Grant W Brown

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104 8,838 45 93 g-index

122 10,183 10.8 5.63 ext. papers ext. citations avg, IF L-index

#	Paper	IF	Citations
104	Global mapping of the yeast genetic interaction network. <i>Science</i> , 2004 , 303, 808-13	33.3	1700
103	Functional dissection of protein complexes involved in yeast chromosome biology using a genetic interaction map. <i>Nature</i> , 2007 , 446, 806-10	50.4	731
102	Integration of chemical-genetic and genetic interaction data links bioactive compounds to cellular target pathways. <i>Nature Biotechnology</i> , 2004 , 22, 62-9	44.5	527
101	Functional targeting of DNA damage to a nuclear pore-associated SUMO-dependent ubiquitin ligase. <i>Science</i> , 2008 , 322, 597-602	33.3	338
100	Regulation of chromosome replication. <i>Annual Review of Biochemistry</i> , 2000 , 69, 829-80	29.1	330
99	Dissecting DNA damage response pathways by analysing protein localization and abundance changes during DNA replication stress. <i>Nature Cell Biology</i> , 2012 , 14, 966-76	23.4	322
98	CX-5461 is a DNA G-quadruplex stabilizer with selective lethality in BRCA1/2 deficient tumours. <i>Nature Communications</i> , 2017 , 8, 14432	17.4	251
97	Quantitative analysis of fitness and genetic interactions in yeast on a genome scale. <i>Nature Methods</i> , 2010 , 7, 1017-24	21.6	251
96	A genome-wide screen for methyl methanesulfonate-sensitive mutants reveals genes required for S phase progression in the presence of DNA damage. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 16934-9	11.5	234
95	BLAP75/RMI1 promotes the BLM-dependent dissolution of homologous recombination intermediates. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 4068-73	11.5	222
94	Identification of protein complexes required for efficient sister chromatid cohesion. <i>Molecular Biology of the Cell</i> , 2004 , 15, 1736-45	3.5	198
93	Unification of Protein Abundance Datasets Yields a Quantitative Saccharomyces cerevisiae Proteome. <i>Cell Systems</i> , 2018 , 6, 192-205.e3	10.6	186
92	The synthetic genetic interaction spectrum of essential genes. <i>Nature Genetics</i> , 2005 , 37, 1147-52	36.3	185
91	Mapping the cellular response to small molecules using chemogenomic fitness signatures. <i>Science</i> , 2014 , 344, 208-11	33.3	174
90	RMI, a new OB-fold complex essential for Bloom syndrome protein to maintain genome stability. <i>Genes and Development</i> , 2008 , 22, 2843-55	12.6	153
89	RMI1/NCE4, a suppressor of genome instability, encodes a member of the RecQ helicase/Topo III complex. <i>EMBO Journal</i> , 2005 , 24, 2024-33	13	139
88	Systematic analysis of complex genetic interactions. <i>Science</i> , 2018 , 360,	33.3	128

(2014-2003)

87	Elg1 forms an alternative RFC complex important for DNA replication and genome integrity. <i>EMBO Journal</i> , 2003 , 22, 4304-13	13	127
86	A Genetic Map of the Response to DNA Damage in Human Cells. <i>Cell</i> , 2020 , 182, 481-496.e21	56.2	122
85	Diversity of eukaryotic DNA replication origins revealed by genome-wide analysis of chromatin structure. <i>PLoS Genetics</i> , 2010 , 6, e1001092	6	104
84	The origin recognition complex links replication, sister chromatid cohesion and transcriptional silencing in Saccharomyces cerevisiae. <i>Genetics</i> , 2004 , 167, 579-91	4	94
83	HELB Is a Feedback Inhibitor of DNA End Resection. <i>Molecular Cell</i> , 2016 , 61, 405-418	17.6	92
82	Top3lis an RNA topoisomerase that works with fragile X syndrome protein to promote synapse formation. <i>Nature Neuroscience</i> , 2013 , 16, 1238-47	25.5	92
81	Purification of Hsk1, a minichromosome maintenance protein kinase from fission yeast. <i>Journal of Biological Chemistry</i> , 1998 , 273, 22083-90	5.4	92
80	The MMS22L-TONSL complex mediates recovery from replication stress and homologous recombination. <i>Molecular Cell</i> , 2010 , 40, 619-31	17.6	85
79	Genetic dissection of parallel sister-chromatid cohesion pathways. <i>Genetics</i> , 2007 , 176, 1417-29	4	79
78	Suppression of genomic instability by SLX5 and SLX8 in Saccharomyces cerevisiae. <i>DNA Repair</i> , 2006 , 5, 336-46	4.3	79
77	Exploiting DNA Replication Stress for Cancer Treatment. Cancer Research, 2019, 79, 1730-1739	10.1	76
76	Endogenous DNA replication stress results in expansion of dNTP pools and a mutator phenotype. <i>EMBO Journal</i> , 2012 , 31, 895-907	13	76
75	Slx4 regulates DNA damage checkpoint-dependent phosphorylation of the BRCT domain protein Rtt107/Esc4. <i>Molecular Biology of the Cell</i> , 2006 , 17, 539-48	3.5	75
74	A survey of essential gene function in the yeast cell division cycle. <i>Molecular Biology of the Cell</i> , 2006 , 17, 4736-47	3.5	74
73	Schizosaccharomyces pombe Hsk1p is a potential cds1p target required for genome integrity. <i>Molecular and Cellular Biology</i> , 2000 , 20, 7922-32	4.8	69
72	The endonuclease Cue2 cleaves mRNAs at stalled ribosomes during No Go Decay. <i>ELife</i> , 2019 , 8,	8.9	69
71	New azole antifungal agents with novel modes of action: synthesis and biological studies of new tridentate ligands based on pyrazole and triazole. <i>European Journal of Medicinal Chemistry</i> , 2011 , 46, 4117-24	6.8	58
70	Haploinsufficiency of an RB-E2F1-Condensin II complex leads to aberrant replication and aneuploidy. <i>Cancer Discovery</i> , 2014 , 4, 840-53	24.4	57

69	Putting genetic interactions in context through a global modular decomposition. <i>Genome Research</i> , 2011 , 21, 1375-87	9.7	55
68	Human topoisomerase Illalpha is a single-stranded DNA decatenase that is stimulated by BLM and RMI1. <i>Journal of Biological Chemistry</i> , 2010 , 285, 21426-36	5.4	51
67	Budding yeast Mms22 and Mms1 regulate homologous recombination induced by replisome blockage. <i>DNA Repair</i> , 2008 , 7, 811-8	4.3	49
66	Regulation of rtt107 recruitment to stalled DNA replication forks by the cullin rtt101 and the rtt109 acetyltransferase. <i>Molecular Biology of the Cell</i> , 2008 , 19, 171-80	3.5	49
65	Functional annotation of chemical libraries across diverse biological processes. <i>Nature Chemical Biology</i> , 2017 , 13, 982-993	11.7	48
64	The INO80 chromatin remodeling complex prevents polyploidy and maintains normal chromatin structure at centromeres. <i>Genes and Development</i> , 2012 , 26, 2590-603	12.6	47
63	Global analysis of SUMO chain function reveals multiple roles in chromatin regulation. <i>Journal of Cell Biology</i> , 2013 , 201, 145-63	7.3	47
62	A role for USP7 in DNA replication. <i>Molecular and Cellular Biology</i> , 2014 , 34, 132-45	4.8	45
61	A conserved domain of Schizosaccharomyces pombe dfp1(+) is uniquely required for chromosome stability following alkylation damage during S phase. <i>Molecular and Cellular Biology</i> , 2002 , 22, 4477-90	4.8	45
60	Monoclonal antibodies to the major nonstructural nuclear protein of minute virus of mice. <i>Virology</i> , 1991 , 181, 35-45	3.6	45
59	Smc5/6 Mediated Sumoylation of the Sgs1-Top3-Rmi1 Complex Promotes Removal of Recombination Intermediates. <i>Cell Reports</i> , 2016 , 16, 368-378	10.6	45
58	The Monoterpene Carvacrol Generates Endoplasmic Reticulum Stress in the Pathogenic Fungus Candida albicans. <i>Antimicrobial Agents and Chemotherapy</i> , 2015 , 59, 4584-92	5.9	43
57	Progerin-Induced Replication Stress Facilitates Premature Senescence in Hutchinson-Gilford Progeria Syndrome. <i>Molecular and Cellular Biology</i> , 2017 , 37,	4.8	38
56	Dampening DNA damage checkpoint signalling via coordinated BRCT domain interactions. <i>EMBO Journal</i> , 2015 , 34, 1704-17	13	35
55	Comparative chemogenomics to examine the mechanism of action of dna-targeted platinum-acridine anticancer agents. <i>ACS Chemical Biology</i> , 2012 , 7, 1892-901	4.9	34
54	Slx4 and Rtt107 control checkpoint signalling and DNA resection at double-strand breaks. <i>Nucleic Acids Research</i> , 2016 , 44, 669-82	20.1	33
53	Cdc7 kinases (DDKs) and checkpoint responses: lessons from two yeasts. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2003 , 532, 21-7	3.3	32
52	Chemical-genetic profiling of imidazo[1,2-a]pyridines and -pyrimidines reveals target pathways conserved between yeast and human cells. <i>PLoS Genetics</i> , 2008 , 4, e1000284	6	31

51	Controlling initiation during the cell cycle. DNA replication. <i>Current Biology</i> , 1996 , 6, 229-33	6.3	31
50	Assembly of Slx4 signaling complexes behind DNA replication forks. <i>EMBO Journal</i> , 2015 , 34, 2182-97	13	30
49	Isolation of the genes encoding the 51-kilodalton and 28-kilodalton subunits of Crithidia fasciculata replication protein A. <i>Molecular and Biochemical Parasitology</i> , 1994 , 63, 135-42	1.9	28
48	Rad5 Recruits Error-Prone DNA Polymerases for Mutagenic Repair of ssDNA Gaps on Undamaged Templates. <i>Molecular Cell</i> , 2019 , 73, 900-914.e9	17.6	27
47	RMI1 promotes DNA replication fork progression and recovery from replication fork stress. <i>Molecular and Cellular Biology</i> , 2012 , 32, 3054-64	4.8	22
46	Intersection of calorie restriction and magnesium in the suppression of genome-destabilizing RNA-DNA hybrids. <i>Nucleic Acids Research</i> , 2016 , 44, 8870-8884	20.1	20
45	Genome rearrangements caused by depletion of essential DNA replication proteins in Saccharomyces cerevisiae. <i>Genetics</i> , 2012 , 192, 147-60	4	19
44	P-body proteins regulate transcriptional rewiring to promote DNA replication stress resistance. <i>Nature Communications</i> , 2017 , 8, 558	17.4	18
43	Flap endonuclease overexpression drives genome instability and DNA damage hypersensitivity in a PCNA-dependent manner. <i>Nucleic Acids Research</i> , 2018 , 46, 5634-5650	20.1	18
42	A high-throughput yeast assay identifies synergistic drug combinations. <i>Assay and Drug Development Technologies</i> , 2013 , 11, 299-307	2.1	16
41	The N- and C-termini of Elg1 contribute to the maintenance of genome stability. <i>DNA Repair</i> , 2008 , 7, 1221-32	4.3	16
40	Exploring Quantitative Yeast Phenomics with Single-Cell Analysis of DNA Damage Foci. <i>Cell Systems</i> , 2016 , 3, 264-277.e10	10.6	16
39	Mms1 and Mms22 stabilize the replisome during replication stress. <i>Molecular Biology of the Cell</i> , 2011 , 22, 2396-408	3.5	15
38	Mapping DNA damage-dependent genetic interactions in yeast via party mating and barcode fusion genetics. <i>Molecular Systems Biology</i> , 2018 , 14, e7985	12.2	15
37	E4F1 is a master regulator of CHK1-mediated functions. <i>Cell Reports</i> , 2015 , 11, 210-9	10.6	14
36	Leveraging DNA damage response signaling to identify yeast genes controlling genome stability. <i>G3: Genes, Genomes, Genetics</i> , 2015 , 5, 997-1006	3.2	14
35	Termination of Replication Stress Signaling via Concerted Action of the Slx4 Scaffold and the PP4 Phosphatase. <i>Genetics</i> , 2015 , 201, 937-49	4	13
34	Analysis of Replicating Yeast Chromosomes by DNA Combing. <i>Cold Spring Harbor Protocols</i> , 2016 , 2016, pdb.prot085118	1.2	13

33	MTE1 Functions with MPH1 in Double-Strand Break Repair. <i>Genetics</i> , 2016 , 203, 147-57	4	12
32	Purification and characterization of DNA ligase I from the trypanosomatid Crithidia fasciculata. <i>Nucleic Acids Research</i> , 1992 , 20, 3905-10	20.1	11
31	RNF168 regulates R-loop resolution and genomic stability in BRCA1/2-deficient tumors. <i>Journal of Clinical Investigation</i> , 2021 , 131,	15.9	11
30	The Budding Yeast "Saccharomyces cerevisiae" as a Drug Discovery Tool to Identify Plant-Derived Natural Products with Anti-Proliferative Properties. <i>Evidence-based Complementary and Alternative Medicine</i> , 2011 , 2011, 954140	2.3	9
29	High-throughput fluorescence microscopic analysis of protein abundance and localization in budding yeast. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2016 , 51, 110-9	8.7	8
28	Replication protein A from the trypanosomatid Crithidia fasciculata is inactive in the primosome assembly step of SV40 DNA replication. <i>Molecular and Biochemical Parasitology</i> , 1993 , 59, 323-5	1.9	8
27	Post-replication repair: Rad5/HLTF regulation, activity on undamaged templates, and relationship to cancer. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2019 , 54, 301-332	8.7	7
26	Comparative genome hybridization on tiling microarrays to detect aneuploidies in yeast. <i>Methods in Molecular Biology</i> , 2009 , 548, 1-18	1.4	7
25	Genome-Scale Genetic Interactions and Cell Imaging Confirm Cytokinesis as Deleterious to Transient Topoisomerase II Deficiency in. <i>G3: Genes, Genomes, Genetics</i> , 2017 , 7, 3379-3391	3.2	5
24	Genetic Regulation of Dna2 Localization During the DNA Damage Response. <i>G3: Genes, Genomes, Genetics</i> , 2015 , 5, 1937-44	3.2	5
23	BLM and RMI1 alleviate RPA inhibition of TopoIIIdecatenase activity. PLoS ONE, 2012, 7, e41208	3.7	5
22	Sonic hedgehog accelerates DNA replication to cause replication stress promoting cancer initiation in medulloblastoma <i>Nature Cancer</i> , 2020 , 1, 840-854	15.4	5
21	Mistranslating tRNA identifies a deleterious S213P mutation in the allele. <i>Biochemistry and Cell Biology</i> , 2020 , 98, 624-630	3.6	4
20	Single-Molecule Analysis of Replicating Yeast Chromosomes. <i>Cold Spring Harbor Protocols</i> , 2016 , 2016, pdb.top077784	1.2	4
19	Dissecting the DNA damage response using functional genomics approaches in S. cerevisiae. <i>DNA Repair</i> , 2009 , 8, 1110-7	4.3	4
18	DNA Replication Profiling Using Deep Sequencing. <i>Methods in Molecular Biology</i> , 2018 , 1672, 195-207	1.4	3
17	The budding yeast RSC complex maintains ploidy by promoting spindle pole body insertion. <i>Journal of Cell Biology</i> , 2018 , 217, 2445-2462	7.3	3
16	Fanconi anemia signaling and Mus81 cooperate to safeguard development and crosslink repair. Nucleic Acids Research, 2014 , 42, 9807-20	20.1	3

A genetic map of the response to DNA damage in human cells 15 3 Genomic approaches for identifying DNA damage response pathways in S. cerevisiae. Methods in 14 1.7 Enzymology, 2006, 409, 213-35 Schizosaccharomyces pombe Hsk1p Is a Potential Cds1p Target Required for Genome Integrity. 4.8 2 13 Molecular and Cellular Biology, 2000, 20, 7922-7932 Comparative analysis of protein abundance studies to quantify the Saccharomyces cerevisiae proteome 2 12 The amino acid substitution affects cellular response to mistranslation. G3: Genes, Genomes, 11 2 3.2 Genetics, 2021, 11, Functional Annotation of Chemical Libraries across Diverse Biological Processes 10 Chemical-Genetic Interactions with the Proline Analog L-Azetidine-2-Carboxylic Acid in. G3: Genes, 9 3.2 1 Genomes, Genetics, 2020, 10, 4335-4345 A Genome-Wide Screen for Genes Affecting Spontaneous Direct-Repeat Recombination in. G3: 3.2 Genes, Genomes, Genetics, 2020, 10, 1853-1867 Genetic screens identify connections between ribosome recycling and nonsense mediated decay 1 LSD1 is required for euchromatic origin firing and replication timing.. Signal Transduction and *Targeted Therapy*, **2022**, 7, 102 A high-throughput confocal fluorescence microscopy platform to study DNA replication stress in 5 1.4 O yeast cells. Methods in Molecular Biology, 2015, 1300, 1-12 High-throughput platform for yeast morphological profiling predicts the targets of bioactive \circ compounds.. Npj Systems Biology and Applications, 2022, 8, 3 Topoisomerase II deficiency leads to a postreplicative structural shift in all Saccharomyces Ο 4.9 cerevisiae chromosomes. Scientific Reports, 2021, 11, 14940 Clustering with Overlap for Genetic Interaction Networks via Local Search Optimization. Lecture 0.9 Notes in Computer Science, 2011, 326-338 Yeast goes viral: probing SARS-CoV-2 biology using .. Microbial Cell, 2022, 9, 80-83 1 3.9