Philip Hieter

List of Publications by Year
in descending order

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67 papers	10,706 citations	87888 38 h-index	106344 65 g-index
68 all docs	68 docs citations	68 times ranked	12415 citing authors

#	Article	IF	Citations
1	Designer deletion strains derived fromSaccharomyces cerevisiae S288C: A useful set of strains and plasmids for PCR-mediated gene disruption and other applications. Yeast, 1998, 14, 115-132.	1.7	3,028
2	Multifunctional yeast high-copy-number shuttle vectors. Gene, 1992, 110, 119-122.	2.2	1,658
3	Synthetic lethality and cancer. Nature Reviews Genetics, 2017, 18, 613-623.	16.3	444
4	TEL1, an S. cerevisiae homolog of the human gene mutated in ataxia telangiectasia, is functionally related to the yeast checkpoint gene MEC1. Cell, 1995, 82, 831-840.	28.9	372
5	Chromatid cohesion defects may underlie chromosome instability in human colorectal cancers. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 3443-3448.	7.1	361
6	Identification of RFC(Ctf18p, Ctf8p, Dcc1p). Molecular Cell, 2001, 7, 959-970.	9.7	308
7	International Cooperation to Enable the Diagnosis of All Rare Genetic Diseases. American Journal of Human Genetics, 2017, 100, 695-705.	6.2	305
8	A Robust Toolkit for Functional Profiling of the Yeast Genome. Molecular Cell, 2004, 16, 487-496.	9.7	295
9	Identification of a Cullin Homology Region in a Subunit of the Anaphase-Promoting Complex. Science, 1998, 279, 1219-1222.	12.6	234
10	Identification of Protein Complexes Required for Efficient Sister Chromatid Cohesion. Molecular Biology of the Cell, 2004, 15, 1736-1745.	2.1	221
11	Identification of essential components of the S. cerevisiae kinetochore. Cell, 1993, 73, 761-774.	28.9	215
12	R-loop-mediated genome instability in mRNA cleavage and polyadenylation mutants. Genes and Development, 2012, 26, 163-175.	5.9	195
13	Toward a Comprehensive Temperature-Sensitive Mutant Repository of the Essential Genes of Saccharomyces cerevisiae. Molecular Cell, 2008, 30, 248-258.	9.7	189
14	Genome-Wide Profiling of Yeast DNA:RNA Hybrid Prone Sites with DRIP-Chip. PLoS Genetics, 2014, 10, e1004288.	3.5	189
15	The APC11 RING-H2 Finger Mediates E2-Dependent Ubiquitination. Molecular Biology of the Cell, 2000, 11, 2315-2325.	2.1	167
16	Model Organisms Facilitate Rare Disease Diagnosis and Therapeutic Research. Genetics, 2017, 207, 9-27.	2.9	165
17	The Complete Spectrum of Yeast Chromosome Instability Genes Identifies Candidate CIN Cancer Genes and Functional Roles for ASTRA Complex Components. PLoS Genetics, 2011, 7, e1002057.	3.5	156
18	Establishing Genetic Interactions by a Synthetic Dosage Lethality Phenotype. Genetics, 1996, 143, 95-102.	2.9	144

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19	Specific synthetic lethal killing of RAD54B-deficient human colorectal cancer cells by FEN1 silencing. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 3276-3281.	7.1	118
20	KINETOCHORES AND THE CHECKPOINT MECHANISM THAT MONITORS FOR DEFECTS IN THE CHROMOSOME SEGREGATION MACHINERY. Annual Review of Genetics, 1998, 32, 307-337.	7.6	112
21	Ctf3p, the Mis6 budding yeast homolog, interacts with Mcm22p and Mcm16p at the yeast outer kinetochore. Genes and Development, 2002, 16, 101-113.	5.9	111
22	Ctf19p: A Novel Kinetochore Protein in Saccharomyces cerevisiae and a Potential Link between the Kinetochore and Mitotic Spindle. Journal of Cell Biology, 1999, 145, 15-28.	5.2	109
23	The kinetochore and cancer: what's the connection?. Current Opinion in Cell Biology, 2005, 17, 576-582.	5.4	106
24	Genome cross-referencing and XREFdb: Implications for the identification and analysis of genes mutated in human disease. Nature Genetics, 1997, 15, 339-344.	21.4	82
25	Mechanisms of genome instability induced by RNA-processing defects. Trends in Genetics, 2014, 30, 245-253.	6.7	77
26	Complementation of Yeast Genes with Human Genes as an Experimental Platform for Functional Testing of Human Genetic Variants. Genetics, 2015, 201, 1263-1274.	2.9	77
27	An Evolutionarily Conserved Synthetic Lethal Interaction Network Identifies FEN1 as a Broad-Spectrum Target for Anticancer Therapeutic Development. PLoS Genetics, 2013, 9, e1003254.	3.5	76
28	[22] Visual assay for chromosome ploidy. Methods in Enzymology, 1987, 155, 351-372.	1.0	68
29	Overexpression of B-type cyclins alters chromosomal segregation. Oncogene, 2002, 21, 2051-2057.	5.9	67
30	Overexpression screens identify conserved dosage chromosome instability genes in yeast and human cancer. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 9967-9976.	7.1	67
31	Glioblastoma Cells Containing Mutations in the Cohesin Component STAG2 Are Sensitive to PARP Inhibition. Molecular Cancer Therapeutics, 2014, 13, 724-732.	4.1	65
32	Synthetic Lethality of Cohesins with PARPs and Replication Fork Mediators. PLoS Genetics, 2012, 8, e1002574.	3.5	63
33	[54] Analysis of chromosome segregation in Saccharomyces cerevisiae. Methods in Enzymology, 1991, 194, 749-773.	1.0	58
34	Trans-kingdom promiscuity. Nature, 1990, 345, 581-582.	27.8	49
35	Proteasome Nuclear Activity Affects Chromosome Stability by Controlling the Turnover of Mms22, a Protein Important for DNA Repair. PLoS Genetics, 2010, 6, e1000852.	3.5	49
36	Novel Role for a Saccharomyces cerevisiae Nucleoporin, Nup170p, in Chromosome Segregation. Genetics, 2001, 157, 1543-1553.	2.9	48

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37	Canonical DNA Repair Pathways Influence R-Loop-Driven Genome Instability. Journal of Molecular Biology, 2017, 429, 3132-3138.	4.2	47
38	Biogenesis of RNA Polymerases II and III Requires the Conserved GPN Small GTPases in Saccharomyces cerevisiae. Genetics, 2013, 193, 853-864.	2.9	45
39	Recombinational repair of diverged DNAs : a study of homoeologous chromosomes and mammalian YACs in yeast. Molecular Genetics and Genomics, 1992, 234, 65-73.	2.4	41
40	Synthetic dosage lethality. Methods in Enzymology, 2002, 350, 316-326.	1.0	41
41	Protein networksâ€"built by association. Nature Biotechnology, 2000, 18, 1242-1243.	17.5	38
42	An Updated Collection of Sequence Barcoded Temperature-Sensitive Alleles of Yeast Essential Genes. G3: Genes, Genomes, Genetics, 2015, 5, 1879-1887.	1.8	38
43	Expanding family. Nature, 1990, 346, 114-114.	27.8	37
44	The yeast genome â€" a common currency. Nature Genetics, 1996, 13, 253-255.	21.4	37
45	Saccharomyces cerevisiaeGenetics Predicts Candidate Therapeutic Genetic Interactions at the Mammalian Replication Fork. G3: Genes, Genomes, Genetics, 2013, 3, 273-282.	1.8	34
46	Synthetic lethality and cancer: cohesin and PARP at the replication fork. Trends in Genetics, 2013, 29, 290-297.	6.7	31
47	Synthetic Lethal Genetic Interactions That Decrease Somatic Cell Proliferation in Caenorhabditis elegans Identify the Alternative RFC^{CTF18}as a Candidate Cancer Drug Target. Molecular Biology of the Cell, 2009, 20, 5306-5313.	2.1	30
48	The Canadian Rare Diseases Models and Mechanisms (RDMM) Network: Connecting Understudied Genes to Model Organisms. American Journal of Human Genetics, 2020, 106, 143-152.	6.2	30
49	Accumulation of mRNA Coding for the Ctf13p Kinetochore Subunit of Saccharomyces cerevisiae Depends on the Same Factors That Promote Rapid Decay of Nonsense mRNAs. Genetics, 1998, 150, 1019-1035.	2.9	27
50	Genome Destabilizing Mutator Alleles Drive Specific Mutational Trajectories inSaccharomyces cerevisiae. Genetics, 2014, 196, 403-412.	2.9	22
51	Alu sequences in RMSA-1 protein?. Nature, 1994, 370, 106-106.	27.8	17
52	Mutability and mutational spectrum of chromosome transmission fidelity genes. Chromosoma, 2012, 121, 263-275.	2.2	17
53	Dependence of Human Colorectal Cells Lacking the FBW7 Tumor Suppressor on the Spindle Assembly Checkpoint. Genetics, 2015, 201, 885-895.	2.9	17
54	Designer deletion strains derived from Saccharomyces cerevisiae S288C: A useful set of strains and plasmids for PCR-mediated gene disruption and other applications. , 1998, 14, 115.		17

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55	Dosage Mutator Genes in Saccharomyces cerevisiae: A Novel Mutator Mode-of-Action of the Mph1 DNA Helicase. Genetics, 2016, 204, 975-986.	2.9	14
56	Cross-Species Complementation of Nonessential Yeast Genes Establishes Platforms for Testing Inhibitors of Human Proteins. Genetics, 2020, 214, 735-747.	2.9	14
57	Synthetic Cytotoxicity: Digenic Interactions with TEL1/ATM Mutations Reveal Sensitivity to Low Doses of Camptothecin. Genetics, 2014, 197, 611-623.	2.9	11
58	Paralogous synthetic lethality underlies genetic dependencies of the cancer-mutated gene STAG2. Life Science Alliance, 2021, 4, e202101083.	2.8	10
59	A Multimodal Genotoxic Anticancer Drug Characterized by Pharmacogenetic Analysis in Caenorhabditis elegans. Genetics, 2020, 215, 609-621.	2.9	9
60	In Vivo Characterization of the Nonessential Budding Yeast Anaphase-Promoting Complex/Cyclosome Components Swm1p, Mnd2p and Apc9p. Genetics, 2005, 170, 1045-1062.	2.9	8
61	Understanding Rare Disease Pathogenesis: A Grand Challenge for Model Organisms. Genetics, 2014, 198, 443-445.	2.9	8
62	What do yeast proteins do?. Nature, 1999, 402, 362-363.	27.8	5
63	ModelMatcher: A scientistâ€centric online platform to facilitate collaborations between stakeholders of rare and undiagnosed disease research. Human Mutation, 2022, , .	2.5	5
64	The Chromosome Transmission Fidelity Assay for Measuring Chromosome Loss in Yeast. Methods in Molecular Biology, 2018, 1672, 11-19.	0.9	4
65	Modeling DNA trapping of anticancer therapeutic targets using missense mutations identifies dominant synthetic lethal interactions. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, e2100240118.	7.1	3
66	The yeast genome and clinical genetics. Clinical Genetics, 1998, 54, 113-116.	2.0	1
67	Mapping Synthetic Dosage Lethal Genetic Interactions in Saccharomyces cerevisiae. Methods in Molecular Biology, 2021, 2381, 39-56.	0.9	0