

M Todd Washington

List of Publications by Year in descending order

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72
papers

4,380
citations

109321

35
h-index

110387

64
g-index

76
all docs

76
docs citations

76
times ranked

2404
citing authors

#	ARTICLE	IF	CITATIONS
1	Eukaryotic polymerases $\hat{\Gamma}$ and $\hat{\Gamma}$ act sequentially to bypass DNA lesions. <i>Nature</i> , 2000, 406, 1015-1019.	27.8	622
2	Fidelity of Human DNA Polymerase $\hat{\Gamma}$. <i>Journal of Biological Chemistry</i> , 2000, 275, 7447-7450.	3.4	365
3	The Many Roles of PCNA in Eukaryotic DNA Replication. <i>The Enzymes</i> , 2016, 39, 231-254.	1.7	216
4	Fidelity and Processivity of <i>Saccharomyces cerevisiae</i> DNA Polymerase $\hat{\Gamma}$. <i>Journal of Biological Chemistry</i> , 1999, 274, 36835-36838.	3.4	169
5	Human DINB1-encoded DNA polymerase $\hat{\Lambda}$ is a promiscuous extender of mispaired primer termini. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 1910-1914.	7.1	157
6	Bridging the gap: A family of novel DNA polymerases that replicate faulty DNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1999, 96, 12224-12226.	7.1	137
7	Accuracy of thymine-thymine dimer bypass by <i>Saccharomyces cerevisiae</i> DNA polymerase $\hat{\epsilon}$. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 3094-3099.	7.1	137
8	Yeast DNA Polymerase $\hat{\Gamma}$ Utilizes an Induced-Fit Mechanism of Nucleotide Incorporation. <i>Cell</i> , 2001, 107, 917-927.	28.9	126
9	Efficient and Error-Free Replication Past a Minor-Groove DNA Adduct by the Sequential Action of Human DNA Polymerases $\hat{\Gamma}$ and $\hat{\delta}$. <i>Molecular and Cellular Biology</i> , 2004, 24, 5687-5693.	2.3	114
10	Inefficient Bypass of an Abasic Site by DNA Polymerase $\hat{\Gamma}$. <i>Journal of Biological Chemistry</i> , 2001, 276, 6861-6866.	3.4	105
11	Efficient and Error-Free Replication past a Minor-Groove N ² -Guanine Adduct by the Sequential Action of Yeast Rev1 and DNA Polymerase $\hat{\Gamma}$. <i>Molecular and Cellular Biology</i> , 2004, 24, 6900-6906.	2.3	99
12	Structure of monoubiquitinated PCNA and implications for translesion synthesis and DNA polymerase exchange. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 479-484.	8.2	98
13	Biochemical Analysis of Mutant T7 Primase/Helicase Proteins Defective in DNA Binding, Nucleotide Hydrolysis, and the Coupling of Hydrolysis with DNA Unwinding. <i>Journal of Biological Chemistry</i> , 1996, 271, 26825-26834.	3.4	91
14	The dTTPase mechanism of T7 DNA helicase resembles the binding change mechanism of the F1-ATPase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1997, 94, 5012-5017.	7.1	91
15	Requirement of Watson-Crick Hydrogen Bonding for DNA Synthesis by Yeast DNA Polymerase $\hat{\Gamma}$. <i>Molecular and Cellular Biology</i> , 2003, 23, 5107-5112.	2.3	83
16	Translesion Synthesis past Acrolein-derived DNA Adduct, $\hat{\Gamma}$ -Hydroxypropanodeoxyguanosine, by Yeast and Human DNA Polymerase $\hat{\Gamma}$. <i>Journal of Biological Chemistry</i> , 2003, 278, 784-790.	3.4	78
17	Mechanism of nucleotide incorporation opposite a thymine-thymine dimer by yeast DNA polymerase $\hat{\Lambda}$. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 12093-12098.	7.1	78
18	PCNA Structure and Function: Insights from Structures of PCNA Complexes and Post-translationally Modified PCNA. <i>Sub-Cellular Biochemistry</i> , 2012, 62, 281-299.	2.4	76

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19	Variations on a theme: Eukaryotic Y-family DNA polymerases. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2010, 1804, 1113-1123.	2.3	75
20	Accuracy of lesion bypass by yeast and human DNA polymerase $\hat{\Delta}$. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 8355-8360.	7.1	72
21	Mechanism of Efficient and Accurate Nucleotide Incorporation Opposite 7,8-Dihydro-8-Oxoguanine by <i>Saccharomyces cerevisiae</i> DNA Polymerase $\hat{\Gamma}$. <i>Molecular and Cellular Biology</i> , 2005, 25, 2169-2176.	2.3	67
22	Translesion Synthesis: Insights into the Selection and Switching of DNA Polymerases. <i>Genes</i> , 2017, 8, 24.	2.4	64
23	Solution X-ray scattering combined with computational modeling reveals multiple conformations of covalently bound ubiquitin on PCNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 17672-17677.	7.1	61
24	R.I.P. to the PIP: PCNA's binding motif no longer considered specific. <i>BioEssays</i> , 2016, 38, 1117-1122.	2.5	59
25	Human DNA Polymerase $\hat{\Gamma}$ Utilizes Different Nucleotide Incorporation Mechanisms Dependent upon the Template Base. <i>Molecular and Cellular Biology</i> , 2004, 24, 936-943.	2.3	57
26	Srs2 promotes synthesis-dependent strand annealing by disrupting DNA polymerase $\hat{\Gamma}$ -extending D-loops. <i>ELife</i> , 2017, 6, .	6.0	54
27	Evidence for a Watson-Crick Hydrogen Bonding Requirement in DNA Synthesis by Human DNA Polymerase $\hat{\Gamma}$. <i>Molecular and Cellular Biology</i> , 2005, 25, 7137-7143.	2.3	53
28	Mismatch Extension Ability of Yeast and Human DNA Polymerase $\hat{\Gamma}$. <i>Journal of Biological Chemistry</i> , 2001, 276, 2263-2266.	3.4	51
29	PCNA tool belts and polymerase bridges form during translesion synthesis. <i>Nucleic Acids Research</i> , 2016, 44, 8250-8260.	14.5	49
30	Eukaryotic translesion synthesis: Choosing the right tool for the job. <i>DNA Repair</i> , 2018, 71, 127-134.	2.8	46
31	Acidic Residues Critical for the Activity and Biological Function of Yeast DNA Polymerase $\hat{\Gamma}$. <i>Molecular and Cellular Biology</i> , 2001, 21, 2018-2025.	2.3	44
32	The Proliferating Cell Nuclear Antigen (PCNA)-interacting Protein (PIP) Motif of DNA Polymerase $\hat{\Gamma}$ Mediates Its Interaction with the C-terminal Domain of Rev1. <i>Journal of Biological Chemistry</i> , 2016, 291, 8735-8744.	3.4	44
33	The Mechanism of Nucleotide Incorporation by Human DNA Polymerase $\hat{\Gamma}$ Differs from That of the Yeast Enzyme. <i>Molecular and Cellular Biology</i> , 2003, 23, 8316-8322.	2.3	43
34	Human DNA polymerase $\hat{\Delta}$ uses template-primer misalignment as a novel means for extending mispaired termini and for generating single-base deletions. <i>Genes and Development</i> , 2003, 17, 2191-2199.	5.9	40
35	Structurally Distinct Ubiquitin- and Sumo-Modified PCNA: Implications for Their Distinct Roles in the DNA Damage Response. <i>Structure</i> , 2015, 23, 724-733.	3.3	39
36	Yeast DNA polymerase $\hat{\Delta}$ makes functional contacts with the DNA minor groove only at the incoming nucleoside triphosphate. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 5113-5118.	7.1	38

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37	Human DNA polymerase δ forms nonproductive complexes with matched primer termini but not with mismatched primer termini. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 15776-15781.	7.1	38
38	Translesion DNA Synthesis by Yeast DNA Polymerase δ on Templates Containing N ² -Guanine Adducts of 1,3-Butadiene Metabolites. <i>Journal of Biological Chemistry</i> , 2001, 276, 2517-2522.	3.4	35
39	Control of DNA Damage Bypass by Ubiquitylation of PCNA. <i>Genes</i> , 2020, 11, 138.	2.4	35
40	Structure of a Mutant Form of Proliferating Cell Nuclear Antigen That Blocks Translesion DNA Synthesis. <i>Biochemistry</i> , 2008, 47, 13354-13361.	2.5	31
41	Pre-Steady State Kinetic Studies of the Fidelity of Nucleotide Incorporation by Yeast DNA Polymerase δ . <i>Biochemistry</i> , 2010, 49, 7344-7350.	2.5	31
42	Making choices: DNA replication fork recovery mechanisms. <i>Seminars in Cell and Developmental Biology</i> , 2021, 113, 27-37.	5.0	30
43	Crystal Structure of SUMO-Modified Proliferating Cell Nuclear Antigen. <i>Journal of Molecular Biology</i> , 2011, 406, 9-17.	4.2	29
44	PCNA trimer instability inhibits translesion synthesis by DNA polymerase δ and by DNA polymerase ϵ . <i>DNA Repair</i> , 2013, 12, 367-376.	2.8	29
45	Fidelity and Damage Bypass Ability of <i>Schizosaccharomyces pombe</i> Eso1 Protein, Comprised of DNA Polymerase δ and Sister Chromatid Cohesion Protein Ctf7. <i>Journal of Biological Chemistry</i> , 2001, 276, 42857-42862.	3.4	24
46	Dead-End Elimination with a Polarizable Force Field Repacks PCNA Structures. <i>Biophysical Journal</i> , 2015, 109, 816-826.	0.5	24
47	Pre-steady state kinetic studies show that an abasic site is a cognate lesion for the yeast Rev1 protein. <i>DNA Repair</i> , 2011, 10, 1138-1144.	2.8	21
48	Selection, Identification, and Genetic Analysis of Random Mutants in the Cloned Primase/Helicase Gene of Bacteriophage T7. <i>Journal of Biological Chemistry</i> , 1996, 271, 26819-26824.	3.4	20
49	Pre-Steady-State Kinetic Studies of Protein-Template-Directed Nucleotide Incorporation by the Yeast Rev1 Protein. <i>Biochemistry</i> , 2007, 46, 13451-13459.	2.5	19
50	Distinct Structural Alterations in Proliferating Cell Nuclear Antigen Block DNA Mismatch Repair. <i>Biochemistry</i> , 2013, 52, 5611-5619.	2.5	19
51	The C-terminal region of translesion synthesis DNA polymerase δ is partially unstructured and has high conformational flexibility. <i>Nucleic Acids Research</i> , 2018, 46, 2107-2120.	14.5	17
52	Quantifying the Assembly of Multicomponent Molecular Machines by Single-Molecule Total Internal Reflection Fluorescence Microscopy. <i>Methods in Enzymology</i> , 2016, 581, 105-145.	1.0	16
53	Eukaryotic Y-Family Polymerases: A Biochemical and Structural Perspective. <i>Nucleic Acids and Molecular Biology</i> , 2014, , 85-108.	0.2	16
54	Visualizing Rev1 catalyze protein-template DNA synthesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 25494-25504.	7.1	15

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55	Crystal structures of PCNA mutant proteins defective in gene silencing suggest a novel interaction site on the front face of the PCNA ring. <i>PLoS ONE</i> , 2018, 13, e0193333.	2.5	14
56	Increased DNA Unwinding Efficiency of Bacteriophage T7 DNA Helicase Mutant Protein 4A ^Δ /E348K. <i>Journal of Biological Chemistry</i> , 1998, 273, 7880-7887.	3.4	12
57	A charged residue at the subunit interface of PCNA promotes trimer formation by destabilizing alternate subunit interactions. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2009, 65, 560-566.	2.5	12
58	Analyzing the Catalytic Activities and Interactions of Eukaryotic Translesion Synthesis Polymerases. <i>Methods in Enzymology</i> , 2017, 592, 329-356.	1.0	12
59	Structure and Functional Analysis of the BRCT Domain of Translesion Synthesis DNA Polymerase Rev1. <i>Biochemistry</i> , 2013, 52, 254-263.	2.5	11
60	Substitution of a residue contacting the triphosphate moiety of the incoming nucleotide increases the fidelity of yeast DNA polymerase η . <i>Nucleic Acids Research</i> , 2008, 36, 1731-1740.	14.5	10
61	A lag-phase in the reduction of flavin dependent thymidylate synthase (FDTS) revealed a mechanistic missing link. <i>Chemical Communications</i> , 2006, , 1781.	4.1	9
62	KERA: analysis tool for multi-process, multi-state single-molecule data. <i>Nucleic Acids Research</i> , 2021, 49, e53-e53.	14.5	9
63	Identification of New Mutations at the PCNA Subunit Interface that Block Translesion Synthesis. <i>PLoS ONE</i> , 2016, 11, e0157023.	2.5	8
64	Modeling Conformationally Flexible Proteins With X-ray Scattering and Molecular Simulations. <i>Computational and Structural Biotechnology Journal</i> , 2019, 17, 570-578.	4.1	8
65	Conformational flexibility of fork-remodeling helicase Rad5 shown by full-ensemble hybrid methods. <i>PLoS ONE</i> , 2019, 14, e0223875.	2.5	7
66	Conformational Flexibility of Ubiquitin-Modified and SUMO-Modified PCNA Shown by Full-Ensemble Hybrid Methods. <i>Journal of Molecular Biology</i> , 2018, 430, 5294-5303.	4.2	5
67	Mechanism of nucleotide discrimination by the translesion synthesis polymerase Rev1. <i>Nature Communications</i> , 2022, 13, .	12.8	4
68	Recent Advances in Understanding the Structures of Translesion Synthesis DNA Polymerases. <i>Genes</i> , 2022, 13, 915.	2.4	4
69	Structure of DNA polymerase η : capturing the getaway driver. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 1-2.	8.2	3
70	Yeast DNA polymerase η possesses two PIP-like motifs that bind PCNA and Rad6-Rad18 with different specificities. <i>DNA Repair</i> , 2020, 95, 102968.	2.8	3
71	DNA Polymerase Fidelity: Beyond Right and Wrong. <i>Structure</i> , 2016, 24, 1855-1856.	3.3	1
72	PCNA trimer stability and its impact on mutagenesis. <i>FASEB Journal</i> , 2012, 26, lb90.	0.5	0