List of Publications by Year in descending order

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DALE A RAMODEN

#	Article	IF	CITATIONS
1	Ku Recruits the XRCC4-Ligase IV Complex to DNA Ends. Molecular and Cellular Biology, 2000, 20, 2996-3003.	2.3	349
2	A Gradient of Template Dependence Defines Distinct Biological Roles for Family X Polymerases in Nonhomologous End Joining. Molecular Cell, 2005, 19, 357-366.	9.7	294
3	Ku complex interacts with and stimulates the Werner protein. Genes and Development, 2000, 14, 907-912.	5.9	276
4	Association of DNA Polymerase μ (pol μ) with Ku and Ligase IV: Role for pol μ in End-Joining Double-Strand Break Repair. Molecular and Cellular Biology, 2002, 22, 5194-5202.	2.3	270
5	Inflammasome-independent role of AIM2 in suppressing colon tumorigenesis via DNA-PK and Akt. Nature Medicine, 2015, 21, 906-913.	30.7	230
6	Essential Roles for Polymerase Î,-Mediated End Joining in the Repair of Chromosome Breaks. Molecular Cell, 2016, 63, 662-673.	9.7	229
7	The molecular basis and disease relevance of non-homologous DNA end joining. Nature Reviews Molecular Cell Biology, 2020, 21, 765-781.	37.0	217
8	Mechanism of Suppression of Chromosomal Instability by DNA Polymerase POLQ. PLoS Genetics, 2014, 10, e1004654.	3.5	214
9	The DNAâ€dependent protein kinase: the director at the end. Immunological Reviews, 2004, 200, 132-141.	6.0	192
10	Ku is a 5′-dRP/AP lyase that excises nucleotide damage near broken ends. Nature, 2010, 464, 1214-1217.	27.8	171
11	Polymerase Mu Is a DNA-Directed DNA/RNA Polymerase. Molecular and Cellular Biology, 2003, 23, 2309-2315.	2.3	161
12	Organization and dynamics of the nonhomologous end-joining machinery during DNA double-strand break repair. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E2575-84.	7.1	142
13	Werner Protein Is a Target of DNA-dependent Protein Kinase in Vivo and in Vitro, and Its Catalytic Activities Are Regulated by Phosphorylation. Journal of Biological Chemistry, 2002, 277, 18291-18302.	3.4	141
14	Cell-free V(D)J recombination. Nature, 1997, 388, 488-491.	27.8	136
15	Non-homologous End Joining Requires That the DNA-PK Complex Undergo an Autophosphorylation-dependent Rearrangement at DNA Ends. Journal of Biological Chemistry, 2004, 279, 39408-39413.	3.4	123
16	Nonhomologous end joining: A good solution for bad ends. DNA Repair, 2014, 17, 39-51.	2.8	109
17	Genetic determinants of cellular addiction to DNA polymerase theta. Nature Communications, 2019, 10, 4286.	12.8	106
18	Structural insights into NHEJ: Building up an integrated picture of the dynamic DSB repair super complex, one component and interaction at a time. DNA Repair, 2014, 17, 110-120.	2.8	100

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19	Mechanistic basis for microhomology identification and genome scarring by polymerase theta. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 8476-8485.	7.1	96
20	Structural insight into the substrate specificity of DNA Polymerase μ. Nature Structural and Molecular Biology, 2007, 14, 45-53.	8.2	89
21	Ku heterodimer binds to both ends of the Werner protein and functional interaction occurs at the Werner N-terminus. Nucleic Acids Research, 2002, 30, 3583-3591.	14.5	86
22	Radiation-related genomic profile of papillary thyroid carcinoma after the Chernobyl accident. Science, 2021, 372, .	12.6	85
23	Mechanism, cellular functions and cancer roles of polymerase-theta-mediated DNA end joining. Nature Reviews Molecular Cell Biology, 2022, 23, 125-140.	37.0	84
24	Tyrosyl-DNA phosphodiesterase and the repair of 3′-phosphoglycolate-terminated DNA double-strand breaks. DNA Repair, 2009, 8, 901-911.	2.8	72
25	The fidelity of the ligation step determines how ends are resolved during nonhomologous end joining. Nature Communications, 2014, 5, 4286.	12.8	69
26	Ribonucleotide incorporation enables repair of chromosome breaks by nonhomologous end joining. Science, 2018, 361, 1126-1129.	12.6	69
27	A specific loop in human DNA polymerase mu allows switching between creative and DNA-instructed synthesis. Nucleic Acids Research, 2006, 34, 4572-4582.	14.5	65
28	Genomic instability due to V(D)J recombination-associated transposition. Genes and Development, 2006, 20, 1575-1582.	5.9	65
29	Essential role for polymerase specialization in cellular nonhomologous end joining. Proceedings of the United States of America, 2015, 112, E4537-45.	7.1	61
30	Werner Protein Cooperates with the XRCC4-DNA Ligase IV Complex in End-Processing. Biochemistry, 2008, 47, 7548-7556.	2.5	59
31	Dual Modes of Interaction between XRCC4 and Polynucleotide Kinase/Phosphatase. Journal of Biological Chemistry, 2010, 285, 37619-37629.	3.4	57
32	Sustained active site rigidity during synthesis by human DNA polymerase μ. Nature Structural and Molecular Biology, 2014, 21, 253-260.	8.2	57
33	End-bridging is required for pol μ to efficiently promote repair of noncomplementary ends by nonhomologous end joining. Nucleic Acids Research, 2008, 36, 3085-3094.	14.5	54
34	DNA Ligase IV Guides End-Processing Choice during Nonhomologous End Joining. Cell Reports, 2017, 20, 2810-2819.	6.4	53
35	Sibling rivalry: competition between Pol X family members in V(D)J recombination and general double strand break repair. Immunological Reviews, 2004, 200, 156-164.	6.0	52
36	DNA repair factor RAD18 and DNA polymerase Poll [®] confer tolerance of oncogenic DNA replication stress. Journal of Cell Biology, 2017, 216, 3097-3115.	5.2	52

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37	Template strand scrunching during DNA gap repair synthesis by human polymerase λ. Nature Structural and Molecular Biology, 2009, 16, 967-972.	8.2	49
38	Specificity of the dRP/AP Lyase of Ku Promotes Nonhomologous End Joining (NHEJ) Fidelity at Damaged Ends*. Journal of Biological Chemistry, 2012, 287, 13686-13693.	3.4	47
39	Translesion Synthesis Past Platinum DNA Adducts by Human DNA Polymerase μâ€. Biochemistry, 2003, 42, 1777-1788.	2.5	41
40	Polymerases in Nonhomologous End Joining: Building a Bridge over Broken Chromosomes. Antioxidants and Redox Signaling, 2011, 14, 2509-2519.	5.4	41
41	Loading of the Nonhomologous End Joining Factor, Ku, on Protein-occluded DNA Ends. Journal of Biological Chemistry, 2007, 282, 10605-10613.	3.4	36
42	Structural accommodation of ribonucleotide incorporation by the DNA repair enzyme polymerase Mu. Nucleic Acids Research, 2017, 45, 9138-9148.	14.5	36
43	Bridging of double-stranded breaks by the nonhomologous end-joining ligation complex is modulated by DNA end chemistry. Nucleic Acids Research, 2017, 45, 1872-1878.	14.5	35
44	A comparison of BRCT domains involved in nonhomologous end-joining: Introducing the solution structure of the BRCT domain of polymerase lambda. DNA Repair, 2008, 7, 1340-1351.	2.8	33
45	DNA polymerases in nonhomologous end joining: Are there any benefits to standing out from the crowd?. Environmental and Molecular Mutagenesis, 2012, 53, 741-751.	2.2	30
46	WRN Exonuclease activity is blocked by specific oxidatively induced base lesions positioned in either DNA strand. Nucleic Acids Research, 2008, 36, 4975-4987.	14.5	26
47	Oxidative DNA-protein crosslinks formed in mammalian cells by abasic site lyases involved in DNA repair, 2020, 87, 102773.	2.8	26
48	Solution Structure of Polymerase μ's BRCT Domain Reveals an Element Essential for Its Role in Nonhomologous End Joining. Biochemistry, 2007, 46, 12100-12110.	2.5	25
49	Activity of ribonucleotide reductase helps determine how cells repair DNA double strand breaks. DNA Repair, 2009, 8, 1258-1263.	2.8	24
50	Reversal of DNA damage induced Topoisomerase 2 DNA–protein crosslinks by Tdp2. Nucleic Acids Research, 2016, 44, 3829-3844.	14.5	23
51	Trimming of damaged $3\hat{a}\in^2$ overhangs of DNA double-strand breaks by the Metnase and Artemis endonucleases. DNA Repair, 2013, 12, 422-432.	2.8	22
52	V(D)J recombination: Born to be wild. Seminars in Cancer Biology, 2010, 20, 254-260.	9.6	21
53	Substrate preference of Gen endonucleases highlights the importance of branched structures as DNA damage repair intermediates. Nucleic Acids Research, 2017, 45, 5333-5348.	14.5	21
54	Mechanisms driving chromosomal translocations: lost in time and space. Oncogene, 2021, 40, 4263-4270.	5.9	21

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55	DNA polymerase theta suppresses mitotic crossing over. PLoS Genetics, 2021, 17, e1009267.	3.5	19
56	Requirements for 5′dRP/AP lyase activity in Ku. Nucleic Acids Research, 2014, 42, 11136-11143.	14.5	18
57	Dual inhibition of DNA-PK and DNA polymerase theta overcomes radiation resistance induced by p53 deficiency. NAR Cancer, 2020, 2, zcaa038.	3.1	18
58	Marker-free quantification of repair pathway utilization at Cas9-induced double-strand breaks. Nucleic Acids Research, 2021, 49, 5095-5105.	14.5	14
59	Regulation of human polλ by ATM-mediated phosphorylation during non-homologous end joining. DNA Repair, 2017, 51, 31-45.	2.8	13
60	Resolution of complex ends by Nonhomologous end joining - better to be lucky than good?. Genome Integrity, 2012, 3, 10.	1.0	12
61	Polμ tumor variants decrease the efficiency and accuracy of NHEJ. Nucleic Acids Research, 2017, 45, 10018-10031.	14.5	9
62	Nonhomologous end joining of complex DNA double-strand breaks with proximal thymine glycol and interplay with base excision repair. DNA Repair, 2016, 41, 16-26.	2.8	8
63	High-Throughput Analysis of DNA Break-Induced Chromosome Rearrangements by Amplicon Sequencing. Methods in Enzymology, 2018, 601, 111-144.	1.0	8
64	Unexpected behavior of DNA polymerase Mu opposite template 8-oxo-7,8-dihydro-2′-guanosine. Nucleic Acids Research, 2019, 47, 9410-9422.	14.5	8
65	Analysis of diverse double-strand break synapsis with Polλ reveals basis for unique substrate specificity in nonhomologous end-joining. Nature Communications, 2022, 13, .	12.8	7
66	Structural snapshots of human DNA polymerase μ engaged on a DNA double-strand break. Nature Communications, 2020, 11, 4784.	12.8	6
67	The <i>Drosophila melanogaster</i> Ortholog of RFWD3 Functions Independently of RAD51 During DNA Repair. G3: Genes, Genomes, Genetics, 2020, 10, 999-1004.	1.8	2