
132	Functional domains required for the Saccharomyces cerevisiae Mus81-Mms4 endonuclease complex formation and nuclear localization. DNA Repair, 2003, 2, 1435-1447.	2.8	23
133	A single amino acid substitution in MSH5 results in DNA alkylation tolerance. Gene, 2003, 315, 177-182.	2.2	14
134	Energetics and Specificity of Interactions within UbÂ·UevÂ·Ubc13 Human Ubiquitin Conjugation Complexes. Biochemistry, 2003, 42, 7922-7930.	2.5	42
135	Compromised DNA Repair Enhances Sensitivity of the Yeast RNR3-lacZ Genotoxicity Testing System. Toxicological Sciences, 2003, 75, 82-88.	3.1	20
136	An NMR-based Model of the Ubiquitin-bound Human Ubiquitin Conjugation Complex Mms2Â·Ubc13. Journal of Biological Chemistry, 2003, 278, 13151-13158.	3.4	86
137	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
138	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
139	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
140	Structural and functional conservation of error-free DNA postreplication repair in Schizosaccharomyces pombe. DNA Repair, 2002, 1, 869-880.	2.8	20
141	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
142	Roles of mouse UBC13 in DNA postreplication repair and Lys63-linked ubiquitination. Gene, 2002, 285, 183-191.	2.2	32
143	MMS1 protects against replication-dependent DNA damage in Saccharomyces cerevisiae. Molecular Genetics and Genomics, 2002, 266, 848-857.	2.1	32
144	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

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145	DNA postreplication repair and mutagenesis in Saccharomyces cerevisiae. Mutation Research DNA Repair, 2001, 486, 167-184.	3.7	208
146	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
147	Isolation by phage display and characterization of a single-chain antibody specific for O6-methyldeoxyguanosine. Science Bulletin, 2001, 46, 1024-1029.	1.7	5
148	Crystal structure of the human ubiquitin conjugating enzyme complex, hMms2-hUbc13. Nature Structural Biology, 2001, 8, 669-673.	9.7	138
149	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
150	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
151	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
152	Improving synthetic lethal screens by regulating the yeast centromere sequence. Genome, 2000, 43, 910-917.	2.0	8
153	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
154	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
155	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
156	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
157	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
158	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
159	Up-regulation of CIR1/CROC1 expression upon cell immortalization and in tumor-derived human cell lines. Oncogene, 1998, 17, 1321-1326.	5.9	31
160	Defects in base excision repair combined with elevated intracellular dCTP levels dramatically reduce mutation induction in yeast by ethyl methanesulfonate andN-methyl-Nâ€²-nitro-N-nitrosoguanidine. , 1998, 32, 173-178.		6
161	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
162	Isolation of hMRE11B: failure to complement yeast mre11 defects due to species-specific protein interactions. Gene, 1998, 225, 107-116.	2.2	13

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163	Identification, chromosomal mapping and tissue-specific expression of hREV3 encoding a putative human DNA polymerase zeta. Carcinogenesis, 1998, 19, 945-949.	2.8	49
164	Bidirectional regulation of two DNAâ€damageâ€inducible genes, MAG1 and DDI1 , from Saccharomyces cerevisiae. Molecular Microbiology, 1997, 23, 777-789.	2.5	45
165	The repair of DNA methylation damage in Saccharomyces cerevisiae. Current Genetics, 1996, 30, 461-468.	1.7	98
166	The 2Î¼m plasmid of laboratory yeast strains is a type-1/type-2 hybrid. , 1996, 12, 809-813.		3
167	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
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