

Petr Cejka

List of Publications by Year in descending order

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Version: 2024-02-01

80
papers

6,467
citations

76294

40
h-index

74108

75
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93
all docs

93
docs citations

93
times ranked

5727
citing authors

#	ARTICLE	IF	CITATIONS
1	The CDK1-TOPBP1-PLK1 axis regulates the Bloomâ€™s syndrome helicase BLM to suppress crossover recombination in somatic cells. <i>Science Advances</i> , 2022, 8, eabk0221.	4.7	13
2	Mre11-Rad50 oligomerization promotes DNA double-strand break repair. <i>Nature Communications</i> , 2022, 13, 2374.	5.8	15
3	Strand annealing and motor driven activities of SMARCAL1 and ZRANB3 are stimulated by RAD51 and the paralog complex. <i>Nucleic Acids Research</i> , 2022, 50, 8008-8022.	6.5	18
4	MRE11-RAD50-NBS1 Complex Is Sufficient to Promote Transcription by RNA Polymerase II at Double-Strand Breaks by Melting DNA Ends. <i>Cell Reports</i> , 2021, 34, 108565.	2.9	43
5	Sae2 and Rif2 regulate MRX endonuclease activity at DNA double-strand breaks in opposite manners. <i>Cell Reports</i> , 2021, 34, 108906.	2.9	17
6	Single-molecule studies illuminate the function of RAD51 paralogs. <i>Molecular Cell</i> , 2021, 81, 898-900.	4.5	4
7	The Pif1 helicase is actively inhibited during meiotic recombination which restrains gene conversion tract length. <i>Nucleic Acids Research</i> , 2021, 49, 4522-4533.	6.5	16
8	Inhibition of MRN activity by a telomere protein motif. <i>Nature Communications</i> , 2021, 12, 3856.	5.8	20
9	Molecular basis of the dual role of the Mlh1-Mlh3 endonuclease in MMR and in meiotic crossover formation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	18
10	Crossover or non-crossover outcomes: tailored processing of homologous recombination intermediates. <i>Current Opinion in Genetics and Development</i> , 2021, 71, 39-47.	1.5	10
11	Distinct RPA domains promote recruitment and the helicase-nuclease activities of Dna2. <i>Nature Communications</i> , 2021, 12, 6521.	5.8	9
12	DNA End Resection: Mechanism and Control. <i>Annual Review of Genetics</i> , 2021, 55, 285-307.	3.2	105
13	Exo1 recruits Cdc5 polo kinase to MutL ³ to ensure efficient meiotic crossover formation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 30577-30588.	3.3	28
14	MRNIP is a replication fork protection factor. <i>Science Advances</i> , 2020, 6, eaba5974.	4.7	16
15	Regulation of the MLH1â€™MLH3 endonuclease in meiosis. <i>Nature</i> , 2020, 586, 618-622.	13.7	88
16	Phosphorylated CtIP bridges DNA to promote annealing of broken ends. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 21403-21412.	3.3	21
17	The MRE11 complex: A versatile toolkit for the repair of broken DNA. <i>DNA Repair</i> , 2020, 91-92, 102869.	1.3	62
18	MCM8IP activates the MCM8-9 helicase to promote DNA synthesis and homologous recombination upon DNA damage. <i>Nature Communications</i> , 2020, 11, 2948.	5.8	28

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19	Phosphorylation of the RecQ Helicase Sgs1/BLM Controls Its DNA Unwinding Activity during Meiosis and Mitosis. <i>Developmental Cell</i> , 2020, 53, 706-723.e5.	3.1	26
20	CtIP promotes the motor activity of DNA2 to accelerate long-range DNA end resection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 8859-8869.	3.3	51
21	Regulated Proteolysis of MutS ³ Controls Meiotic Crossing Over. <i>Molecular Cell</i> , 2020, 78, 168-183.e5.	4.5	33
22	The iron-sulphur cluster in human DNA2 is required for all biochemical activities of DNA2. <i>Communications Biology</i> , 2020, 3, 322.	2.0	13
23	DNA Bridging by the Homologous Recombination Component CtIP Investigated on the Single DNA Molecule Level. <i>Biophysical Journal</i> , 2020, 118, 30a.	0.2	0
24	The internal region of CtIP negatively regulates DNA end resection. <i>Nucleic Acids Research</i> , 2020, 48, 5485-5498.	6.5	12
25	A Disease-Causing Single Amino Acid Deletion in the Coiled-Coil Domain of RAD50 Impairs MRE11 Complex Functions in Yeast and Humans. <i>Cell Reports</i> , 2020, 33, 108559.	2.9	7
26	Sumoylation regulates the stability and nuclease activity of <i>Saccharomyces cerevisiae</i> Dna2. <i>Communications Biology</i> , 2019, 2, 174.	2.0	11
27	Competing interaction partners modulate the activity of Sgs1 helicase during <sc>DNA</sc> end resection. <i>EMBO Journal</i> , 2019, 38, e101516.	3.5	21
28	Seeing is believing: DNA zipping promotes DNA repair. <i>Journal of Biological Chemistry</i> , 2019, 294, 3321-3322.	1.6	0
29	NBS1 promotes the endonuclease activity of the MRE11-RAD50 complex by sensing CtIP phosphorylation. <i>EMBO Journal</i> , 2019, 38, .	3.5	63
30	Stepwise 5' DNA end-specific resection of DNA breaks by the Mre11-Rad50-Xrs2 and Sae2 nuclease ensemble. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 5505-5513.	3.3	49
31	A meiotic XPF-ERCC1-like complex recognizes joint molecule recombination intermediates to promote crossover formation. <i>Genes and Development</i> , 2018, 32, 283-296.	2.7	98
32	Main steps in DNA double-strand break repair: an introduction to homologous recombination and related processes. <i>Chromosoma</i> , 2018, 127, 187-214.	1.0	242
33	BRCA2 controls DNA:RNA hybrid level at DSBs by mediating RNase H2 recruitment. <i>Nature Communications</i> , 2018, 9, 5376.	5.8	176
34	Regulatory control of DNA end resection by Sae2 phosphorylation. <i>Nature Communications</i> , 2018, 9, 4016.	5.8	64
35	Methods to Study DNA End Resection II: Biochemical Reconstitution Assays. <i>Methods in Enzymology</i> , 2018, 600, 67-106.	0.4	16
36	Methods to Study DNA End Resection I: Recombinant Protein Purification. <i>Methods in Enzymology</i> , 2018, 600, 25-66.	0.4	29

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37	The Mre11-Nbs1 Interface Is Essential for Viability and Tumor Suppression. <i>Cell Reports</i> , 2017, 18, 496-507.	2.9	39
38	The motor activity of DNA2 functions as an ssDNA translocase to promote DNA end resection. <i>Genes and Development</i> , 2017, 31, 493-502.	2.7	39
39	Complex assistance for DNA invasion. <i>Nature</i> , 2017, 550, 342-343.	13.7	4
40	Restoration of Replication Fork Stability in BRCA1- and BRCA2-Deficient Cells by Inactivation of SNF2-Family Fork Remodelers. <i>Molecular Cell</i> , 2017, 68, 414-430.e8.	4.5	295
41	SAMHD1 Promotes DNA End Resection to Facilitate DNA Repair by Homologous Recombination. <i>Cell Reports</i> , 2017, 20, 1921-1935.	2.9	147
42	Physiological protein blocks direct the Mre11-Rad50-Xrs2 and Sae2 nuclease complex to initiate DNA end resection. <i>Genes and Development</i> , 2017, 31, 2325-2330.	2.7	106
43	Concerted action of the MutL ² heterodimer and Mer3 helicase regulates the global extent of meiotic gene conversion. <i>ELife</i> , 2017, 6, .	2.8	67
44	The MMS22L-TONSL heterodimer directly promotes RAD51-dependent recombination upon replication stress. <i>EMBO Journal</i> , 2016, 35, 2584-2601.	3.5	64
45	Xrs2 Dependent and Independent Functions of the Mre11-Rad50 Complex. <i>Molecular Cell</i> , 2016, 64, 405-415.	4.5	66
46	Phosphorylated CtIP Functions as a Co-factor of the MRE11-RAD50-NBS1 Endonuclease in DNA End Resection. <i>Molecular Cell</i> , 2016, 64, 940-950.	4.5	237
47	RECQL4 Promotes DNA End Resection in Repair of DNA Double-Strand Breaks. <i>Cell Reports</i> , 2016, 16, 161-173.	2.9	81
48	Replication intermediates that escape Dna2 activity are processed by Holliday junction resolvase Yen1. <i>Nature Communications</i> , 2016, 7, 13157.	5.8	31
49	Force regulated dynamics of RPA on a DNA fork. <i>Nucleic Acids Research</i> , 2016, 44, 5837-5848.	6.5	31
50	H4K20me0 marks post-replicative chromatin and recruits the TONSL-MMS22L DNA repair complex. <i>Nature</i> , 2016, 534, 714-718.	13.7	172
51	Human DNA2 possesses a cryptic DNA unwinding activity that functionally integrates with BLM or WRN helicases. <i>ELife</i> , 2016, 5, .	2.8	59
52	The <i>Saccharomyces cerevisiae</i> Dna2 can function as a sole nuclease in the processing of Okazaki fragments in DNA replication. <i>Nucleic Acids Research</i> , 2015, 43, 7888-7897.	6.5	40
53	Top3-Rmi1 Dissolve Rad51-Mediated D Loops by a Topoisomerase-Based Mechanism. <i>Molecular Cell</i> , 2015, 57, 595-606.	4.5	103
54	DNA2 drives processing and restart of reversed replication forks in human cells. <i>Journal of Cell Biology</i> , 2015, 208, 545-562.	2.3	280

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55	DNA End Resection: Nucleases Team Up with the Right Partners to Initiate Homologous Recombination. <i>Journal of Biological Chemistry</i> , 2015, 290, 22931-22938.	1.6	179
56	DNA2 Cooperates with the WRN and BLM RecQ Helicases to Mediate Long-range DNA End Resection in Human Cells. <i>Journal of Biological Chemistry</i> , 2014, 289, 27314-27326.	1.6	162
57	The <i>Saccharomyces cerevisiae</i> Mlh1-Mlh3 Heterodimer Is an Endonuclease That Preferentially Binds to Holliday Junctions. <i>Journal of Biological Chemistry</i> , 2014, 289, 5674-5686.	1.6	116
58	Sae2 promotes dsDNA endonuclease activity within Mre11-Rad50-Xrs2 to resect DNA breaks. <i>Nature</i> , 2014, 514, 122-125.	13.7	364
59	Structural and mechanistic insight into Holliday-junction dissolution by Topoisomerase III \pm and RMI1. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 261-268.	3.6	71
60	Ribonucleotides Misincorporated into DNA Act as Strand-Discrimination Signals in Eukaryotic Mismatch Repair. <i>Molecular Cell</i> , 2013, 50, 323-332.	4.5	139
61	Pif1 family helicases suppress genome instability at G-quadruplex motifs. <i>Nature</i> , 2013, 497, 458-462.	13.7	403
62	Relationship of DNA degradation by <i>Saccharomyces cerevisiae</i> Exonuclease 1 and its stimulation by RPA and Mre11-Rad50-Xrs2 to DNA end resection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E1661-8.	3.3	110
63	Nuclease activity of <i>Saccharomyces cerevisiae</i> Dna2 inhibits its potent DNA helicase activity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E1992-2001.	3.3	52
64	Decatenation of DNA by the <i>S. cerevisiae</i> Sgs1-Top3-Rmi1 and RPA Complex: A Mechanism for Disentangling Chromosomes. <i>Molecular Cell</i> , 2012, 47, 886-896.	4.5	92
65	Rmi1 stimulates decatenation of double Holliday junctions during dissolution by Sgs1-Top3. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 1377-1382.	3.6	175
66	DNA end resection by Dna2-Sgs1-RPA and its stimulation by Top3-Rmi1 and Mre11-Rad50-Xrs2. <i>Nature</i> , 2010, 467, 112-116.	13.7	421
67	The Full-length <i>Saccharomyces cerevisiae</i> Sgs1 Protein Is a Vigorous DNA Helicase That Preferentially Unwinds Holliday Junctions. <i>Journal of Biological Chemistry</i> , 2010, 285, 8290-8301.	1.6	106
68	Interplay of DNA Repair Pathways Controls Methylation Damage Toxicity in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2008, 179, 1835-1844.	1.2	16
69	Homologous Recombination Rescues Mismatch-Repair-Dependent Cytotoxicity of SN1-Type Methylating Agents in <i>S. cerevisiae</i> . <i>Current Biology</i> , 2005, 15, 1395-1400.	1.8	33
70	Somatic hypermutation and mismatch repair in non-B Δ cells. <i>European Journal of Immunology</i> , 2005, 35, 2222-2229.	1.6	3
71	Expression of the MutL Homologue hMLH3 in Human Cells and its Role in DNA Mismatch Repair. <i>Cancer Research</i> , 2005, 65, 10759-10766.	0.4	105
72	High Doses of SN1 Type Methylating Agents Activate DNA Damage Signaling Cascades that are Largely Independent of Mismatch Repair. <i>Cell Cycle</i> , 2005, 4, 473-477.	1.3	40

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73	Dependence of the Cytotoxicity of DNA-Damaging Agents on the Mismatch Repair Status of Human Cells. <i>Cancer Research</i> , 2004, 64, 3391-3394.	0.4	102
74	Mismatch repair-dependent G2 checkpoint induced by low doses of SN1 type methylating agents requires the ATR kinase. <i>Genes and Development</i> , 2004, 18, 1331-1344.	2.7	206
75	Is mismatch repair really required for ionizing radiation-induced DNA damage signaling?. <i>Nature Genetics</i> , 2004, 36, 432-433.	9.4	18
76	Methylation-induced G2/M arrest requires a full complement of the mismatch repair protein hMLH1. <i>EMBO Journal</i> , 2003, 22, 2245-2254.	3.5	160
77	Differential killing of mismatch repair-deficient and -proficient cells: towards the therapy of tumors with microsatellite instability. <i>Cancer Research</i> , 2003, 63, 8113-7.	0.4	7
78	Mismatch repair-dependent transcriptome changes in human cells treated with the methylating agent N-methyl-n'-nitro-N-nitrosoguanidine. <i>Cancer Research</i> , 2003, 63, 8158-66.	0.4	18
79	Dissection of the Functions of the <i>Saccharomyces cerevisiae</i> RAD6 Postreplicative Repair Group in Mutagenesis and UV Sensitivity. <i>Genetics</i> , 2001, 159, 953-963.	1.2	45
80	Mechanism of Replication Fork Reversal and Protection by Human RAD51 and RAD51 Paralogs. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0