Jeremy M Stark

List of Publications by Year
in descending order

63 papers	6,408 citations	101543 36 h-index	123424 61 g-index
67 all docs	67 docs citations	67 times ranked	7775 citing authors

#	Article	IF	Citations
1	Microarray screening reveals two non-conventional SUMO-binding modules linked to DNA repair by non-homologous end-joining. Nucleic Acids Research, 2022, 50, 4732-4754.	14.5	4
2	The importance of DNAPKcs for blunt DNA end joining is magnified when XLF is weakened. Nature Communications, 2022, 13, .	12.8	9
3	m ⁶ A deposition is regulated by PRMT1â€mediated arginine methylation of METTL14 in its disordered Câ€terminal region. EMBO Journal, 2021, 40, e106309.	7.8	30
4	Polζ reverse transcribes RNA and promotes RNA-templated DNA repair. Science Advances, 2021, 7, .	10.3	51
5	R-Loop Associated Mitotic Stress Confers Vulnerabilities in Splicing Factor Mutant Leukemia. Blood, 2021, 138, 3713-3713.	1.4	0
6	Functional deficiency of DNA repair gene EXO5 results in androgen-induced genomic instability and prostate tumorigenesis. Oncogene, 2020, 39, 1246-1259.	5.9	8
7	53BP1 Enforces Distinct Pre- and Post-resection Blocks on Homologous Recombination. Molecular Cell, 2020, 77, 26-38.e7.	9.7	85
8	The canonical non-homologous end joining factor XLF promotes chromosomal deletion rearrangements in human cells. Journal of Biological Chemistry, 2020, 295, 125-137.	3.4	12
9	RNF8 has both KU-dependent and independent roles in chromosomal break repair. Nucleic Acids Research, 2020, 48, 6032-6052.	14.5	15
10	The RAD52 S346X variant reduces risk of developing breast cancer in carriers of pathogenic germline BRCA2 mutations. Molecular Oncology, 2020, 14, 1124-1133.	4.6	13
11	USP22 Interacts with PALB2 and Promotes Chemotherapy Resistance via Homologous Recombination of DNA Double-Strand Breaks. Molecular Cancer Research, 2020, 18, 424-435.	3.4	12
12	BLM has Contrary Effects on Repeat-Mediated Deletions, based on the Distance of DNA DSBs to a Repeat and Repeat Divergence. Cell Reports, 2020, 30, 1342-1357.e4.	6.4	17
13	XLF acts as a flexible connector during non-homologous end joining. ELife, 2020, 9, .	6.0	22
14	Distinct roles of RAD52 and POLQ in chromosomal break repair and replication stress response. PLoS Genetics, 2019, 15, e1008319.	3.5	60
15	Electrophilic fatty acids impair RAD51 function and potentiate the effects of DNA-damaging agents on growth of triple-negative breast cells. Journal of Biological Chemistry, 2019, 294, 397-404.	3.4	16
16	Repeat-mediated deletions can be induced by a chromosomal break far from a repeat, but multiple pathways suppress such rearrangements. Genes and Development, 2018, 32, 524-536.	5.9	35
17	C-NHEJ without indels is robust and requires synergistic function of distinct XLF domains. Nature Communications, 2018, 9, 2484.	12.8	75
18	The Anticancer Activity of a First-in-class Small-molecule Targeting PCNA. Clinical Cancer Research, 2018, 24, 6053-6065.	7.0	27

#	Article	IF	Citations
19	Contribution of canonical nonhomologous end joining to chromosomal rearrangements is enhanced by ATM kinase deficiency. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 728-733.	7.1	28
20	PRPF8 is important for BRCA1-mediated homologous recombination. Oncotarget, 2017, 8, 93319-93337.	1.8	15
21	Myelodysplasia-associated mutations in serine/arginine-rich splicing factor SRSF2 lead to alternative splicing of CDC25C. BMC Molecular Biology, 2016, 17, 18.	3.0	7
22	Tetratricopeptide repeat factor XAB2 mediates the end resection step of homologous recombination. Nucleic Acids Research, 2016, 44, 5702-5716.	14.5	26
23	Regulation of Single-Strand Annealing and its Role in Genome Maintenance. Trends in Genetics, 2016, 32, 566-575.	6.7	344
24	RNF4 regulates DNA double-strand break repair in a cell cycle-dependent manner. Cell Cycle, 2016, 15, 787-798.	2.6	23
25	Heavy Metal Exposure Influences Double Strand Break DNA Repair Outcomes. PLoS ONE, 2016, 11, e0151367.	2.5	107
26	EXO1 is critical for embryogenesis and the DNA damage response in mice with a hypomorphicNbs1allele. Nucleic Acids Research, 2015, 43, 7371-7387.	14.5	16
27	DNA Damage Response Factors from Diverse Pathways, Including DNA Crosslink Repair, Mediate Alternative End Joining. PLoS Genetics, 2015, 11, e1004943.	3.5	114
28	An RNF168 fragment defective for focal accumulation at DNA damage is proficient for inhibition of homologous recombination in BRCA1 deficient cells. Nucleic Acids Research, 2014, 42, 7720-7733.	14.5	28
29	TGFÎ² Induces â€œBRCAnessâ€•and Sensitivity to PARP Inhibition in Breast Cancer by Regulating DNA-Repair Genes. Molecular Cancer Research, 2014, 12, 1597-1609.	3.4	56
30	A PCNA-Derived Cell Permeable Peptide Selectively Inhibits Neuroblastoma Cell Growth. PLoS ONE, 2014, 9, e94773.	2.5	22
31	Visualization of local DNA unwinding by Mre11/Rad50/Nbs1 using single-molecule FRET. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 18868-18873.	7.1	55
32	HP1 promotes tumor suppressor BRCA1 functions during the DNA damage response. Nucleic Acids Research, 2013, 41, 5784-5798.	14.5	83
33	The interaction between CtIP and BRCA1 is not essential for resection-mediated DNA repair or tumor suppression. Journal of Cell Biology, 2013, 201, 693-707.	5.2	71
34	The HSV-1 Exonuclease, UL12, Stimulates Recombination by a Single Strand Annealing Mechanism. PLoS Pathogens, 2012, 8, e1002862.	4.7	80
35	Suberoylanilide Hydroxamic Acid as a Radiosensitizer through Modulation of RAD51 Protein and Inhibition of Homology-Directed Repair in Multiple Myeloma. Molecular Cancer Research, 2012, 10, 1052-1064.	3.4	47
36	Examining the roles of DNA2 during mammalian end resection. Cell Cycle, 2012, 11, 4111-4111.	2.6	0

#	Article	IF	Citations
37	Ring Finger Nuclear Factor RNF168 Is Important for Defects in Homologous Recombination Caused by Loss of the Breast Cancer Susceptibility Factor BRCA1. Journal of Biological Chemistry, 2012, 287, 40618-40628.	3.4	44
38	RI-1: a chemical inhibitor of RAD51 that disrupts homologous recombination in human cells. Nucleic Acids Research, 2012, 40, 7347-7357.	14.5	154
39	A Dual Role for UVRAG in Maintaining Chromosomal Stability Independent of Autophagy. Developmental Cell, 2012, 22, 1001-1016.	7.0	90
40	I-SceI-Based Assays to Examine Distinct Repair Outcomes of Mammalian Chromosomal Double Strand Breaks. Methods in Molecular Biology, 2012, 920, 379-391.	0.9	271
41	Chronic myelogenous leukemia stem and progenitor cells demonstrate chromosomal instability related to repeated breakage-fusion-bridge cycles mediated by increased nonhomologous end joining. Blood, 2012, 119, 6187-6197.	1.4	42
42	Subtelomeric regions in mammalian cells are deficient in DNA double-strand break repair. DNA Repair, 2011, 10, 536-544.	2.8	34
43	Trex2 Enables Spontaneous Sister Chromatid Exchanges Without Facilitating DNA Double-Strand Break Repair. Genetics, 2011, 188, 787-797.	2.9	15
44	The relative efficiency of homology-directed repair has distinct effects on proper anaphase chromosome separation. Nucleic Acids Research, 2011, 39, 5935-5944.	14.5	41
45	Interhomolog recombination and loss of heterozygosity in wild-type and Bloom syndrome helicase (BLM)-deficient mammalian cells. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 11971-11976.	7.1	72
46	Protein phosphatase PP6 is required for homology-directed repair of DNA double-strand breaks. Cell Cycle, 2011, 10, 1411-1419.	2.6	45
47	Correct End Use during End Joining of Multiple Chromosomal Double Strand Breaks Is Influenced by Repair Protein RAD50, DNA-dependent Protein Kinase DNA-PKcs, and Transcription Context. Journal of Biological Chemistry, 2011, 286, 42470-42482.	3.4	95
48	Mammalian Fbh1 is important to restore normal mitotic progression following decatenation stress. DNA Repair, 2010, 9, 708-717.	2.8	18
49	Physical Interaction of RECQ5 Helicase with RAD51 Facilitates Its Anti-recombinase Activity. Journal of Biological Chemistry, 2010, 285, 15739-15745.	3.4	78
50	ATM Limits Incorrect End Utilization during Non-Homologous End Joining of Multiple Chromosome Breaks. PLoS Genetics, 2010, 6, e1001194.	3.5	43
51	53BP1 Inhibits Homologous Recombination in Brca1-Deficient Cells by Blocking Resection of DNA Breaks. Cell, 2010, 141, 243-254.	28.9	1,406
52	Limiting the Persistence of a Chromosome Break Diminishes Its Mutagenic Potential. PLoS Genetics, 2009, 5, e1000683.	3.5	77
53	Alternative-NHEJ Is a Mechanistically Distinct Pathway of Mammalian Chromosome Break Repair. PLoS Genetics, 2008, 4, e1000110.	3.5	708
54	RECQL5/Recql5 helicase regulates homologous recombination and suppresses tumor formation via disruption of Rad51 presynaptic filaments. Genes and Development, 2007, 21, 3073-3084.	5.9	283

#	Article	IF	Citations
55	Suppression of the DNA repair defects of BRCA2-deficient cells with heterologous protein fusions. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 8768-8773.	7.1	91
56	Genetic Steps of Mammalian Homologous Repair with Distinct Mutagenic Consequences. Molecular and Cellular Biology, 2004, 24, 9305-9316.	2.3	439
57	Rad51 overexpression promotes alternative double-strand break repair pathways and genome instability. Oncogene, 2004, 23, 546-553.	5.9	216
58	Extensive Loss of Heterozygosity Is Suppressed during Homologous Repair of Chromosomal Breaks. Molecular and Cellular Biology, 2003, 23, 733-743.	2.3	110
59	ATP Hydrolysis by Mammalian RAD51 Has a Key Role during Homology-directed DNA Repair. Journal of Biological Chemistry, 2002, 277, 20185-20194.	3.4	124
60	Variant XRCC3 implicated in cancer is functional in homology-directed repair of double-strand breaks. Oncogene, 2002, 21, 4176-4180.	5.9	107
61	Double-strand breaks and tumorigenesis. Trends in Cell Biology, 2001, 11, S52-S59.	7.9	135
62	The Relative Strengths of SR Protein-mediated Associations of Alternative and Constitutive Exons Can Influence Alternative Splicing. Journal of Biological Chemistry, 1999, 274, 29838-29842.	3.4	12
63	Multiple Regions of Yeast Ribosomal Protein L1 Are Important for Its Interaction with 5 S rRNA and Assembly into Ribosomes. Journal of Biological Chemistry, 1995, 270, 30148-30156.	3.4	43