

# Martin Kupiec

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

128  
papers

4,709  
citations

37  
h-index

64  
g-index

136  
ext. papers

5,570  
ext. citations

8.6  
avg, IF

5.69  
L-index

#	Paper	IF	Citations
128	Metabolic remodeling maintains a reducing environment for rapid activation of the yeast DNA replication checkpoint.. <i>EMBO Journal</i> , <b>2022</b> , e108290	13	2
127	TOR complex 2 contributes to regulation of gene expression via inhibiting Gcn5 recruitment to subtelomeric and DNA replication stress genes.. <i>PLoS Genetics</i> , <b>2022</b> , 18, e1010061	6	0
126	Histones on fire: the effect of Dun1 and Mrc1 on origin firing and replication of hyper-acetylated genomes. <i>Current Genetics</i> , <b>2021</b> , 67, 501-510	2.9	1
125	Noise buffering by biomolecular condensates in glucose sensing. <i>Current Opinion in Cell Biology</i> , <b>2021</b> , 69, 1-6	9	1
124	DNA damage bypass pathways and their effect on mutagenesis in yeast. <i>FEMS Microbiology Reviews</i> , <b>2021</b> , 45,	15.1	4
123	The Amazing Acrobat: Yeast's Histone H3K56 Juggles Several Important Roles While Maintaining Perfect Balance. <i>Genes</i> , <b>2021</b> , 12,	4.2	1
122	A novel role for Dun1 in the regulation of origin firing upon hyper-acetylation of H3K56. <i>PLoS Genetics</i> , <b>2021</b> , 17, e1009391	6	3
121	Access to PCNA by Srs2 and Elg1 Controls the Choice between Alternative Repair Pathways in <i>Saccharomyces cerevisiae</i> . <i>MBio</i> , <b>2020</b> , 11,	7.8	9
120	How yeast cells deal with stalled replication forks. <i>Current Genetics</i> , <b>2020</b> , 66, 911-915	2.9	5
119	G2G: A web-server for the prediction of human synthetic lethal interactions. <i>Computational and Structural Biotechnology Journal</i> , <b>2020</b> , 18, 1028-1031	6.8	1
118	TOR Complex 2- independent mutations in the regulatory PIF pocket of Gad8AKT1/SGK1 define separate branches of the stress response mechanisms in fission yeast. <i>PLoS Genetics</i> , <b>2020</b> , 16, e1009196	6	1
117	Telomeres and stress in yeast cells: When genes and environment interact. <i>Fungal Biology</i> , <b>2020</b> , 124, 311-315	2.8	3
116	A role for the yeast PCNA unloader Elg1 in eliciting the DNA damage checkpoint. <i>Current Genetics</i> , <b>2020</b> , 66, 79-84	2.9	6
115	Genome architecture and stability in the <i>Saccharomyces cerevisiae</i> knockout collection. <i>Nature</i> , <b>2019</b> , 573, 416-420	50.4	24
114	Carbon catabolite repression: not only for glucose. <i>Current Genetics</i> , <b>2019</b> , 65, 1321-1323	2.9	6
113	The Yeast PCNA Unloader Elg1 RFC-Like Complex Plays a Role in Eliciting the DNA Damage Checkpoint. <i>MBio</i> , <b>2019</b> , 10,	7.8	7
112	Carbon Catabolite Repression in Yeast is Not Limited to Glucose. <i>Scientific Reports</i> , <b>2019</b> , 9, 6491	4.9	22

111	Comparative Analysis of Normalization Methods for Network Propagation. <i>Frontiers in Genetics</i> , <b>2019</b> , 10, 4	4.5	8
110	The cytosolic form of aspartate aminotransferase is required for full activation of TOR complex 1 in fission yeast. <i>Journal of Biological Chemistry</i> , <b>2019</b> , 294, 18244-18255	5.4	4
109	WebPropagate: A Web Server for Network Propagation. <i>Journal of Molecular Biology</i> , <b>2018</b> , 430, 2231-2236	2.3	3
108	Spontaneous Changes in Ploidy Are Common in Yeast. <i>Current Biology</i> , <b>2018</b> , 28, 825-835.e4	6.3	35
107	Pivotal roles of PCNA loading and unloading in heterochromatin function. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2018</b> , 115, E2030-E2039	11.5	20
106	Rnr1's role in telomere elongation cannot be replaced by Rnr3: a role beyond dNTPs?. <i>Current Genetics</i> , <b>2018</b> , 64, 547-550	2.9	7
105	A reversible liquid drop aggregation controls glucose response in yeast. <i>Current Genetics</i> , <b>2018</b> , 64, 785-788	2.9	15
104	Tight Regulation of Srs2 Helicase Activity Is Crucial for Proper Functioning of DNA Repair Mechanisms. <i>G3: Genes, Genomes, Genetics</i> , <b>2018</b> , 8, 1615-1626	3.2	8
103	Frequent ploidy changes in growing yeast cultures. <i>Current Genetics</i> , <b>2018</b> , 64, 1001-1004	2.9	23
102	Do long telomeres affect cellular fitness?. <i>Current Genetics</i> , <b>2018</b> , 64, 173-176	2.9	10
101	The Main Role of Srs2 in DNA Repair Depends on Its Helicase Activity, Rather than on Its Interactions with PCNA or Rad51. <i>MBio</i> , <b>2018</b> , 9,	7.8	6
100	The extent of ribosome queuing in budding yeast. <i>PLoS Computational Biology</i> , <b>2018</b> , 14, e1005951	5	40
99	The evolutionarily conserved factor Sus1/ENY2 plays a role in telomere length maintenance. <i>Current Genetics</i> , <b>2018</b> , 64, 635-644	2.9	4
98	Mec1 is needed for extensive telomere elongation in response to ethanol in yeast. <i>Current Genetics</i> , <b>2018</b> , 64, 223-234	2.9	9
97	TOR complex 2 in fission yeast is required for chromatin-mediated gene silencing and assembly of heterochromatic domains at subtelomeres. <i>Journal of Biological Chemistry</i> , <b>2018</b> , 293, 8138-8150	5.4	15
96	Ubiquitylation-dependent oligomerization regulates activity of Nedd4 ligases. <i>EMBO Journal</i> , <b>2017</b> , 36, 425-440	13	37
95	A structure-function analysis of the yeast Elg1 protein reveals the importance of PCNA unloading in genome stability maintenance. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, 3189-3203	20.1	18
94	A New Method, "Reverse Yeast Two-Hybrid Array" (RYTHA), Identifies Mutants that Dissociate the Physical Interaction Between Elg1 and Slx5. <i>Genetics</i> , <b>2017</b> , 206, 1683-1697	4	

93	Long Telomeres Do Not Affect Cellular Fitness in Yeast. <i>MBio</i> , <b>2017</b> , 8,	7.8	6
92	The Std1 Activator of the Snf1/AMPK Kinase Controls Glucose Response in Yeast by a Regulated Protein Aggregation. <i>Molecular Cell</i> , <b>2017</b> , 68, 1120-1133.e3	17.6	26
91	GLADIATOR: a global approach for elucidating disease modules. <i>Genome Medicine</i> , <b>2017</b> , 9, 48	14.4	10
90	Rnr1, but not Rnr3, facilitates the sustained telomerase-dependent elongation of telomeres. <i>PLoS Genetics</i> , <b>2017</b> , 13, e1007082	6	12
89	Utilizing yeast chemogenomic profiles for the prediction of pharmacogenomic associations in humans. <i>Scientific Reports</i> , <b>2016</b> , 6, 23703	4.9	3
88	Gad8 Protein Is Found in the Nucleus Where It Interacts with the Mlul Cell Cycle Box-binding Factor (MBF) Transcriptional Complex to Regulate the Response to DNA Replication Stress. <i>Journal of Biological Chemistry</i> , <b>2016</b> , 291, 9371-81	5.4	18
87	Systematic identification and correction of annotation errors in the genetic interaction map of <i>Saccharomyces cerevisiae</i> . <i>Nucleic Acids Research</i> , <b>2016</b> , 44, e50	20.1	11
86	Mixed Integer Linear Programming based machine learning approach identifies regulators of telomerase in yeast. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, e93	20.1	8
85	Role of the ESCRT Complexes in Telomere Biology. <i>MBio</i> , <b>2016</b> , 7,	7.8	8
84	Alternative clamp loaders/unloaders. <i>FEMS Yeast Research</i> , <b>2016</b> , 16,	3.1	7
83	Elg1, a central player in genome stability. <i>Mutation Research - Reviews in Mutation Research</i> , <b>2015</b> , 763, 267-79	7	12
82	Cross-Talk between Carbon Metabolism and the DNA Damage Response in <i>S. cerevisiae</i> . <i>Cell Reports</i> , <b>2015</b> , 12, 1865-75	10.6	25
81	Regulation of Elg1 activity by phosphorylation. <i>Cell Cycle</i> , <b>2015</b> , 14, 3689-97	4.7	10
80	TORC1 Regulates Developmental Responses to Nitrogen Stress via Regulation of the GATA Transcription Factor Gaf1. <i>MBio</i> , <b>2015</b> , 6, e00959	7.8	22
79	Biology of telomeres: lessons from budding yeast. <i>FEMS Microbiology Reviews</i> , <b>2014</b> , 38, 144-71	15.1	62
78	A method for predicting protein-protein interaction types. <i>PLoS ONE</i> , <b>2014</b> , 9, e90904	3.7	12
77	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. <i>Journal of Biological Chemistry</i> , <b>2014</b> , 289, 21727-37	5.4	29
76	Glycan degradation (GlyDeR) analysis predicts mammalian gut microbiota abundance and host diet-specific adaptations. <i>MBio</i> , <b>2014</b> , 5,	7.8	27

75	Isp7 Is a Novel Regulator of Amino Acid Uptake in the TOR Signaling Pathway. <i>Molecular and Cellular Biology</i> , <b>2014</b> , 34, 1535-1535	4.8	78
74	Telomere length kinetics assay (TELKA) sorts the telomere length maintenance (tlm) mutants into functional groups. <i>Nucleic Acids Research</i> , <b>2014</b> , 42, 6314-25	20.1	10
73	A high-throughput chemical screen with FDA approved drugs reveals that the antihypertensive drug Spironolactone impairs cancer cell survival by inhibiting homology directed repair. <i>Nucleic Acids Research</i> , <b>2014</b> , 42, 5689-701	20.1	28
72	Genome-wide studies of telomere biology in budding yeast. <i>Microbial Cell</i> , <b>2014</b> , 1, 70-80	3.9	4
71	Genomic instability and repair mediated by common repeated sequences. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2013</b> , 110, 19664-5	11.5	2
70	Effect of nuclear architecture on the efficiency of double-strand break repair. <i>Nature Cell Biology</i> , <b>2013</b> , 15, 694-9	23.4	88
69	Environmental stresses disrupt telomere length homeostasis. <i>PLoS Genetics</i> , <b>2013</b> , 9, e1003721	6	70
68	Nature vs nurture: interplay between the genetic control of telomere length and environmental factors. <i>Cell Cycle</i> , <b>2013</b> , 12, 3465-70	4.7	15
67	TORC2 is required to maintain genome stability during S phase in fission yeast. <i>Journal of Biological Chemistry</i> , <b>2013</b> , 288, 19649-60	5.4	21
66	Genetic and physical interactions between the yeast ELG1 gene and orthologs of the Fanconi anemia pathway. <i>Cell Cycle</i> , <b>2013</b> , 12, 1625-36	4.7	12
65	A genetic screen for high copy number suppressors of the synthetic lethality between <i>elg1Δ</i> and <i>srs2Δ</i> in yeast. <i>G3: Genes, Genomes, Genetics</i> , <b>2013</b> , 3, 917-26	3.2	8
64	Systematic identification of gene annotation errors in the widely used yeast mutation collections. <i>Nature Methods</i> , <b>2012</b> , 9, 373-8	21.6	58
63	The importance of being modified: PCNA modification and DNA damage response. <i>Cell Cycle</i> , <b>2012</b> , 11, 2620-3	4.7	17
62	TOR links starvation responses to telomere length maintenance. <i>Cell Cycle</i> , <b>2012</b> , 11, 2268-71	4.7	10
61	Chromosomal duplication is a transient evolutionary solution to stress. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2012</b> , 109, 21010-5	11.5	232
60	The Rad1-Rad10 nuclease promotes chromosome translocations between dispersed repeats. <i>Nature Structural and Molecular Biology</i> , <b>2012</b> , 19, 964-71	17.6	33
59	Composite effects of gene determinants on the translation speed and density of ribosomes. <i>Genome Biology</i> , <b>2011</b> , 12, R110	18.3	151
58	Tor complex 1 controls telomere length by affecting the level of Ku. <i>Current Biology</i> , <b>2011</b> , 21, 2115-20	6.3	26

57	The role of Holliday junction resolvases in the repair of spontaneous and induced DNA damage. <i>Nucleic Acids Research</i> , <b>2011</b> , 39, 7009-19	20.1	37
56	Roles of RSC, Rad59, and cohesin in double-strand break repair. <i>Molecular and Cellular Biology</i> , <b>2011</b> , 31, 3921-3	4.8	5
55	Elg1, the major subunit of an alternative RFC complex, interacts with SUMO-processing proteins. <i>Cell Cycle</i> , <b>2011</b> , 10, 2894-903	4.7	22
54	An anti-checkpoint activity for rif1. <i>PLoS Genetics</i> , <b>2011</b> , 7, e1002421	6	4
53	Elg1, an alternative subunit of the RFC clamp loader, preferentially interacts with SUMOylated PCNA. <i>EMBO Journal</i> , <b>2010</b> , 29, 2611-22	13	76
52	Proteasome nuclear activity affects chromosome stability by controlling the turnover of Mms22, a protein important for DNA repair. <i>PLoS Genetics</i> , <b>2010</b> , 6, e1000852	6	42
51	The ELG1 clamp loader plays a role in sister chromatid cohesion. <i>PLoS ONE</i> , <b>2009</b> , 4, e5497	3.7	48
50	Higher-order genomic organization of cellular functions in yeast. <i>Journal of Computational Biology</i> , <b>2009</b> , 16, 303-16	1.7	8
49	Toward accurate reconstruction of functional protein networks. <i>Molecular Systems Biology</i> , <b>2009</b> , 5, 248	12.2	80
48	A genome-wide screen for essential yeast genes that affect telomere length maintenance. <i>Nucleic Acids Research</i> , <b>2009</b> , 37, 3840-9	20.1	63
47	A complex-centric view of protein network evolution. <i>Nucleic Acids Research</i> , <b>2009</b> , 37, e88	20.1	23
46	Developmentally regulated MAPK pathways modulate heterochromatin in <i>Saccharomyces cerevisiae</i> . <i>Nucleic Acids Research</i> , <b>2009</b> , 37, 4839-49	20.1	8
45	TOR complex 2 controls gene silencing, telomere length maintenance, and survival under DNA-damaging conditions. <i>Molecular and Cellular Biology</i> , <b>2009</b> , 29, 4584-94	4.8	49
44	Analysis of repair mechanism choice during homologous recombination. <i>Nucleic Acids Research</i> , <b>2009</b> , 37, 5081-92	20.1	47
43	Adaptive prediction of environmental changes by microorganisms. <i>Nature</i> , <b>2009</b> , 460, 220-4	50.4	371
42	Finding a match: how do homologous sequences get together for recombination?. <i>Nature Reviews Genetics</i> , <b>2008</b> , 9, 27-37	30.1	137
41	A systems-level approach to mapping the telomere length maintenance gene circuitry. <i>Molecular Systems Biology</i> , <b>2008</b> , 4, 172	12.2	45
40	From E-MAPs to module maps: dissecting quantitative genetic interactions using physical interactions. <i>Molecular Systems Biology</i> , <b>2008</b> , 4, 209	12.2	59

39	A role for the yeast cell cycle/splicing factor Cdc40 in the G1/S transition. <i>Current Genetics</i> , <b>2007</b> , 51, 123-40	2.9	16
38	Genetic interactions in yeast: is robustness going bust?. <i>Molecular Systems Biology</i> , <b>2007</b> , 3, 97	12.2	6
37	The Elg1 replication factor C-like complex: a novel guardian of genome stability. <i>DNA Repair</i> , <b>2005</b> , 4, 409-17	4.3	38
36	Evidence for abundant transcription of non-coding regions in the <i>Saccharomyces cerevisiae</i> genome. <i>BMC Genomics</i> , <b>2005</b> , 6, 93	4.5	19
35	The yeast VPS genes affect telomere length regulation. <i>Current Genetics</i> , <b>2005</b> , 47, 18-28	2.9	36
34	The <i>Saccharomyces cerevisiae</i> gene CDC40/PRP17 controls cell cycle progression through splicing of the ANC1 gene. <i>Nucleic Acids Research</i> , <b>2004</b> , 32, 2529-40	20.1	33
33	A genome-wide screen for <i>Saccharomyces cerevisiae</i> deletion mutants that affect telomere length. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2004</b> , 101, 8658-63	11.5	268
32	The CDK regulates repair of double-strand breaks by homologous recombination during the cell cycle. <i>EMBO Journal</i> , <b>2004</b> , 23, 4868-75	13	303
31	DSB repair: the yeast paradigm. <i>DNA Repair</i> , <b>2004</b> , 3, 797-797	4.3	
30	DSB repair: the yeast paradigm. <i>DNA Repair</i> , <b>2004</b> , 3, 797-815	4.3	129
29	The compact chromatin structure of a Ty repeated sequence suppresses recombination hotspot activity in <i>Saccharomyces cerevisiae</i> . <i>Molecular Cell</i> , <b>2004</b> , 15, 221-31	17.6	40
28	New insights into the mechanism of homologous recombination in yeast. <i>Mutation Research - Reviews in Mutation Research</i> , <b>2004</b> , 566, 231-48	7	62
27	ELG1, a yeast gene required for genome stability, forms a complex related to replication factor C. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2003</b> , 100, 9906-11	11.5	109
26	Pitfalls of the synthetic lethality screen in <i>Saccharomyces cerevisiae</i> : an improved design. <i>Current Genetics</i> , <b>2003</b> , 43, 62-9	2.9	19
25	Molecular dissection of mitotic recombination in the yeast <i>Saccharomyces cerevisiae</i> . <i>Molecular and Cellular Biology</i> , <b>2003</b> , 23, 1403-17	4.8	99
24	The checkpoint protein Rad24 of <i>Saccharomyces cerevisiae</i> is involved in processing double-strand break ends and in recombination partner choice. <i>Molecular and Cellular Biology</i> , <b>2003</b> , 23, 6585-96	4.8	54
23	Control of meiotic recombination initiation: a role for the environment?. <i>Current Genetics</i> , <b>2002</b> , 42, 129-39		28
22	Mutations in genes of <i>Saccharomyces cerevisiae</i> encoding pre-mRNA splicing factors cause cell cycle arrest through activation of the spindle checkpoint. <i>Nucleic Acids Research</i> , <b>2002</b> , 30, 4361-70	20.1	40

21	Deletion of the SRS2 gene suppresses elevated recombination and DNA damage sensitivity in rad5 and rad18 mutants of <i>Saccharomyces cerevisiae</i> . <i>Mutation Research DNA Repair</i> , <b>2001</b> , 486, 137-46		53
20	Recombination between divergent sequences leads to cell death in a mismatch-repair-independent manner. <i>Current Genetics</i> , <b>2000</b> , 38, 23-32	2.9	12
19	Functional analyses of interacting factors involved in both pre-mRNA splicing and cell cycle progression in <i>Saccharomyces cerevisiae</i> . <i>Rna</i> , <b>2000</b> , 6, 1565-72	5.8	48
18	The relationship between homology length and crossing over during the repair of a broken chromosome. <i>Journal of Biological Chemistry</i> , <b>2000</b> , 275, 30833-8	5.4	55
17	Extensive genetic interactions between PRP8 and PRP17/CDC40, two yeast genes involved in pre-mRNA splicing and cell cycle progression. <i>Genetics</i> , <b>2000</b> , 154, 61-71	4	36
16	Genetic and physical interactions between factors involved in both cell cycle progression and pre-mRNA splicing in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , <b>2000</b> , 156, 1503-17	4	96
15	The identification and characterization of a novel splicing protein, Isy1p, of <i>Saccharomyces cerevisiae</i> . <i>Rna</i> , <b>1999</b> , 5, 360-8	5.8	35
14	Characterization of the role played by the RAD59 gene of <i>Saccharomyces cerevisiae</i> in ectopic recombination. <i>Current Genetics</i> , <b>1999</b> , 36, 13-20	2.9	33
13	Homology search and choice of homologous partner during mitotic recombination. <i>Molecular and Cellular Biology</i> , <b>1999</b> , 19, 4134-42	4.8	79
12	Genetic interactions between mutants of the Error-prone repair group of <i>Saccharomyces cerevisiae</i> and their effect on recombination and mutagenesis. <i>Mutation Research DNA Repair</i> , <b>1998</b> , 407, 135-45		72
11	Identification and functional analysis of hPRP17, the human homologue of the PRP17/CDC40 yeast gene involved in splicing and cell cycle control. <i>Rna</i> , <b>1998</b> , 4, 1304-12	5.8	35
10	Damage-induced ectopic recombination in the yeast <i>Saccharomyces cerevisiae</i> . <i>Mutation Research DNA Repair</i> , <b>1997</b> , 384, 33-44		12
9	The role of <i>Saccharomyces cerevisiae</i> Cdc40p in DNA replication and mitotic spindle formation and/or maintenance. <i>Molecular Genetics and Genomics</i> , <b>1995</b> , 247, 123-36		41
8	Donation of information to the unbroken chromosome in double-strand break repair. <i>Current Genetics</i> , <b>1993</b> , 23, 414-22	2.9	13
7	Effect of donor copy number on the rate of gene conversion in the yeast <i>Saccharomyces cerevisiae</i> . <i>Molecular Genetics and Genomics</i> , <b>1992</b> , 235, 97-103		14
6	The RAD50 gene of <i>Saccharomyces cerevisiae</i> is not essential for vegetative growth. <i>Current Genetics</i> , <b>1986</b> , 10, 487-9	2.9	5
5	Regulation of the RAD6 gene of <i>Saccharomyces cerevisiae</i> in the mitotic cell cycle and in meiosis. <i>Molecular Genetics and Genomics</i> , <b>1986</b> , 203, 538-43		29
4	DNA-repair characterization of cdc40-1, a cell-cycle mutant of <i>Saccharomyces cerevisiae</i> . <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , <b>1986</b> , 162, 33-40	3.3	12



3	Cloning and mapping of CDC40, a <i>Saccharomyces cerevisiae</i> gene with a role in DNA repair. <i>Current Genetics</i> , <b>1985</b> , 9, 253-7	2.9	27
2	Arrest of the mitotic cell cycle and of meiosis in <i>Saccharomyces cerevisiae</i> by MMS. <i>Molecular Genetics and Genomics</i> , <b>1985</b> , 201, 558-564		21
1	Cloning and mapping of the RAD50 gene of <i>Saccharomyces cerevisiae</i> . <i>Molecular Genetics and Genomics</i> , <b>1984</b> , 193, 525-31		21