Martin Kupiec

List of Publications by Citations

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128	4,709	37	64
papers	citations	h-index	g-index
136	5,570	8.6	5.69
ext. papers	ext. citations	avg, IF	L-index

#	Paper	IF	Citations
128	Adaptive prediction of environmental changes by microorganisms. *Nature*, **2009**, 460, 220-4	50.4	371
127	The CDK regulates repair of double-strand breaks by homologous recombination during the cell cycle. *EMBO Journal*, **2004**, 23, 4868-75	13	303
126	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, 8658-63	11.5	268
125	Chromosomal duplication is a transient evolutionary solution to stress. *Proceedings of the National Academy of Sciences of the United States of America*, **2012**, 109, 21010-5	11.5	232
124	Composite effects of gene determinants on the translation speed and density of ribosomes. *Genome Biology*, **2011**, 12, R110	18.3	151
123	Finding a match: how do homologous sequences get together for recombination?. *Nature Reviews Genetics*, **2008**, 9, 27-37	30.1	137
122	DSB repair: the yeast paradigm. *DNA Repair*, **2004**, 3, 797-815	4.3	129
121	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, 9906-11	11.5	109
120	Molecular dissection of mitotic recombination in the yeast Saccharomyces cerevisiae. *Molecular and Cellular Biology*, **2003**, 23, 1403-17	4.8	99
119	Genetic and physical interactions between factors involved in both cell cycle progression and pre-mRNA splicing in Saccharomyces cerevisiae. *Genetics*, **2000**, 156, 1503-17	4	96
118	Effect of nuclear architecture on the efficiency of double-strand break repair. *Nature Cell Biology*, **2013**, 15, 694-9	23.4	88
117	Toward accurate reconstruction of functional protein networks. *Molecular Systems Biology*, **2009**, 5, 248	12.2	80
116	Homology search and choice of homologous partner during mitotic recombination. *Molecular and Cellular Biology*, **1999**, 19, 4134-42	4.8	79
115	Isp7 Is a Novel Regulator of Amino Acid Uptake in the TOR Signaling Pathway. *Molecular and Cellular Biology*, **2014**, 34, 1535-1535	4.8	78
114	Elg1, an alternative subunit of the RFC clamp loader, preferentially interacts with SUMOylated PCNA. *EMBO Journal*, **2010**, 29, 2611-22	13	76
113	Genetic interactions between mutants of the Serror-proneSrepair group of Saccharomyces cerevisiae and their effect on recombination and mutagenesis. *Mutation Research DNA Repair*, **1998** , 407, 135-45		72
112	Environmental stresses disrupt telomere length homeostasis. *PLoS Genetics*, **2013**, 9, e1003721	6	70

111	A genome-wide screen for essential yeast genes that affect telomere length maintenance. *Nucleic Acids Research*, **2009**, 37, 3840-9	20.1	63
110	Biology of telomeres: lessons from budding yeast. *FEMS Microbiology Reviews*, **2014**, 38, 144-71	15.1	62
109	New insights into the mechanism of homologous recombination in yeast. *Mutation Research - Reviews in Mutation Research*, **2004**, 566, 231-48	7	62
108	From E-MAPs to module maps: dissecting quantitative genetic interactions using physical interactions. *Molecular Systems Biology*, **2008**, 4, 209	12.2	59
107	Systematic identification of gene annotation errors in the widely used yeast mutation collections. *Nature Methods*, **2012**, 9, 373-8	21.6	58
106	The relationship between homology length and crossing over during the repair of a broken chromosome. *Journal of Biological Chemistry*, **2000**, 275, 30833-8	5.4	55
105	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, 6585-96	4.8	54
104	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, 137-46		53
103	TOR complex 2 controls gene silencing, telomere length maintenance, and survival under DNA-damaging conditions. *Molecular and Cellular Biology*, **2009**, 29, 4584-94	4.8	49
102	The ELG1 clamp loader plays a role in sister chromatid cohesion. *PLoS ONE*, **2009**, 4, e5497	3.7	48
101	Functional analyses of interacting factors involved in both pre-mRNA splicing and cell cycle progression in Saccharomyces cerevisiae. *Rna*, **2000**, 6, 1565-72	5.8	48
100	Analysis of repair mechanism choice during homologous recombination. *Nucleic Acids Research*, **2009**, 37, 5081-92	20.1	47
99	A systems-level approach to mapping the telomere length maintenance gene circuitry. *Molecular Systems Biology*, **2008**, 4, 172	12.2	45
98	Proteasome nuclear activity affects chromosome stability by controlling the turnover of Mms22, a protein important for DNA repair. *PLoS Genetics*, **2010**, 6, e1000852	6	42
97	The role of Saccharomyces cerevisiae Cdc40p in DNA replication and mitotic spindle formation and/or maintenance. *Molecular Genetics and Genomics*, **1995**, 247, 123-36		41
96	The extent of ribosome queuing in budding yeast. *PLoS Computational Biology*, **2018**, 14, e1005951	5	40
95	The compact chromatin structure of a Ty repeated sequence suppresses recombination hotspot activity in Saccharomyces cerevisiae. *Molecular Cell*, **2004**, 15, 221-31	17.6	40
94	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, 4361-70	20.1	40

93	The Elg1 replication factor C-like complex: a novel guardian of genome stability. *DNA Repair*, **2005**, 4, 409-17	4.3	38
92	Ubiquitylation-dependent oligomerization regulates activity of Nedd4 ligases. *EMBO Journal*, **2017**, 36, 425-440	13	37
91	The role of Holliday junction resolvases in the repair of spontaneous and induced DNA damage. *Nucleic Acids Research*, **2011**, 39, 7009-19	20.1	37
90	The yeast VPS genes affect telomere length regulation. *Current Genetics*, **2005**, 47, 18-28	2.9	36
89	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	4	36
88	Spontaneous Changes in Ploidy Are Common in Yeast. *Current Biology*, **2018**, 28, 825-835.e4	6.3	35
87	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, 1304-12	5.8	35
86	The identification and characterization of a novel splicing protein, Isy1p, of Saccharomyces cerevisiae. *Rna*, **1999**, 5, 360-8	5.8	35
85	The Rad1-Rad10 nuclease promotes chromosome translocations between dispersed repeats. *Nature Structural and Molecular Biology*, **2012**, 19, 964-71	17.6	33
84	The Saccharomyces cerevisiae gene CDC40/PRP17 controls cell cycle progression through splicing of the ANC1 gene. *Nucleic Acids Research*, **2004**, 32, 2529-40	20.1	33
83	Characterization of the role played by the RAD59 gene of Saccharomyces cerevisiae in ectopic recombination. *Current Genetics*, **1999**, 36, 13-20	2.9	33
82	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, 21727-37	5.4	29
81	Regulation of the RAD6 gene of Saccharomyces cerevisiae in the mitotic cell cycle and in meiosis. *Molecular Genetics and Genomics*, **1986**, 203, 538-43		29
80	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, 5689-701	20.1	28
79	Control of meiotic recombination initiation: a role for the environment?. *Current Genetics*, **2002**, 42, 129-39	2.9	28
78	Glycan degradation (GlyDeR) analysis predicts mammalian gut microbiota abundance and host diet-specific adaptations. *MBio*, **2014**, 5,	7.8	27
77	Cloning and mapping of CDC40, a Saccharomyces cerevisiae gene with a role in DNA repair. *Current Genetics*, **1985**, 9, 253-7	2.9	27
76	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	17.6	26

75	Tor complex 1 controls telomere length by affecting the level of Ku. *Current Biology*, **2011**, 21, 2115-20	6.3	26
74	Cross-Talk between Carbon Metabolism and the DNA Damage Response in S. cerevisiae. *Cell Reports*, **2015**, 12, 1865-75	10.6	25
73	Genome architecture and stability in the Saccharomyces cerevisiae knockout collection. *Nature*, **2019**, 573, 416-420	50.4	24
72	Frequent ploidy changes in growing yeast cultures. *Current Genetics*, **2018**, 64, 1001-1004	2.9	23
71	A complex-centric view of protein network evolution. *Nucleic Acids Research*, **2009**, 37, e88	20.1	23
70	Carbon Catabolite Repression in Yeast is Not Limited to Glucose. *Scientific Reports*, **2019**, 9, 6491	4.9	22
69	TORC1 Regulates Developmental Responses to Nitrogen Stress via Regulation of the GATA Transcription Factor Gaf1. *MBio*, **2015**, 6, e00959	7.8	22
68	Elg1, the major subunit of an alternative RFC complex, interacts with SUMO-processing proteins. *Cell Cycle*, **2011**, 10, 2894-903	4.7	22
67	TORC2 is required to maintain genome stability during S phase in fission yeast. *Journal of Biological Chemistry*, **2013**, 288, 19649-60	5.4	21
66	Cloning and mapping of the RAD50 gene of Saccharomyces cerevisiae. *Molecular Genetics and Genomics*, **1984**, 193, 525-31		21
65	Arrest of the mitotic cell cycle and of meiosis in Saccharomyces cerevisiae by MMS. *Molecular Genetics and Genomics*, **1985**, 201, 558-564		21
64	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	11.5	20
63	Pitfalls of the synthetic lethality screen in Saccharomyces cerevisiae: an improved design. *Current Genetics*, **2003**, 43, 62-9	2.9	19
62	Evidence for abundant transcription of non-coding regions in the Saccharomyces cerevisiae genome. *BMC Genomics*, **2005**, 6, 93	4.5	19
61	A structure-function analysis of the yeast Elg1 protein reveals the importance of PCNA unloading in genome stability maintenance. *Nucleic Acids Research*, **2017**, 45, 3189-3203	20.1	18
60	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, 9371-81	5.4	18
59	The importance of being modified: PCNA modification and DNA damage response. *Cell Cycle*, **2012**, 11, 2620-3	4.7	17
58	A role for the yeast cell cycle/splicing factor Cdc40 in the G1/S transition. *Current Genetics*, **2007**, 51, 123-40	2.9	16

57	A reversible liquid drop aggregation controls glucose response in yeast. *Current Genetics*, **2018**, 64, 785-788	2.9	15
56	Nature vs nurture: interplay between the genetic control of telomere length and environmental factors. *Cell Cycle*, **2013**, 12, 3465-70	4.7	15
55	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	5.4	15
54	Effect of donor copy number on the rate of gene conversion in the yeast Saccharomyces cerevisiae. *Molecular Genetics and Genomics*, **1992**, 235, 97-103		14
53	Donation of information to the unbroken chromosome in double-strand break repair. *Current Genetics*, **1993**, 23, 414-22	2.9	13
52	Elg1, a central player in genome stability. *Mutation Research - Reviews in Mutation Research*, **2015**, 763, 267-79	7	12
51	A method for predicting protein-protein interaction types. *PLoS ONE*, **2014**, 9, e90904	3.7	12
50	Genetic and physical interactions between the yeast ELG1 gene and orthologs of the Fanconi anemia pathway. *Cell Cycle*, **2013**, 12, 1625-36	4.7	12
49	Damage-induced ectopic recombination in the yeast Saccharomyces cerevisiae. *Mutation Research DNA Repair*, **1997**, 384, 33-44		12
48	Recombination between divergent sequences leads to cell death in a mismatch-repair-independent manner. *Current Genetics*, **2000**, 38, 23-32	2.9	12
47	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	3.3	12
46	Rnr1, but not Rnr3, facilitates the sustained telomerase-dependent elongation of telomeres. *PLoS Genetics*, **2017**, 13, e1007082	6	12
45	Systematic identification and correction of annotation errors in the genetic interaction map of Saccharomyces cerevisiae. *Nucleic Acids Research*, **2016**, 44, e50	20.1	11
44	Regulation of Elg1 activity by phosphorylation. *Cell Cycle*, **2015**, 14, 3689-97	4.7	10
43	Do long telomeres affect cellular fitness?. *Current Genetics*, **2018**, 64, 173-176	2.9	10
42	GLADIATOR: a global approach for elucidating disease modules. *Genome Medicine*, **2017**, 9, 48	14.4	10
41	Telomere length kinetics assay (TELKA) sorts the telomere length maintenance (tlm) mutants into functional groups. *Nucleic Acids Research*, **2014**, 42, 6314-25	20.1	10
40	TOR links starvation responses to telomere length maintenance. *Cell Cycle*, **2012**, 11, 2268-71	4.7	10

39	Access to PCNA by Srs2 and Elg1 Controls the Choice between Alternative Repair Pathways in Saccharomyces cerevisiae. *MBio*, **2020**, 11,	7.8	9
38	Mec1 is needed for extensive telomere elongation in response to ethanol in yeast. *Current Genetics*, **2018**, 64, 223-234	2.9	9
37	Comparative Analysis of Normalization Methods for Network Propagation. *Frontiers in Genetics*, **2019**, 10, 4	4.5	8
36	Tight Regulation of Srs2 Helicase Activity Is Crucial for Proper Functioning of DNA Repair Mechanisms. *G3: Genes, Genomes, Genetics*, **2018**, 8, 1615-1626	3.2	8
35	Mixed Integer Linear Programming based machine learning approach identifies regulators of telomerase in yeast. *Nucleic Acids Research*, **2016**, 44, e93	20.1	8
34	A genetic screen for high copy number suppressors of the synthetic lethality between elg1 and srs2 in yeast. *G3: Genes, Genomes, Genetics*, **2013**, 3, 917-26	3.2	8
33	Higher-order genomic organization of cellular functions in yeast. *Journal of Computational Biology*, **2009**, 16, 303-16	1.7	8
32	Developmentally regulated MAPK pathways modulate heterochromatin in Saccharomyces cerevisiae. *Nucleic Acids Research*, **2009**, 37, 4839-49	20.1	8
31	Role of the ESCRT Complexes in Telomere Biology. *MBio*, **2016**, 7,	7.8	8
30	The Yeast PCNA Unloader Elg1 RFC-Like Complex Plays a Role in Eliciting the DNA Damage Checkpoint. *MBio*, **2019**, 10,	7.8	7
29	Rnr1's role in telomere elongation cannot be replaced by Rnr3: a role beyond dNTPs?. *Current Genetics*, **2018**, 64, 547-550	2.9	7
28	Alternative clamp loaders/unloaders. *FEMS Yeast Research*, **2016**, 16,	3.1	7
27	Carbon catabolite repression: not only for glucose. *Current Genetics*, **2019**, 65, 1321-1323	2.9	6
26	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,	7.8	6
25	Long Telomeres Do Not Affect Cellular Fitness in Yeast. *MBio*, **2017**, 8,	7.8	6
24	Genetic interactions in yeast: is robustness going bust?. *Molecular Systems Biology*, **2007**, 3, 97	12.2	6
23	A role for the yeast PCNA unloader Elg1 in eliciting the DNA damage checkpoint. *Current Genetics*, **2020**, 66, 79-84	2.9	6
22	How yeast cells deal with stalled replication forks. *Current Genetics*, **2020**, 66, 911-915	2.9	5

21	Roles of RSC, Rad59, and cohesin in double-strand break repair. *Molecular and Cellular Biology*, **2011** , 31, 3921-3	4.8	5
20	The RAD50 gene of Saccharomyces cerevisiae is not essential for vegetative growth. *Current Genetics*, **1986**, 10, 487-9	2.9	5
19	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	5.4	4
18	An anti-checkpoint activity for rif1. *PLoS Genetics*, **2011**, 7, e1002421	6	4
17	Genome-wide studies of telomere biology in budding yeast. *Microbial Cell*, **2014**, 1, 70-80	3.9	4
16	DNA damage bypass pathways and their effect on mutagenesis in yeast. *FEMS Microbiology Reviews* , **2021**, 45,	15.1	4
15	The evolutionarily conserved factor Sus1/ENY2 plays a role in telomere length maintenance. *Current Genetics*, **2018**, 64, 635-644	2.9	4
14	WebPropagate: A Web Server for Network Propagation. *Journal of Molecular Biology*, **2018**, 430, 2231-2236	6.9	3
13	Utilizing yeast chemogenomic profiles for the prediction of pharmacogenomic associations in humans. *Scientific Reports*, **2016**, 6, 23703	4.9	3
12	Telomeres and stress in yeast cells: When genes and environment interact. *Fungal Biology*, **2020**, 124, 311-315	2.8	3
11	A novel role for Dun1 in the regulation of origin firing upon hyper-acetylation of H3K56. *PLoS Genetics*, **2021**, 17, e1009391	6	3
10	Genomic instability and repair mediated by common repeated sequences. *Proceedings of the National Academy of Sciences of the United States of America*, **2013**, 110, 19664-5	11.5	2
9	Metabolic remodeling maintains a reducing environment for rapid activation of the yeast DNA replication checkpoint.. *EMBO Journal*, **2022**, e108290	13	2
8	G2G: A web-server for the prediction of human synthetic lethal interactions. *Computational and Structural Biotechnology Journal*, **2020**, 18, 1028-1031	6.8	1
7	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	6	1
6	Histones on fire: the effect of Dun1 and Mrc1 on origin firing and replication of hyper-acetylated genomes. *Current Genetics*, **2021**, 67, 501-510	2.9	1
5	Noise buffering by biomolecular condensates in glucose sensing. *Current Opinion in Cell Biology*, **2021**, 69, 1-6	9	1
4	The Amazing Acrobat: YeastSs Histone H3K56 Juggles Several Important Roles While Maintaining Perfect Balance. *Genes*, **2021**, 12,	4.2	1

LIST OF PUBLICATIONS

3	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	6	0
2	A New Method, "Reverse Yeast Two-Hybrid Array" (RYTHA), Identifies Mutants that Dissociate the Physical Interaction Between Elg1 and Slx5. *Genetics*, **2017**, 206, 1683-1697	4	
1	DSB repair: the yeast paradigm. *DNA Repair*, **2004**, 3, 797-797	4.3	