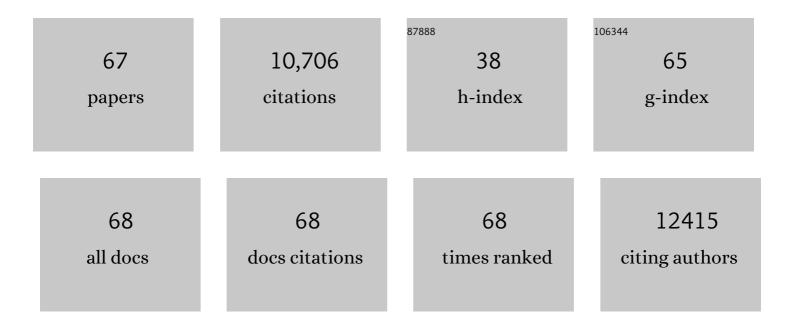
List of Publications by Year in descending order

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DHILID HIFTED

#	Article	IF	CITATIONS
1	ModelMatcher: A scientistâ€centric online platform to facilitate collaborations between stakeholders of rare and undiagnosed disease research. Human Mutation, 2022, , .	2.5	5
2	Mapping Synthetic Dosage Lethal Genetic Interactions in Saccharomyces cerevisiae. Methods in Molecular Biology, 2021, 2381, 39-56.	0.9	0
3	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
4	Paralogous synthetic lethality underlies genetic dependencies of the cancer-mutated gene <i>STAG2</i> . Life Science Alliance, 2021, 4, e202101083.	2.8	10
5	A Multimodal Genotoxic Anticancer Drug Characterized by Pharmacogenetic Analysis in <i>Caenorhabditis elegans</i> . Genetics, 2020, 215, 609-621.	2.9	9
6	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
7	Cross-Species Complementation of Nonessential Yeast Genes Establishes Platforms for Testing Inhibitors of Human Proteins. Genetics, 2020, 214, 735-747.	2.9	14
8	The Chromosome Transmission Fidelity Assay for Measuring Chromosome Loss in Yeast. Methods in Molecular Biology, 2018, 1672, 11-19.	0.9	4
9	International Cooperation to Enable the Diagnosis of All Rare Genetic Diseases. American Journal of Human Genetics, 2017, 100, 695-705.	6.2	305
10	Model Organisms Facilitate Rare Disease Diagnosis and Therapeutic Research. Genetics, 2017, 207, 9-27.	2.9	165
11	Synthetic lethality and cancer. Nature Reviews Genetics, 2017, 18, 613-623.	16.3	444
12	Canonical DNA Repair Pathways Influence R-Loop-Driven Genome Instability. Journal of Molecular Biology, 2017, 429, 3132-3138.	4.2	47
13	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
14	Dosage Mutator Genes in <i>Saccharomyces cerevisiae</i> : A Novel Mutator Mode-of-Action of the Mph1 DNA Helicase. Genetics, 2016, 204, 975-986.	2.9	14
15	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
16	An Updated Collection of Sequence Barcoded Temperature-Sensitive Alleles of Yeast Essential Genes. G3: Genes, Genomes, Genetics, 2015, 5, 1879-1887.	1.8	38
17	Dependence of Human Colorectal Cells Lacking the FBW7 Tumor Suppressor on the Spindle Assembly Checkpoint. Genetics, 2015, 201, 885-895.	2.9	17
18	Genome-Wide Profiling of Yeast DNA:RNA Hybrid Prone Sites with DRIP-Chip. PLoS Genetics, 2014, 10, e1004288.	3.5	189

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19	Synthetic Cytotoxicity: Digenic Interactions with TEL1/ATM Mutations Reveal Sensitivity to Low Doses of Camptothecin. Genetics, 2014, 197, 611-623.	2.9	11
20	Genome Destabilizing Mutator Alleles Drive Specific Mutational Trajectories in <i>Saccharomyces cerevisiae</i> . Genetics, 2014, 196, 403-412.	2.9	22
21	Glioblastoma Cells Containing Mutations in the Cohesin Component <i>STAG2</i> Are Sensitive to PARP Inhibition. Molecular Cancer Therapeutics, 2014, 13, 724-732.	4.1	65
22	Understanding Rare Disease Pathogenesis: A Grand Challenge for Model Organisms. Genetics, 2014, 198, 443-445.	2.9	8
23	Mechanisms of genome instability induced by RNA-processing defects. Trends in Genetics, 2014, 30, 245-253.	6.7	77
24	Synthetic lethality and cancer: cohesin and PARP at the replication fork. Trends in Genetics, 2013, 29, 290-297.	6.7	31
25	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
26	Biogenesis of RNA Polymerases II and III Requires the Conserved GPN Small GTPases in <i>Saccharomyces cerevisiae</i> . Genetics, 2013, 193, 853-864.	2.9	45
27	<i>Saccharomyces cerevisiae</i> Genetics Predicts Candidate Therapeutic Genetic Interactions at the Mammalian Replication Fork. G3: Genes, Genomes, Genetics, 2013, 3, 273-282.	1.8	34
28	Synthetic Lethality of Cohesins with PARPs and Replication Fork Mediators. PLoS Genetics, 2012, 8, e1002574.	3.5	63
29	R-loop-mediated genome instability in mRNA cleavage and polyadenylation mutants. Genes and Development, 2012, 26, 163-175.	5.9	195
30	Mutability and mutational spectrum of chromosome transmission fidelity genes. Chromosoma, 2012, 121, 263-275.	2.2	17
31	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
32	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
33	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
34	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
35	Toward a Comprehensive Temperature-Sensitive Mutant Repository of the Essential Genes of Saccharomyces cerevisiae. Molecular Cell, 2008, 30, 248-258.	9.7	189
36	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

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37	The kinetochore and cancer: what's the connection?. Current Opinion in Cell Biology, 2005, 17, 576-582.	5.4	106
38	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
39	Identification of Protein Complexes Required for Efficient Sister Chromatid Cohesion. Molecular Biology of the Cell, 2004, 15, 1736-1745.	2.1	221
40	A Robust Toolkit for Functional Profiling of the Yeast Genome. Molecular Cell, 2004, 16, 487-496.	9.7	295
41	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
42	Synthetic dosage lethality. Methods in Enzymology, 2002, 350, 316-326.	1.0	41
43	Overexpression of B-type cyclins alters chromosomal segregation. Oncogene, 2002, 21, 2051-2057.	5.9	67
44	Identification of RFC(Ctf18p, Ctf8p, Dcc1p). Molecular Cell, 2001, 7, 959-970.	9.7	308
45	Novel Role for a <i>Saccharomyces cerevisiae</i> Nucleoporin, Nup170p, in Chromosome Segregation. Genetics, 2001, 157, 1543-1553.	2.9	48
46	Protein networks—built by association. Nature Biotechnology, 2000, 18, 1242-1243.	17.5	38
47	The APC11 RING-H2 Finger Mediates E2-Dependent Ubiquitination. Molecular Biology of the Cell, 2000, 11, 2315-2325.	2.1	167
48	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
49	What do yeast proteins do?. Nature, 1999, 402, 362-363.	27.8	5
50	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
51	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
52	Identification of a Cullin Homology Region in a Subunit of the Anaphase-Promoting Complex. Science, 1998, 279, 1219-1222.	12.6	234
53	The yeast genome and clinical genetics. Clinical Genetics, 1998, 54, 113-116.	2.0	1
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	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
56	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
57	The yeast genome — a common currency. Nature Genetics, 1996, 13, 253-255.	21.4	37
58	Establishing Genetic Interactions by a Synthetic Dosage Lethality Phenotype. Genetics, 1996, 143, 95-102.	2.9	144
59	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
60	Alu sequences in RMSA-1 protein?. Nature, 1994, 370, 106-106.	27.8	17
61	Identification of essential components of the S. cerevisiae kinetochore. Cell, 1993, 73, 761-774.	28.9	215
62	Multifunctional yeast high-copy-number shuttle vectors. Gene, 1992, 110, 119-122.	2.2	1,658
63	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
64	[54] Analysis of chromosome segregation in Saccharomyces cerevisiae. Methods in Enzymology, 1991, 194, 749-773.	1.0	58
65	Trans-kingdom promiscuity. Nature, 1990, 345, 581-582.	27.8	49
66	Expanding family. Nature, 1990, 346, 114-114.	27.8	37
67	[22] Visual assay for chromosome ploidy. Methods in Enzymology, 1987, 155, 351-372.	1.0	68