Katarzyna Bebenek

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/3958375/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	DNA Replication Fidelity. Annual Review of Biochemistry, 2000, 69, 497-529.	11.1	896
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	Somatic mutation hotspots correlate with DNA polymerase η error spectrum. Nature Immunology, 2001, 2, 530-536.	14.5	282
4	Functions of DNA Polymerases. Advances in Protein Chemistry, 2004, 69, 137-165.	4.4	225
5	ldentification of an Intrinsic 5′-Deoxyribose-5-phosphate Lyase Activity in Human DNA Polymerase λ. Journal of Biological Chemistry, 2001, 276, 34659-34663.	3.4	215
6	[18] Analyzing fidelity of DNA polymerases. Methods in Enzymology, 1995, 262, 217-232.	1.0	191
7	DNA Polymerase λ, a Novel DNA Repair Enzyme in Human Cells. Journal of Biological Chemistry, 2002, 277, 13184-13191.	3.4	166
8	The X family portrait: Structural insights into biological functions of X family polymerases. DNA Repair, 2007, 6, 1709-1725.	2.8	158
9	Replication infidelity via a mismatch with Watson–Crick geometry. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 1862-1867.	7.1	148
10	A closed conformation for the Pol λ catalytic cycle. Nature Structural and Molecular Biology, 2005, 12, 97-98.	8.2	138
11	Exonucleolytic Proofreading during Replication of Repetitive DNA. Biochemistry, 1996, 35, 1046-1053.	2.5	113
12	A minor groove binding track in reverse transcriptase. Nature Structural Biology, 1997, 4, 194-197.	9.7	111
13	The Frameshift Infidelity of Human DNA Polymerase λ. Journal of Biological Chemistry, 2003, 278, 34685-34690.	3.4	101
14	Structural Analysis of Strand Misalignment during DNA Synthesis by a Human DNA Polymerase. Cell, 2006, 124, 331-342.	28.9	94
15	Structural insight into the substrate specificity of DNA Polymerase μ. Nature Structural and Molecular Biology, 2007, 14, 45-53.	8.2	89
16	Role of the catalytic metal during polymerization by DNA polymerase lambda. DNA Repair, 2007, 6, 1333-1340.	2.8	62
17	Alternative solutions and new scenarios for translesion DNA synthesis by human PrimPol. DNA Repair, 2015, 29, 127-138.	2.8	59
18	Sustained active site rigidity during synthesis by human DNA polymerase μ. Nature Structural and Molecular Biology, 2014, 21, 253-260.	8.2	57

Katarzyna Bebenek

#	Article	IF	CITATIONS
19	Biochemical Properties of Saccharomyces cerevisiae DNA Polymerase IV. Journal of Biological Chemistry, 2005, 280, 20051-20058.	3.4	56
20	Time-lapse crystallography snapshots of a double-strand break repair polymerase in action. Nature Communications, 2017, 8, 253.	12.8	54
21	Structure–Function Studies of DNA Polymerase λ. Biochemistry, 2014, 53, 2781-2792.	2.5	52
22	Template strand scrunching during DNA gap repair synthesis by human polymerase λ. Nature Structural and Molecular Biology, 2009, 16, 967-972.	8.2	49
23	The catalytic cycle for ribonucleotide incorporation by human DNA Pol λ. Nucleic Acids Research, 2012, 40, 7518-7527.	14.5	48
24	Structures of DNA-bound human ligase IV catalytic core reveal insights into substrate binding and catalysis. Nature Communications, 2018, 9, 2642.	12.8	37
25	Substrateâ€induced DNA strand misalignment during catalytic cycling by DNA polymerase λ. EMBO Reports, 2008, 9, 459-464.	4.5	36
26	Structural accommodation of ribonucleotide incorporation by the DNA repair enzyme polymerase Mu. Nucleic Acids Research, 2017, 45, 9138-9148.	14.5	36
27	Loop 1 modulates the fidelity of DNA polymerase Â. Nucleic Acids Research, 2010, 38, 5419-5431.	14.5	34
28	Creative template-dependent synthesis by human polymerase mu. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E4530-6.	7.1	26
29	A Molecular Dynamics Model of HIV-1 Reverse Transcriptase Complexed with DNA: Comparison with Experimental Structures. Journal of Molecular Modeling, 2000, 6, 575-586.	1.8	9
30	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
31	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
32	Structural snapshots of human DNA polymerase μ engaged on a DNA double-strand break. Nature Communications, 2020, 11, 4784.	12.8	6
33	Structures of the Leishmania infantum polymerase beta. DNA Repair, 2014, 18, 1-9.	2.8	5
34	DNA polymerase mu: An inflexible scaffold for substrate flexibility. DNA Repair, 2020, 93, 102932.	2.8	2
35	Structural Insights into the Specificity of 8-Oxo-7,8-dihydro-2′-deoxyguanosine Bypass by Family X DNA Polymerases. Genes, 2022, 13, 15.	2.4	2
36	32nd Annual Meeting of European Environmental Mutagen Society. DNA Repair, 2003, 2, 765-781.	2.8	1