Dale A Ramsden

List of Publications by Year
in descending order

67 papers	5,385 citations	81900 39 h-index	98798 67 g-index
70 all docs	70 docs citations	70 times ranked	4316 citing authors

#	Article	IF	Citations
1	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
2	Analysis of diverse double-strand break synapsis with PolÎ» reveals basis for unique substrate specificity in nonhomologous end-joining. Nature Communications, 2022, 13, .	12.8	7
3	DNA polymerase theta suppresses mitotic crossing over. PLoS Genetics, 2021, 17, e1009267.	3.5	19
4	Radiation-related genomic profile of papillary thyroid carcinoma after the Chernobyl accident. Science, 2021, 372, .	12.6	85
5	Marker-free quantification of repair pathway utilization at Cas9-induced double-strand breaks. Nucleic Acids Research, 2021, 49, 5095-5105.	14.5	14
6	Mechanisms driving chromosomal translocations: lost in time and space. Oncogene, 2021, 40, 4263-4270.	5.9	21
7	Oxidative DNA-protein crosslinks formed in mammalian cells by abasic site lyases involved in DNA repair. DNA Repair, 2020, 87, 102773.	2.8	26
8	Structural snapshots of human DNA polymerase Î¼ engaged on a DNA double-strand break. Nature Communications, 2020, 11, 4784.	12.8	6
9	The molecular basis and disease relevance of non-homologous DNA end joining. Nature Reviews Molecular Cell Biology, 2020, 21, 765-781.	37.0	217
10	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
11	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
12	Dual inhibition of DNA-PK and DNA polymerase theta overcomes radiation resistance induced by p53 deficiency. NAR Cancer, 2020, 2, zcaa038.	3.1	18
13	Unexpected behavior of DNA polymerase Mu opposite template 8-oxo-7,8-dihydro-2â€²-guanosine. Nucleic Acids Research, 2019, 47, 9410-9422.	14.5	8
14	Genetic determinants of cellular addiction to DNA polymerase theta. Nature Communications, 2019, 10, 4286.	12.8	106
15	Ribonucleotide incorporation enables repair of chromosome breaks by nonhomologous end joining. Science, 2018, 361, 1126-1129.	12.6	69
16	High-Throughput Analysis of DNA Break-Induced Chromosome Rearrangements by Amplicon Sequencing. Methods in Enzymology, 2018, 601, 111-144.	1.0	8
17	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
18	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

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19	Regulation of human polÎ» by ATM-mediated phosphorylation during non-homologous end joining. DNA Repair, 2017, 51, 31-45.	2.8	13
20	DNA repair factor RAD18 and DNA polymerase PolÎº confer tolerance of oncogenic DNA replication stress. Journal of Cell Biology, 2017, 216, 3097-3115.	5.2	52
21	DNA Ligase IV Guides End-Processing Choice during Nonhomologous End Joining. Cell Reports, 2017, 20, 2810-2819.	6.4	53
22	PolÎ¼ tumor variants decrease the efficiency and accuracy of NHEJ. Nucleic Acids Research, 2017, 45, 10018-10031.	14.5	9
23	Structural accommodation of ribonucleotide incorporation by the DNA repair enzyme polymerase Mu. Nucleic Acids Research, 2017, 45, 9138-9148.	14.5	36
24	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
25	Reversal of DNA damage induced Topoisomerase 2 DNAâ€“protein crosslinks by Tdp2. Nucleic Acids Research, 2016, 44, 3829-3844.	14.5	23
26	Essential Roles for Polymerase Î¸-Mediated End Joining in the Repair of Chromosome Breaks. Molecular Cell, 2016, 63, 662-673.	9.7	229
27	Inflammasome-independent role of AIM2 in suppressing colon tumorigenesis via DNA-PK and Akt. Nature Medicine, 2015, 21, 906-913.	30.7	230
28	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
29	Essential role for polymerase specialization in cellular nonhomologous end joining. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E4537-45.	7.1	61
30	Mechanism of Suppression of Chromosomal Instability by DNA Polymerase POLQ. PLoS Genetics, 2014, 10, e1004654.	3.5	214
31	Sustained active site rigidity during synthesis by human DNA polymerase Î¼. Nature Structural and Molecular Biology, 2014, 21, 253-260.	8.2	57
32	Requirements for 5â€²dRP/AP lyase activity in Ku. Nucleic Acids Research, 2014, 42, 11136-11143.	14.5	18
33	The fidelity of the ligation step determines how ends are resolved during nonhomologous end joining. Nature Communications, 2014, 5, 4286.	12.8	69
34	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
35	Nonhomologous end joining: A good solution for bad ends. DNA Repair, 2014, 17, 39-51.	2.8	109
36	Trimming of damaged 3â€² overhangs of DNA double-strand breaks by the Metnase and Artemis endonucleases. DNA Repair, 2013, 12, 422-432.	2.8	22

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37	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
38	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
39	Resolution of complex ends by Nonhomologous end joining - better to be lucky than good?. Genome Integrity, 2012, 3, 10.	1.0	12
40	Polymerases in Nonhomologous End Joining: Building a Bridge over Broken Chromosomes. Antioxidants and Redox Signaling, 2011, 14, 2509-2519.	5.4	41
41	V(D)J recombination: Born to be wild. Seminars in Cancer Biology, 2010, 20, 254-260.	9.6	21
42	Ku is a 5â€²-dRP/AP lyase that excises nucleotide damage near broken ends. Nature, 2010, 464, 1214-1217.	27.8	171
43	Dual Modes of Interaction between XRCC4 and Polynucleotide Kinase/Phosphatase. Journal of Biological Chemistry, 2010, 285, 37619-37629.	3.4	57
44	Tyrosyl-DNA phosphodiesterase and the repair of 3â€²-phosphoglycolate-terminated DNA double-strand breaks. DNA Repair, 2009, 8, 901-911.	2.8	72
45	Activity of ribonucleotide reductase helps determine how cells repair DNA double strand breaks. DNA Repair, 2009, 8, 1258-1263.	2.8	24
46	Template strand scrunching during DNA gap repair synthesis by human polymerase Î». Nature Structural and Molecular Biology, 2009, 16, 967-972.	8.2	49
47	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
48	Werner Protein Cooperates with the XRCC4-DNA Ligase IV Complex in End-Processing. Biochemistry, 2008, 47, 7548-7556.	2.5	59
49	End-bridging is required for pol Î¼ to efficiently promote repair of noncomplementary ends by nonhomologous end joining. Nucleic Acids Research, 2008, 36, 3085-3094.	14.5	54
50	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
51	Loading of the Nonhomologous End Joining Factor, Ku, on Protein-occluded DNA Ends. Journal of Biological Chemistry, 2007, 282, 10605-10613.	3.4	36
52	Solution Structure of Polymerase Î¼'s BRCT Domain Reveals an Element Essential for Its Role in Nonhomologous End Joining. Biochemistry, 2007, 46, 12100-12110.	2.5	25
53	Structural insight into the substrate specificity of DNA Polymerase Î¼. Nature Structural and Molecular Biology, 2007, 14, 45-53.	8.2	89
54	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

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55	Genomic instability due to V(D)J recombination-associated transposition. Genes and Development, 2006, 20, 1575-1582.	5.9	65
56	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
57	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
58	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
59	The DNAâ€dependent protein kinase: the director at the end. Immunological Reviews, 2004, 200, 132-141.	6.0	192
60	Polymerase Mu Is a DNA-Directed DNA/RNA Polymerase. Molecular and Cellular Biology, 2003, 23, 2309-2315.	2.3	161
61	Translesion Synthesis Past Platinum DNA Adducts by Human DNA Polymerase Î¼â€. Biochemistry, 2003, 42, 1777-1788.	2.5	41
62	Association of DNA Polymerase Î¼ (pol Î¼) with Ku and Ligase IV: Role for pol Î¼ in End-Joining Double-Strand Break Repair. Molecular and Cellular Biology, 2002, 22, 5194-5202.	2.3	270
63	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
64	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
65	Ku Recruits the XRCC4-Ligase IV Complex to DNA Ends. Molecular and Cellular Biology, 2000, 20, 2996-3003.	2.3	349
66	Ku complex interacts with and stimulates the Werner protein. Genes and Development, 2000, 14, 907-912.	5.9	276
67	Cell-free V(D)J recombination. Nature, 1997, 388, 488-491.	27.8	136