Martin Kupiec

List of Publications by Year
in descending order

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131 papers	5,973 citations	81743 39 h-index	91712 69 g-index
136 all docs	136 docs citations	136 times ranked	6583 citing authors

#	Article	IF	Citations
1	Adaptive prediction of environmental changes by microorganisms. Nature, 2009, 460, 220-224.	13.7	488
2	The CDK regulates repair of double-strand breaks by homologous recombination during the cell cycle. EMBO Journal, 2004, 23, 4868-4875.	3.5	334
3	A genome-wide screen for Saccharomyces cerevisiae deletion mutants that affect telomere length. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 8658-8663.	3.3	317
4	Chromosomal duplication is a transient evolutionary solution to stress. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 21010-21015.	3.3	311
5	Composite effects of gene determinants on the translation speed and density of ribosomes. Genome Biology, 2011, 12, R110.	13.9	185
6	Finding a match: how do homologous sequences get together for recombination?. Nature Reviews Genetics, 2008, 9, 27-37.	7.7	162
7	DSB repair: the yeast paradigm. DNA Repair, 2004, 3, 797-815.	1.3	146
8	ELG1, a yeast gene required for genome stability, forms a complex related to replication factor C. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 9906-9911.	3.3	135
9	Effect of nuclear architecture on the efficiency of double-strand break repair. Nature Cell Biology, 2013, 15, 694-699.	4.6	117
10	Molecular Dissection of Mitotic Recombination in the Yeast Saccharomyces cerevisiae. Molecular and Cellular Biology, 2003, 23, 1403-1417.	1.1	114
11	Genetic and Physical Interactions Between Factors Involved in Both Cell Cycle Progression and Pre-mRNA Splicing in <i>Saccharomyces cerevisiae</i>. Genetics, 2000, 156, 1503-1517.	1.2	108
12	Elg1, an alternative subunit of the RFC clamp loader, preferentially interacts with SUMOylated PCNA. EMBO Journal, 2010, 29, 2611-2622.	3.5	104
13	Toward accurate reconstruction of functional protein networks. Molecular Systems Biology, 2009, 5, 248.	3.2	90
14	Environmental Stresses Disrupt Telomere Length Homeostasis. PLoS Genetics, 2013, 9, e1003721.	1.5	89
15	Genetic interactions between mutants of the `error-prone' repair group of Saccharomyces cerevisiae and their effect on recombination and mutagenesis. Mutation Research DNA Repair, 1998, 407, 135-145.	3.8	86
16	Homology Search and Choice of Homologous Partner during Mitotic Recombination. Molecular and Cellular Biology, 1999, 19, 4134-4142.	1.1	86
17	Biology of telomeres: lessons from budding yeast. FEMS Microbiology Reviews, 2014, 38, 144-171.	3.9	86
18	A genome-wide screen for essential yeast genes that affect telomere length maintenance. Nucleic Acids Research, 2009, 37, 3840-3849.	6.5	83

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19	Systematic identification of gene annotation errors in the widely used yeast mutation collections. Nature Methods, 2012, 9, 373-378.	9.0	78
20	New insights into the mechanism of homologous recombination in yeast. Mutation Research - Reviews in Mutation Research, 2004, 566, 231-248.	2.4	75
21	Genome architecture and stability in the Saccharomyces cerevisiae knockout collection. Nature, 2019, 573, 416-420.	13.7	72
22	Spontaneous Changes in Ploidy Are Common in Yeast. Current Biology, 2018, 28, 825-835.e4.	1.8	71
23	From Eâ€MAPs to module maps: dissecting quantitative genetic interactions using physical interactions. Molecular Systems Biology, 2008, 4, 209.	3.2	69
24	The Relationship between Homology Length and Crossing Over during the Repair of a Broken Chromosome. Journal of Biological Chemistry, 2000, 275, 30833-30838.	1.6	65
25	The Checkpoint Protein Rad24 of Saccharomyces cerevisiae Is Involved in Processing Double-Strand Break Ends and in Recombination Partner Choice. Molecular and Cellular Biology, 2003, 23, 6585-6596.	1.1	65
26	Deletion of the SRS2 gene suppresses elevated recombination and DNA damage sensitivity in rad5 and rad18 mutants of Saccharomyces cerevisiae. Mutation Research DNA Repair, 2001, 486, 137-146.	3.8	60
27	The Elg1 Clamp Loader Plays a Role in Sister Chromatid Cohesion. PLoS ONE, 2009, 4, e5497.	1.1	58
28	TOR Complex 2 Controls Gene Silencing, Telomere Length Maintenance, and Survival under DNA-Damaging Conditions. Molecular and Cellular Biology, 2009, 29, 4584-4594.	1.1	55
29	Analysis of repair mechanism choice during homologous recombination. Nucleic Acids Research, 2009, 37, 5081-5092.	6.5	55
30	The extent of ribosome queuing in budding yeast. PLoS Computational Biology, 2018, 14, e1005951.	1.5	55
31	Functional analyses of interacting factors involved in both pre-mRNA splicing and cell cycle progression in Saccharomyces cerevisiae. Rna, 2000, 6, 1565-1572.	1.6	53
32	A systemsâ€level approach to mapping the telomere length maintenance gene circuitry. Molecular Systems Biology, 2008, 4, 172.	3.2	52
33	Ubiquitylationâ€dependent oligomerization regulates activity of Nedd4 ligases. EMBO Journal, 2017, 36, 425-440.	3.5	51
34	Cloning and mapping of CDC40, a Saccharomyces cerevisiae gene with a role in DNA repair. Current Genetics, 1985, 9, 253-257.	0.8	50
35	The Elg1 replication factor C-like complex: a novel guardian of genome stability. DNA Repair, 2005, 4, 409-417.	1.3	49
36	Proteasome Nuclear Activity Affects Chromosome Stability by Controlling the Turnover of Mms22, a Protein Important for DNA Repair. PLoS Genetics, 2010, 6, e1000852.	1.5	49

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37	The Compact Chromatin Structure of a Ty Repeated Sequence Suppresses Recombination Hotspot Activity in Saccharomyces cerevisiae. Molecular Cell, 2004, 15, 221-231.	4.5	48
38	The role ofSaccharomyces cerevisiae Cdc40p in DNA replication and mitotic spindle formation and/or maintenance. Molecular Genetics and Genomics, 1995, 247, 123-136.	2.4	46
39	The role of Holliday junction resolvases in the repair of spontaneous and induced DNA damage. Nucleic Acids Research, 2011, 39, 7009-7019.	6.5	46
40	Mutations in genes of Saccharomyces cerevisiae encoding pre-mRNA splicing factors cause cell cycle arrest through activation of the spindle checkpoint. Nucleic Acids Research, 2002, 30, 4361-4370.	6.5	44
41	Carbon Catabolite Repression in Yeast is Not Limited to Glucose. Scientific Reports, 2019, 9, 6491.	1.6	43
42	Elg1, the major subunit of an alternative RFC complex, interacts with SUMO-processing proteins. Cell Cycle, 2011, 10, 2894-2903.	1.3	42
43	Extensive Genetic Interactions Between PRP8 and PRP17/CDC40, Two Yeast Genes Involved in Pre-mRNA Splicing and Cell Cycle Progression. Genetics, 2000, 154, 61-71.	1.2	42
44	The Rad1-Rad10 nuclease promotes chromosome translocations between dispersed repeats. Nature Structural and Molecular Biology, 2012, 19, 964-971.	3.6	40
45	Identification and functional analysis of hPRP17, the human homologue of the PRP17/CDC40 yeast gene involved in splicing and cell cycle control. Rna, 1998, 4, 1304-1312.	1.6	39
46	The identification and characterization of a novel splicing protein, Isy1p, of Saccharomyces cerevisiae. Rna, 1999, 5, 360-368.	1.6	39
47	Characterization of the role played by the RAD59 gene of Saccharomyces cerevisiae in ectopic recombination. Current Genetics, 1999, 36, 13-20.	0.8	39
48	The yeast VPS genes affect telomere length regulation. Current Genetics, 2005, 47, 18-28.	0.8	39
49	Cross-Talk between Carbon Metabolism and the DNA Damage Response in S.Âcerevisiae. Cell Reports, 2015, 12, 1865-1875.	2.9	38
50	Pivotal roles of PCNA loading and unloading in heterochromatin function. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E2030-E2039.	3.3	38
51	The Saccharomyces cerevisiae gene CDC40/PRP17 controls cell cycle progression through splicing of the ANC1 gene. Nucleic Acids Research, 2004, 32, 2529-2540.	6.5	35
52	Glucose Activates TORC2-Gad8 Protein via Positive Regulation of the cAMP/cAMP-dependent Protein Kinase A (PKA) Pathway and Negative Regulation of the Pmk1 Protein-Mitogen-activated Protein Kinase Pathway. Journal of Biological Chemistry, 2014, 289, 21727-21737.	1.6	35
53	Glycan Degradation (GlyDeR) Analysis Predicts Mammalian Gut Microbiota Abundance and Host Diet-Specific Adaptations. MBio, 2014, 5, .	1.8	35
54	A high-throughput chemical screen with FDA approved drugs reveals that the antihypertensive drug Spironolactone impairs cancer cell survival by inhibiting homology directed repair. Nucleic Acids Research, 2014, 42, 5689-5701.	6.5	35

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55	A structureâ€"function analysis of the yeast Elg1 protein reveals the importance of PCNA unloading in genome stability maintenance. Nucleic Acids Research, 2017, 45, gkw1348.	6.5	34
56	Regulation of the RAD6 gene of Saccharomyces cerevisiae in the mitotic cell cycle and in meiosis. Molecular Genetics and Genomics, 1986, 203, 538-543.	2.4	33
57	Tor Complex 1 Controls Telomere Length by Affecting the Level of Ku. Current Biology, 2011, 21, 2115-2120.	1.8	33
58	The Std1 Activator of the Snf1/AMPK Kinase Controls Glucose Response in Yeast by a Regulated Protein Aggregation. Molecular Cell, 2017, 68, 1120-1133.e3.	4.5	33
59	TORC1 Regulates Developmental Responses to Nitrogen Stress via Regulation of the GATA Transcription Factor Gaf1. MBio, 2015, 6, e00959.	1.8	32
60	Frequent ploidy changes in growing yeast cultures. Current Genetics, 2018, 64, 1001-1004.	0.8	32
61	Arrest of the mitotic cell cycle and of meiosis in Saccharomyces cerevisiae by MMS. Molecular Genetics and Genomics, 1985, 201, 558-564.	2.4	31
62	Control of meiotic recombination initiation: a role for the environment?. Current Genetics, 2002, 42, 129-139.	0.8	29
63	Cloning and mapping of the RAD50 gene of Saccharomyces cerevisiae. Molecular Genetics and Genomics, 1984, 193, 525-531.	2.4	28
64	PCNA Loaders and Unloadersâ€"One Ring That Rules Them All. Genes, 2021, 12, 1812.	1.0	28
65	TORC2 Is Required to Maintain Genome Stability during S Phase in Fission Yeast. Journal of Biological Chemistry, 2013, 288, 19649-19660.	1.6	25
66	A complex-centric view of protein network evolution. Nucleic Acids Research, 2009, 37, e88-e88.	6.5	24
67	Evidence for abundant transcription of non-coding regions in the Saccharomyces cerevisiae genome. BMC Genomics, 2005, 6, 93.	1.2	23
68	Nature vs nurture: Interplay between the genetic control of telomere length and environmental factors. Cell Cycle, 2013, 12, 3465-3470.	1.3	23
69	Gad8 Protein Is Found in the Nucleus Where It Interacts with the MluI Cell Cycle Box-binding Factor (MBF) Transcriptional Complex to Regulate the Response to DNA Replication Stress. Journal of Biological Chemistry, 2016, 291, 9371-9381.	1.6	23
70	GLADIATOR: a global approach for elucidating disease modules. Genome Medicine, 2017, 9, 48.	3.6	23
71	Pitfalls of the synthetic lethality screen in Saccharomyces cerevisiae: an improved design. Current Genetics, 2003, 43, 62-69.	0.8	22
72	A reversible liquid drop aggregation controls glucose response in yeast. Current Genetics, 2018, 64, 785-788.	0.8	21

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73	Carbon catabolite repression: not only for glucose. Current Genetics, 2019, 65, 1321-1323.	0.8	21
74	TOR complex 2 in fission yeast is required for chromatin-mediated gene silencing and assembly of heterochromatic domains at subtelomeres. Journal of Biological Chemistry, 2018, 293, 8138-8150.	1.6	20
75	Rnr1, but not Rnr3, facilitates the sustained telomerase-dependent elongation of telomeres. PLoS Genetics, 2017, 13, e1007082.	1.5	20
76	A role for the yeast cell cycle/splicing factor Cdc40 in the G1/S transition. Current Genetics, 2007, 51, 123-140.	0.8	19
77	Systematic identification and correction of annotation errors in the genetic interaction map of<i>Saccharomyces cerevisiae</i>. Nucleic Acids Research, 2016, 44, e50-e50.	6.5	19
78	Effect of donor copy number on the rate of gene conversion in the yeast Saccharomyces cerevisiae. Molecular Genetics and Genomics, 1992, 235, 97-103.	2.4	18
79	The importance of being modified: PCNA modification and DNA damage response. Cell Cycle, 2012, 11, 2620-2623.	1.3	18
80	A Method for Predicting Protein-Protein Interaction Types. PLoS ONE, 2014, 9, e90904.	1.1	18
81	Access to PCNA by Srs2 and Elg1 Controls the Choice between Alternative Repair Pathways in Saccharomyces cerevisiae. MBio, 2020, 11, .	1.8	18
82	Comparative Analysis of Normalization Methods for Network Propagation. Frontiers in Genetics, 2019, 10, 4.	1.1	17
83	DNA damage bypass pathways and their effect on mutagenesis in yeast. FEMS Microbiology Reviews, 2021, 45, .	3.9	17
84	DNA-repair characterization of cdc40-1, a cell-cycle mutant of Saccharomyces cerevisiae. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 1986, 162, 33-40.	0.4	16
85	Donation of information to the unbroken chromosome in double-strand break repair. Current Genetics, 1993, 23, 414-422.	0.8	16
86	TOR links starvation responses to telomere length maintenance. Cell Cycle, 2012, 11, 2268-2271.	1.3	15
87	Genetic and physical interactions between the yeast<i>ELG1</i>gene and orthologs of the Fanconi anemia pathway. Cell Cycle, 2013, 12, 1625-1636.	1.3	15
88	A Genetic Screen for High Copy Number Suppressors of the Synthetic Lethality Between<i>elg1Î”</i>and<i>srs2Î”</i>in Yeast. G3: Genes, Genomes, Genetics, 2013, 3, 917-926.	0.8	15
89	Elg1, a central player in genome stability. Mutation Research - Reviews in Mutation Research, 2015, 763, 267-279.	2.4	15
90	Alternative clamp loaders/unloaders. FEMS Yeast Research, 2016, 16, fow084.	1.1	15

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91	Long Telomeres Do Not Affect Cellular Fitness in Yeast. MBio, 2017, 8, .	1.8	15
92	Do long telomeres affect cellular fitness?. Current Genetics, 2018, 64, 173-176.	0.8	15
93	Mec1ATR is needed for extensive telomere elongation in response to ethanol in yeast. Current Genetics, 2018, 64, 223-234.	0.8	15
94	Damage-induced ectopic recombination in the yeast Saccharomyces cerevisiae. Mutation Research DNA Repair, 1997, 384, 33-44.	3.8	14
95	Telomere length kinetics assay (TELKA) sorts the telomere length maintenance (tlm) mutants into functional groups. Nucleic Acids Research, 2014, 42, 6314-6325.	6.5	14
96	Regulation of Elg1 activity by phosphorylation. Cell Cycle, 2015, 14, 3689-3697.	1.3	13
97	Recombination between divergent sequences leads to cell death in a mismatch-repair-independent manner. Current Genetics, 2000, 38, 23-32.	0.8	12
98	How yeast cells deal with stalled replication forks. Current Genetics, 2020, 66, 911-915.	0.8	12
99	Higher-Order Genomic Organization of Cellular Functions in Yeast. Journal of Computational Biology, 2009, 16, 303-316.	0.8	11
100	Developmentally regulated MAPK pathways modulate heterochromatin in Saccharomyces cerevisiae. Nucleic Acids Research, 2009, 37, 4839-4849.	6.5	11
101	Role of the ESCRT Complexes in Telomere Biology. MBio, 2016, 7, .	1.8	11
102	Tight Regulation of Srs2 Helicase Activity Is Crucial for Proper Functioning of DNA Repair Mechanisms. G3: Genes, Genomes, Genetics, 2018, 8, 1615-1626.	0.8	11
103	The Yeast PCNA Unloader Elg1 RFC-Like Complex Plays a Role in Eliciting the DNA Damage Checkpoint. MBio, 2019, 10, .	1.8	11
104	Mixed Integer Linear Programming based machine learning approach identifies<i>regulators</i>of telomerase in yeast. Nucleic Acids Research, 2016, 44, e93-e93.	6.5	10
105	The RAD50 gene of Saccharomyces cerevisiae is not essential for vegetative growth. Current Genetics, 1986, 10, 487-489.	0.8	9
106	A novel role for Dun1 in the regulation of origin firing upon hyper-acetylation of H3K56. PLoS Genetics, 2021, 17, e1009391.	1.5	9
107	Rnr1â€™s role in telomere elongation cannot be replaced by Rnr3: a role beyond dNTPs?. Current Genetics, 2018, 64, 547-550.	0.8	8
108	The Main Role of Srs2 in DNA Repair Depends on Its Helicase Activity, Rather than on Its Interactions with PCNA or Rad51. MBio, 2018, 9, .	1.8	8

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109	The cytosolic form of aspartate aminotransferase is required for full activation of TOR complex 1 in fission yeast. Journal of Biological Chemistry, 2019, 294, 18244-18255.	1.6	8
110	Genome-wide studies of telomere biology in budding yeast. Microbial Cell, 2014, 1, 70-80.	1.4	8
111	Metabolic remodeling maintains a reducing environment for rapid activation of the yeast DNA replication checkpoint. EMBO Journal, 2022, 41, e108290.	3.5	8
112	WebPropagate: A Web Server for Network Propagation. Journal of Molecular Biology, 2018, 430, 2231-2236.	2.0	7
113	Telomeres and stress in yeast cells: When genes and environment interact. Fungal Biology, 2020, 124, 311-315.	1.1	7
114	A role for the yeast PCNA unloader Elg1 in eliciting the DNA damage checkpoint. Current Genetics, 2020, 66, 79-84.	0.8	7
115	The Amazing Acrobat: Yeastâ€™s Histone H3K56 Juggles Several Important Roles While Maintaining Perfect Balance. Genes, 2021, 12, 342.	1.0	7
116	Genetic interactions in yeast: is robustness going bust?. Molecular Systems Biology, 2007, 3, 97.	3.2	6
117	The evolutionarily conserved factor Sus1/ENY2 plays a role in telomere length maintenance. Current Genetics, 2018, 64, 635-644.	0.8	6
118	Roles of RSC, Rad59, and Cohesin in Double-Strand Break Repair. Molecular and Cellular Biology, 2011, 31, 3921-3923.	1.1	5
119	An Anti-Checkpoint Activity for Rif1. PLoS Genetics, 2011, 7, e1002421.	1.5	5
120	Utilizing yeast chemogenomic profiles for the prediction of pharmacogenomic associations in humans. Scientific Reports, 2016, 6, 23703.	1.6	4
121	S. cerevisiae Cells Can Grow without the Pds5 Cohesin Subunit. MBio, 2022, 13, .	1.8	4
122	G2G: A web-server for the prediction of human synthetic lethal interactions. Computational and Structural Biotechnology Journal, 2020, 18, 1028-1031.	1.9	3
123	TOR Complex 2- independent mutations in the regulatory PIF pocket of Gad8AKT1/SGK1 define separate branches of the stress response mechanisms in fission yeast. PLoS Genetics, 2020, 16, e1009196.	1.5	3
124	Establishment of sister chromatid cohesion: The role of the clamp loaders. Cell Cycle, 2010, 9, 4615-4615.	1.3	2
125	Genomic instability and repair mediated by common repeated sequences. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 19664-19665.	3.3	2
126	Editorial from the new Editor-in-Chief. Current Genetics, 2015, 61, 1-2.	0.8	2

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127	Noise buffering by biomolecular condensates in glucose sensing. Current Opinion in Cell Biology, 2021, 69, 1-6.	2.6	2
128	TOR complex 2 contributes to regulation of gene expression via inhibiting Gcn5 recruitment to subtelomeric and DNA replication stress genes. PLoS Genetics, 2022, 18, e1010061.	1.5	2
129	Histones on fire: the effect of Dun1 and Mrc1 on origin firing and replication of hyper-acetylated genomes. Current Genetics, 2021, 67, 501-510.	0.8	1
130	DSB repair: the yeast paradigm. DNA Repair, 2004, 3, 797-797.	1.3	0
131	A New Method, â€œReverse Yeast Two-Hybrid Arrayâ€•(RYTHA), Identifies Mutants that Dissociate the Physical Interaction Between Elg1 and Slx5. Genetics, 2017, 206, 1683-1697.	1.2	0