Eric A Hendrickson

List of Publications by Year
in descending order

56 papers	3,025 citations	186265 28 h-index	168389 53 g-index
58 all docs	58 docs citations	58 times ranked	4194 citing authors

#	Article	IF	Citations
1	DNA2 drives processing and restart of reversed replication forks in human cells. Journal of Cell Biology, 2015, 208, 545-562.	5.2	280
2	Chromosomal Translocations in Human Cells Are Generated by Canonical Nonhomologous End-Joining. Molecular Cell, 2014, 55, 829-842.	9.7	278
3	Ku Regulates the Non-Homologous End Joining Pathway Choice of DNA Double-Strand Break Repair in Human Somatic Cells. PLoS Genetics, 2010, 6, e1000855.	3.5	198
4	Ku86 is essential in human somatic cells. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 832-837.	7.1	172
5	Ku86 represses lethal telomere deletion events in human somatic cells. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 12430-12435.	7.1	141
6	ATRX represses alternative lengthening of telomeres. Oncotarget, 2015, 6, 16543-16558.	1.8	135
7	DNA-dependent Protein Kinase Is a Target for a CPP32-like Apoptotic Protease. Journal of Biological Chemistry, 1996, 271, 25035-25040.	3.4	112
8	The Catalytic Subunit of DNA-Dependent Protein Kinase Regulates Proliferation, Telomere Length, and Genomic Stability in Human Somatic Cells. Molecular and Cellular Biology, 2008, 28, 6182-6195.	2.3	107
9	Regulation of Telomere Length and Suppression of Genomic Instability in Human Somatic Cells by Ku86. Molecular and Cellular Biology, 2004, 24, 5050-5059.	2.3	91
10	The HSV-1 Exonuclease, UL12, Stimulates Recombination by a Single Strand Annealing Mechanism. PLoS Pathogens, 2012, 8, e1002862.	4.7	80
11	Mechanisms of precise genome editing using oligonucleotide donors. Genome Research, 2017, 27, 1099-1111.	5.5	76
12	<i>Ku70</i> , an essential gene, modulates the frequency of rAAV-mediated gene targeting in human somatic cells. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 8703-8708.	7.1	75
13	The fidelity of the ligation step determines how ends are resolved during nonhomologous end joining. Nature Communications, 2014, 5, 4286.	12.8	69
14	CtIP mediates replication fork recovery in a FANCD2-regulated manner. Human Molecular Genetics, 2014, 23, 3695-3705.	2.9	68
15	FANCI Regulates Recruitment of the FA Core Complex at Sites of DNA Damage Independently of FANCD2. PLoS Genetics, 2015, 11, e1005563.	3.5	67
16	Radiosensitization by PARP Inhibition in DNA Repair Proficient and Deficient Tumor Cells: Proliferative Recovery in Senescent Cells. Radiation Research, 2016, 185, 229.	1.5	66
17	Escape from Telomere-Driven Crisis Is DNA Ligase III Dependent. Cell Reports, 2014, 8, 1063-1076.	6.4	65
18	Preventing over-resection by DNA2 helicase/nuclease suppresses repair defects in Fanconi anemia cells. Cell Cycle, 2014, 13, 1540-1550.	2.6	58

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19	Cockayne syndrome group B protein regulates <scp>DNA</scp> doubleâ€strand break repair and checkpoint activation. EMBO Journal, 2015, 34, 1399-1416.	7.8	57
20	DNA-PKcs promotes chromatin decondensation to facilitate initiation of the DNA damage response. Nucleic Acids Research, 2019, 47, 9467-9479.	14.5	55
21	A versatile reporter system for CRISPR-mediated chromosomal rearrangements. Genome Biology, 2015, 16, 111.	9.6	52
22	XRCC4/XLF Interaction Is Variably Required for DNA Repair and Is Not Required for Ligase IV Stimulation. Molecular and Cellular Biology, 2015, 35, 3017-3028.	2.3	50
23	DNA ligase III and DNA ligase IV carry out genetically distinct forms of end joining in human somatic cells. DNA Repair, 2014, 21, 97-110.	2.8	47
24	Chromothripsis during telomere crisis is independent of NHEJ, and consistent with a replicative origin. Genome Research, 2019, 29, 737-749.	5.5	47
25	Human LIGIV is synthetically lethal with the loss of Rad54B-dependent recombination and is required for certain chromosome fusion events induced by telomere dysfunction. Nucleic Acids Research, 2013, 41, 1734-1749.	14.5	44
26	The Mechanism of Gene Targeting in Human Somatic Cells. PLoS Genetics, 2014, 10, e1004251.	3.5	44
27	Mutations to Ku reveal differences in human somatic cell lines. DNA Repair, 2008, 7, 762-774.	2.8	38
28	Sister chromatid telomere fusions, but not NHEJ-mediated inter-chromosomal telomere fusions, occur independently of DNA ligases 3 and 4. Genome Research, 2016, 26, 588-600.	5.5	38
29	CTC1â€STN1 coordinates Gâ€and Câ€strand synthesis to regulate telomere length. Aging Cell, 2018, 17, e12783.	6.7	35
30	FANCI and FANCD2 have common as well as independent functions during the cellular replication stress response. Nucleic Acids Research, 2017, 45, 11837-11857.	14.5	34
31	High-throughput identification of noncoding functional SNPs via type IIS enzyme restriction. Nature Genetics, 2018, 50, 1180-1188.	21.4	31
32	EXO1 resection at G-quadruplex structures facilitates resolution and replication. Nucleic Acids Research, 2020, 48, 4960-4975.	14.5	26
33	Restoration of ATM Expression in DNA-PKcsâ€“Deficient Cells Inhibits Signal End Joining. Journal of Immunology, 2016, 196, 3032-3042.	0.8	24
34	Human somatic cells deficient for RAD52 are impaired for viral integration and compromised for most aspects of homology-directed repair. DNA Repair, 2017, 55, 64-75.	2.8	24
35	Restoration of X-ray and etoposide resistance, Ku-end binding activity and V(D)J recombination to the Chinese hamster sxi-3 mutant by a hamster Ku86 cDNA. Mutation Research DNA Repair, 1996, 363, 43-56.	3.7	23
36	Bi-allelic MCM10 variants associated with immune dysfunction and cardiomyopathy cause telomere shortening. Nature Communications, 2021, 12, 1626.	12.8	22

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37	A role for XLF in DNA repair and recombination in human somatic cells. DNA Repair, 2014, 15, 39-53.	2.8	21
38	Functional cross talk between the Fanconi anemia and ATRX/DAXX histone chaperone pathways promotes replication fork recovery. Human Molecular Genetics, 2020, 29, 1083-1095.	2.9	21
39	DNA Ligase 1 is an essential mediator of sister chromatid telomere fusions in G2 cell cycle phase. Nucleic Acids Research, 2019, 47, 2402-2424.	14.5	19
40	Histone Deacetylase Inhibitors Selectively Target Homology Dependent DNA Repair Defective Cells and Elevate Non-Homologous Endjoining Activity. PLoS ONE, 2014, 9, e87203.	2.5	17
41	Telomere fusions and translocations: a bridge too far?. Current Opinion in Genetics and Development, 2020, 60, 85-91.	3.3	17
42	TDP1 suppresses mis-joining of radiomimetic DNA double-strand breaks and cooperates with Artemis to promote optimal nonhomologous end joining. Nucleic Acids Research, 2018, 46, 8926-8939.	14.5	15
43	PARP1 is required for preserving telomeric integrity but is dispensable for A-NHEJ. Oncotarget, 2018, 9, 34821-34837.	1.8	14
44	CtIP is essential for telomere replication. Nucleic Acids Research, 2019, 47, 8927-8940.	14.5	13
45	Absence of XRCC4 and its paralogs in human cells reveal differences in outcomes for DNA repair and V(D)J recombination. DNA Repair, 2020, 85, 102738.	2.8	10
46	Telomere replicationâ€"When the going gets tough. DNA Repair, 2020, 94, 102875.	2.8	9
47	RAD52: Viral Friend or Foe?. Cancers, 2020, 12, 399.	3.7	9
48	Gene Targeting in Human Somatic Cells. , 2008, , 509-525.		8
49	Telomeres and Chromosomal Translocations. Advances in Experimental Medicine and Biology, 2018, 1044, 89-112.	1.6	5
50	PARP inhibition prevents escape from a telomere-driven crisis and inhibits cell immortalisation. Oncotarget, 2018, 9, 37549-37563.	1.8	4
51	POLQ suppresses genome instability and alterations inÂDNA repeat tract lengths. NAR Cancer, 2022, 4, .	3.1	3
52	Alternative end joining, clonal evolution, and escape from a telomere-driven crisis. Molecular and Cellular Oncology, 2015, 2, e975623.	0.7	2
53	Both the classical and alternative non-homologous end joining pathways contribute to the fusion of drastically shortened telomeres induced by TRF2 overexpression. Cell Cycle, 2019, 18, 880-888.	2.6	2
54	Functional validation of TERT and TERC variants of uncertain significance in patients with short telomere syndromes. Blood Cancer Journal, 2020, 10, 120.	6.2	2

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55	Conversion Tract Analysis of Homology-Directed Genome Editing Using Oligonucleotide Donors. Methods in Molecular Biology, 2019, 1999, 131-144.	0.9	1
56	FANCN Hypomorphic Mutation Retains BRCA1 Binding Domain. Blood, 2016, 128, 2676-2676.	1.4	0