

# Michael Lisby

## List of Publications by Year in descending order

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116  
papers

7,805  
citations

70961

41  
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58464

82  
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124  
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124  
docs citations

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times ranked

6593  
citing authors

#	ARTICLE	IF	CITATIONS
1	Chromosome-scale assembly and whole-genome sequencing of 266 giant panda roundworms provide insights into their evolution, adaptation and potential drug targets. <i>Molecular Ecology Resources</i> , 2022, 22, 768-785.	2.2	6
2	The chromosome-scale genomes of <i>Dipterocarpus turbinatus</i> and <i>Hopea hainanensis</i> (Dipterocarpaceae) provide insights into fragrant oleoresin biosynthesis and hardwood formation. <i>Plant Biotechnology Journal</i> , 2022, 20, 538-553.	4.1	21
3	Genomes shed light on the evolution of <i>Begonia</i> , a mega-diverse genus. <i>New Phytologist</i> , 2022, 234, 295-310.	3.5	18
4	Telomeric C-circles localize at nuclear pore complexes in <i>Saccharomyces cerevisiae</i> . <i>EMBO Journal</i> , 2022, 41, e108736.	3.5	7
5	SCAI promotes error-free repair of DNA interstrand crosslinks via the Fanconi anemia pathway. <i>EMBO Reports</i> , 2022, 23, e53639.	2.0	12
6	The <i>Cycas</i> genome and the early evolution of seed plants. <i>Nature Plants</i> , 2022, 8, 389-401.	4.7	80
7	Spatiotemporal transcriptomic atlas of mouse organogenesis using DNA nanoball-patterned arrays. <i>Cell</i> , 2022, 185, 1777-1792.e21.	13.5	437
8	Functions of TopBP1 in preserving genome integrity during mitosis. <i>Seminars in Cell and Developmental Biology</i> , 2021, 113, 57-64.	2.3	26
9	The Rad51 paralog complex Rad55-Rad57 acts as a molecular chaperone during homologous recombination. <i>Molecular Cell</i> , 2021, 81, 1043-1057.e8.	4.5	45
10	Rad52 SUMOylation functions as a molecular switch that determines a balance between the Rad51- and Rad59-dependent survivors. <i>IScience</i> , 2021, 24, 102231.	1.9	12
11	Topoisomerase II deficiency leads to a postreplicative structural shift in all <i>Saccharomyces cerevisiae</i> chromosomes. <i>Scientific Reports</i> , 2021, 11, 14940.	1.6	2
12	A complex of BRCA2 and PP2A-B56 is required for DNA repair by homologous recombination. <i>Nature Communications</i> , 2021, 12, 5748.	5.8	24
13	The <i>Clausena lansium</i> (Wampee) genome reveal new insights into the carbazole alkaloids biosynthesis pathway. <i>Genomics</i> , 2021, 113, 3696-3704.	1.3	11
14	DNA Double-Strand Break-Induced Gene Amplification in Yeast. <i>Methods in Molecular Biology</i> , 2021, 2153, 239-252.	0.4	1
15	Ethanol exposure increases mutation rate through error-prone polymerases. <i>Nature Communications</i> , 2020, 11, 3664.	5.8	29
16	Protocol for Purification of Human ZGRF1 and Its Regulatory Function on RAD51-Mediated D-Loop Formation. <i>STAR Protocols</i> , 2020, 1, 100099.	0.5	0
17	The ZGRF1 Helicase Promotes Recombinational Repair of Replication-Blocking DNA Damage in Human Cells. <i>Cell Reports</i> , 2020, 32, 107849.	2.9	9
18	A distinct role for recombination repair factors in an early cellular response to transcription-replication conflicts. <i>Nucleic Acids Research</i> , 2020, 48, 5467-5484.	6.5	23

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19	Folliculin variants linked to Birt-Hogg-Dubé syndrome are targeted for proteasomal degradation. <i>PLoS Genetics</i> , 2020, 16, e1009187.	1.5	16
20	The FANCM family Mph1 helicase localizes to the mitochondria and contributes to mtDNA stability. <i>DNA Repair</i> , 2019, 82, 102684.	1.3	5
21	Guidelines for DNA recombination and repair studies: Cellular assays of DNA repair pathways. <i>Microbial Cell</i> , 2019, 6, 1-64.	1.4	47
22	Esc2 promotes telomere stability in response to DNA replication stress. <i>Nucleic Acids Research</i> , 2019, 47, 4597-4611.	6.5	6
23	Quantitative sensing and signalling of single-stranded DNA during the DNA damage response. <i>Nature Communications</i> , 2019, 10, 944.	5.8	44
24	Fumarase is involved in DNA double-strand break resection through a functional interaction with Sae2. <i>Current Genetics</i> , 2018, 64, 697-712.	0.8	24
25	Regulation of Hed1 and Rad54 binding during maturation of the meiosis-specific presynaptic complex. <i>EMBO Journal</i> , 2018, 37, .	3.5	33
26	FANCD2 binding identifies conserved fragile sites at large transcribed genes in avian cells. <i>Nucleic Acids Research</i> , 2018, 46, 1280-1294.	6.5	43
27	A Critical Role for Dna2 at Unwound Telomeres. <i>Genetics</i> , 2018, 209, 129-141.	1.2	12
28	Imaging of DNA Ultrafine Bridges in Budding Yeast. <i>Methods in Molecular Biology</i> , 2018, 1672, 483-493.	0.4	1
29	Regulation of telomere metabolism by the RNA processing protein Xrn1. <i>Nucleic Acids Research</i> , 2017, 45, 3860-3874.	6.5	6
30	Genome-Scale Genetic Interactions and Cell Imaging Confirm Cytokinesis as Deleterious to Transient Topoisomerase II Deficiency in <i>Saccharomyces cerevisiae</i> . <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 3379-3391.	0.8	8
31	Transcription-replication conflicts at chromosomal fragile sites—consequences in M phase and beyond. <i>Chromosoma</i> , 2017, 126, 213-222.	1.0	17
32	Esc2 promotes Mus81 complex-activity via its SUMO-like and DNA binding domains. <i>Nucleic Acids Research</i> , 2017, 45, 215-230.	6.5	26
33	Editorial: 3Rs tightly intertwined to maintain genome stability. <i>FEMS Yeast Research</i> , 2017, 17, fox003.	1.1	1
34	The Smc5/6 complex regulates the yeast Mph1 helicase at RNA-DNA hybrid-mediated DNA damage. <i>PLoS Genetics</i> , 2017, 13, e1007136.	1.5	47
35	SUMO-Dependent Relocalization of Eroded Telomeres to Nuclear Pore Complexes Controls Telomere Recombination. <i>Cell Reports</i> , 2016, 15, 1242-1253.	2.9	79
36	Pro-recombination Role of Srs2 Protein Requires SUMO (Small Ubiquitin-like Modifier) but Is Independent of PCNA (Proliferating Cell Nuclear Antigen) Interaction. <i>Journal of Biological Chemistry</i> , 2016, 291, 7594-7607.	1.6	19

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37	TopBP1 makes the final call for repair on the verge of cell division. <i>Molecular and Cellular Oncology</i> , 2016, 3, e1093066.	0.3	2
38	The role of HERC2 and RNF8 ubiquitin E3 ligases in the promotion of translesion DNA synthesis in the chicken DT40 cell line. <i>DNA Repair</i> , 2016, 40, 67-76.	1.3	20
39	SUMOylation of Rad52-Rad59 synergistically change the outcome of mitotic recombination. <i>DNA Repair</i> , 2016, 42, 11-25.	1.3	9
40	TOPBP1 regulates RAD51 phosphorylation and chromatin loading and determines PARP inhibitor sensitivity. <i>Journal of Cell Biology</i> , 2016, 212, 281-288.	2.3	70
41	Mte1 interacts with Mph1 and promotes crossover recombination and telomere maintenance. <i>Genes and Development</i> , 2016, 30, 700-717.	2.7	27
42	TopBP1-mediated DNA processing during mitosis. <i>Cell Cycle</i> , 2016, 15, 176-183.	1.3	21
43	Recombinational DNA repair is regulated by compartmentalization of DNA lesions at the nuclear pore complex. <i>BioEssays</i> , 2015, 37, 1287-1292.	1.2	40
44	Top2 and Sgs1-Top3 Act Redundantly to Ensure rDNA Replication Termination. <i>PLoS Genetics</i> , 2015, 11, e1005697.	1.5	15
45	Srs2 promotes Mus81-Mms4-mediated resolution of recombination intermediates. <i>Nucleic Acids Research</i> , 2015, 43, 3626-3642.	6.5	21
46	Compartment-specific aggregases direct distinct nuclear and cytoplasmic aggregate deposition. <i>EMBO Journal</i> , 2015, 34, 778-797.	3.5	243
47	Cmr1/WDR76 defines a nuclear genotoxic stress body linking genome integrity and protein quality control. <i>Nature Communications</i> , 2015, 6, 6533.	5.8	80
48	Biotin starvation causes mitochondrial protein hyperacetylation and partial rescue by the SIRT3-like deacetylase Hst4p. <i>Nature Communications</i> , 2015, 6, 7726.	5.8	47
49	Cell Biology of Mitotic Recombination. <i>Cold Spring Harbor Perspectives in Biology</i> , 2015, 7, a016535.	2.3	54
50	TopBP1 is required at mitosis to reduce transmission of DNA damage to G1 daughter cells. <i>Journal of Cell Biology</i> , 2015, 210, 565-582.	2.3	82
51	Cell cycle regulation of homologous recombination in <i>Saccharomyces cerevisiae</i> . <i>FEMS Microbiology Reviews</i> , 2014, 38, 172-184.	3.9	65
52	Length-dependent processing of telomeres in the absence of telomerase. <i>Nucleic Acids Research</i> , 2014, 42, 3648-3665.	6.5	63
53	DNA secondary structures are associated with recombination in major <i>Plasmodium falciparum</i> variable surface antigen gene families. <i>Nucleic Acids Research</i> , 2014, 42, 2270-2281.	6.5	36
54	Genetic Basis for <i>Saccharomyces cerevisiae</i> Biofilm in Liquid Medium. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 1671-1680.	0.8	36

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55	TopBP1/Dpb11 binds DNA anaphase bridges to prevent genome instability. <i>Journal of Cell Biology</i> , 2014, 204, 45-59.	2.3	93
56	Mechanisms and Regulation of Mitotic Recombination in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2014, 198, 795-835.	1.2	313
57	A cell cycle-regulated Slx4-Dpb11 complex promotes the resolution of DNA repair intermediates linked to stalled replication. <i>Genes and Development</i> , 2014, 28, 1604-1619.	2.7	79
58	Physical mapping and cloning of RAD56. <i>Gene</i> , 2013, 519, 182-186.	1.0	3
59	RPA Coordinates DNA End Resection and Prevents Formation of DNA Hairpins. <i>Molecular Cell</i> , 2013, 50, 589-600.	4.5	225
60	MRX protects fork integrity at protein-DNA barriers, and its absence causes checkpoint activation dependent on chromatin context. <i>Nucleic Acids Research</i> , 2013, 41, 3173-3189.	6.5	17
61	The PCNA Interaction Protein Box Sequence in Rad54 Is an Integral Part of Its ATPase Domain and Is Required for Efficient DNA Repair and Recombination. <i>PLoS ONE</i> , 2013, 8, e82630.	1.1	9
62	Histone H3 Lysine 56 Acetylation and the Response to DNA Replication Fork Damage. <i>Molecular and Cellular Biology</i> , 2012, 32, 154-172.	1.1	77
63	Proteome-wide Analysis of Lysine Acetylation Suggests its Broad Regulatory Scope in <i>Saccharomyces cerevisiae</i> . <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1510-1522.	2.5	255
64	RNF8 and RNF168 but not HERC2 are required for DNA damage-induced ubiquitylation in chicken DT40 cells. <i>DNA Repair</i> , 2012, 11, 892-905.	1.3	22
65	Live Cell Microscopy of DNA Damage Response in <i>Saccharomyces cerevisiae</i> . <i>Methods in Molecular Biology</i> , 2012, 920, 433-443.	0.4	20
66	Optimization of ordered plasmid assembly by gap repair in <i>Saccharomyces cerevisiae</i> . <i>Yeast</i> , 2012, 29, 323-334.	0.8	36
67	Cell Biology of Homologous Recombination in Yeast. <i>Methods in Molecular Biology</i> , 2011, 745, 523-536.	0.4	30
68	Phenylbutyrate inhibits homologous recombination induced by camptothecin and methyl methanesulfonate. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2011, 713, 64-75.	0.4	11
69	Dpb11/TopBP1 plays distinct roles in DNA replication, checkpoint response and homologous recombination. <i>DNA Repair</i> , 2011, 10, 210-224.	1.3	34
70	Bringing Rad52 foci into focus. <i>Journal of Cell Biology</i> , 2011, 194, 665-667.	2.3	13
71	The rad52-Y66A allele alters the choice of donor template during spontaneous chromosomal recombination. <i>DNA Repair</i> , 2010, 9, 23-32.	1.3	7
72	Regulation of homologous recombination at telomeres in budding yeast. <i>FEBS Letters</i> , 2010, 584, 3696-3702.	1.3	14

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73	The Transcription Elongation Factor Bur1-Bur2 Interacts with Replication Protein A and Maintains Genome Stability during Replication Stress. <i>Journal of Biological Chemistry</i> , 2010, 285, 41665-41674.	1.6	18
74	The fate of irreparable DNA double-strand breaks and eroded telomeres at the nuclear periphery. <i>Nucleus</i> , 2010, 1, 158-161.	0.6	7
75	Rad52 SUMOylation affects the efficiency of the DNA repair. <i>Nucleic Acids Research</i> , 2010, 38, 4708-4721.	6.5	85
76	Adaptation to diverse nitrogen-limited environments by deletion or extrachromosomal element formation of the <i>GAP1</i> locus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 18551-18556.	3.3	135
77	The fate of irreparable DNA double-strand breaks and eroded telomeres at the nuclear periphery. <i>Nucleus</i> , 2010, 1, 158-161.	0.6	5
78	Localization of recombination proteins and Srs2 reveals anti-recombinase function in vivo. <i>Journal of Cell Biology</i> , 2009, 185, 969-981.	2.3	72
79	Rad10 exhibits lesion-dependent genetic requirements for recruitment to DNA double-strand breaks in <i>Saccharomyces cerevisiae</i> . <i>Nucleic Acids Research</i> , 2009, 37, 6429-6438.	6.5	10
80	Rad52. <i>Current Biology</i> , 2009, 19, R676-R677.	1.8	80
81	Regulation of rDNA stability by sumoylation. <i>DNA Repair</i> , 2009, 8, 507-516.	1.3	19
82	Choreography of recombination proteins during the DNA damage response. <i>DNA Repair</i> , 2009, 8, 1068-1076.	1.3	103
83	The DNA damage response at eroded telomeres and tethering to the nuclear pore complex. <i>Nature Cell Biology</i> , 2009, 11, 980-987.	4.6	191
84	A two-step model for senescence triggered by a single critically short telomere. <i>Nature Cell Biology</i> , 2009, 11, 988-993.	4.6	151
85	A Flp-nick system to study repair of a single protein-bound nick in vivo. <i>Nature Methods</i> , 2009, 6, 753-757.	9.0	52
86	DNA damage response to eroded telomeres. <i>Cell Cycle</i> , 2009, 8, 3617-3618.	1.3	7
87	Compensatory role for Rad52 during recombinational repair in <i>Ustilago maydis</i> . <i>Molecular Microbiology</i> , 2008, 67, 1156-1168.	1.2	28
88	Rad52 multimerization is important for its nuclear localization in <i>Saccharomyces cerevisiae</i> . <i>DNA Repair</i> , 2008, 7, 57-66.	1.3	18
89	Differential Regulation of the Cellular Response to DNA Double-Strand Breaks in G1. <i>Molecular Cell</i> , 2008, 30, 73-85.	4.5	149
90	Genome-Wide Analysis of Rad52 Foci Reveals Diverse Mechanisms Impacting Recombination. <i>PLoS Genetics</i> , 2007, 3, e228.	1.5	176

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91	Anaphase Onset Before Complete DNA Replication with Intact Checkpoint Responses. <i>Science</i> , 2007, 315, 1411-1415.	6.0	121
92	The Slx5-Slx8 Complex Affects Sumoylation of DNA Repair Proteins and Negatively Regulates Recombination. <i>Molecular and Cellular Biology</i> , 2007, 27, 6153-6162.	1.1	124
93	Dss1 Interaction with Brh2 as a Regulatory Mechanism for Recombinational Repair. <i>Molecular and Cellular Biology</i> , 2007, 27, 2512-2526.	1.1	40
94	The Smc5-Smc6 complex and SUMO modification of Rad52 regulates recombinational repair at the ribosomal gene locus. <i>Nature Cell Biology</i> , 2007, 9, 923-931.	4.6	345
95	Rad52 and Rad59 exhibit both overlapping and distinct functions. <i>DNA Repair</i> , 2007, 6, 27-37.	1.3	34
96	The cell biology of mitotic recombination in <i>Saccharomyces cerevisiae</i> . <i>Topics in Current Genetics</i> , 2007, , 317-333.	0.7	1
97	Systematic hybrid LOH: a new method to reduce false positives and negatives during screening of yeast gene deletion libraries. <i>Yeast</i> , 2006, 23, 1097-1106.	0.8	27
98	Multiple start codons and phosphorylation result in discrete Rad52 protein species. <i>Nucleic Acids Research</i> , 2006, 34, 2587-2597.	6.5	38
99	The Role of DNA Double-Strand Breaks in Spontaneous Homologous Recombination in <i>S. cerevisiae</i> . <i>PLoS Genetics</i> , 2006, 2, e194.	1.5	82
100	Rec2 Interplay with both Brh2 and Rad51 Balances Recombinational Repair in <i>Ustilago maydis</i> . <i>Molecular and Cellular Biology</i> , 2006, 26, 678-688.	1.1	20
101	The Cell Biology of Mitotic Recombination in <i>Saccharomyces Cerevisiae</i> . , 2006, , 317-333.		0
102	Brh2-Dss1 Interplay Enables Properly Controlled Recombination in <i>Ustilago maydis</i> . <i>Molecular and Cellular Biology</i> , 2005, 25, 2547-2557.	1.1	59
103	Localization of checkpoint and repair proteins in eukaryotes. <i>Biochimie</i> , 2005, 87, 579-589.	1.3	59
104	DNA Repair: Keeping It Together. <i>Current Biology</i> , 2004, 14, R994-R996.	1.8	40
105	DNA damage checkpoint and repair centers. <i>Current Opinion in Cell Biology</i> , 2004, 16, 328-334.	2.6	138
106	Choreography of the DNA Damage Response. <i>Cell</i> , 2004, 118, 699-713.	13.5	829
107	Colocalization of multiple DNA double-strand breaks at a single Rad52 repair centre. <i>Nature Cell Biology</i> , 2003, 5, 572-577.	4.6	388
108	Cell Cycle-Regulated Centers of DNA Double-Strand Break Repair. <i>Cell Cycle</i> , 2003, 2, 477-481.	1.3	53

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109	Cell cycle-regulated centers of DNA double-strand break repair. <i>Cell Cycle</i> , 2003, 2, 479-83.	1.3	36
110	Cloning-free genome alterations in <i>saccharomyces cerevisiae</i> using adaptamer-mediated PCR. <i>Methods in Enzymology</i> , 2002, 350, 258-277.	0.4	91
111	Residues within the N-terminal Domain of Human Topoisomerase I Play a Direct Role in Relaxation*. <i>Journal of Biological Chemistry</i> , 2001, 276, 20220-20227.	1.6	49
112	Inhibition of Flp Recombinase by the Topoisomerase I-targeting Drugs, Camptothecin and NSC-314622. <i>Journal of Biological Chemistry</i> , 2001, 276, 6993-6997.	1.6	1
113	Rad52 forms DNA repair and recombination centers during S phase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 8276-8282.	3.3	409
114	Camptothecins Inhibit the Utilization of Hydrogen Peroxide in the Ligation Step of Topoisomerase I Catalysis. <i>Biochemistry</i> , 1998, 37, 10815-10827.	1.2	39
115	The RNA-splicing Factor PSF/p54 Controls DNA-Topoisomerase I Activity by a Direct Interaction. <i>Journal of Biological Chemistry</i> , 1998, 273, 26261-26264.	1.6	82
116	Alcoholysis and Strand Joining by the Flp Site-specific Recombinase. <i>Journal of Biological Chemistry</i> , 1998, 273, 22028-22036.	1.6	5