

M Todd Washington

List of Publications by Year in descending order

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Version: 2024-02-01

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 | Mechanism of nucleotide discrimination by the translesion synthesis polymerase Rev1. <i>Nature Communications</i> , 2022, 13, . | 12.8 | 4 |
| 2 | Recent Advances in Understanding the Structures of Translesion Synthesis DNA Polymerases. <i>Genes</i> , 2022, 13, 915. | 2.4 | 4 |
| 3 | Making choices: DNA replication fork recovery mechanisms. <i>Seminars in Cell and Developmental Biology</i> , 2021, 113, 27-37. | 5.0 | 30 |
| 4 | KERA: analysis tool for multi-process, multi-state single-molecule data. <i>Nucleic Acids Research</i> , 2021, 49, e53-e53. | 14.5 | 9 |
| 5 | 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 |
| 6 | Structure of DNA polymerase $\hat{\Psi}$: capturing the getaway driver. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 1-2. | 8.2 | 3 |
| 7 | Yeast DNA polymerase $\hat{\Psi}$ possesses two PIP-like motifs that bind PCNA and Rad6-Rad18 with different specificities. <i>DNA Repair</i> , 2020, 95, 102968. | 2.8 | 3 |
| 8 | Control of DNA Damage Bypass by Ubiquitylation of PCNA. <i>Genes</i> , 2020, 11, 138. | 2.4 | 35 |
| 9 | 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 |
| 10 | Conformational flexibility of fork-remodeling helicase Rad5 shown by full-ensemble hybrid methods. <i>PLoS ONE</i> , 2019, 14, e0223875. | 2.5 | 7 |
| 11 | The C-terminal region of translesion synthesis DNA polymerase $\hat{\Psi}$ is partially unstructured and has high conformational flexibility. <i>Nucleic Acids Research</i> , 2018, 46, 2107-2120. | 14.5 | 17 |
| 12 | 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 |
| 13 | Eukaryotic translesion synthesis: Choosing the right tool for the job. <i>DNA Repair</i> , 2018, 71, 127-134. | 2.8 | 46 |
| 14 | 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 |
| 15 | Analyzing the Catalytic Activities and Interactions of Eukaryotic Translesion Synthesis Polymerases. <i>Methods in Enzymology</i> , 2017, 592, 329-356. | 1.0 | 12 |
| 16 | Translesion Synthesis: Insights into the Selection and Switching of DNA Polymerases. <i>Genes</i> , 2017, 8, 24. | 2.4 | 64 |
| 17 | Srs2 promotes synthesis-dependent strand annealing by disrupting DNA polymerase $\hat{\Psi}$ -extending D-loops. <i>ELife</i> , 2017, 6, . | 6.0 | 54 |
| 18 | PCNA tool belts and polymerase bridges form during translesion synthesis. <i>Nucleic Acids Research</i> , 2016, 44, 8250-8260. | 14.5 | 49 |

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|----|---|-----|-----------|
| 19 | Identification of New Mutations at the PCNA Subunit Interface that Block Translesion Synthesis. PLoS ONE, 2016, 11, e0157023. | 2.5 | 8 |
| 20 | R.I.P. to the PIP: PCNA-binding motif no longer considered specific. BioEssays, 2016, 38, 1117-1122. | 2.5 | 59 |
| 21 | The Many Roles of PCNA in Eukaryotic DNA Replication. The Enzymes, 2016, 39, 231-254. | 1.7 | 216 |
| 22 | DNA Polymerase Fidelity: Beyond Right and Wrong. Structure, 2016, 24, 1855-1856. | 3.3 | 1 |
| 23 | Quantifying the Assembly of Multicomponent Molecular Machines by Single-Molecule Total Internal Reflection Fluorescence Microscopy. Methods in Enzymology, 2016, 581, 105-145. | 1.0 | 16 |
| 24 | The Proliferating Cell Nuclear Antigen (PCNA)-interacting Protein (PIP) Motif of DNA Polymerase δ Mediates Its Interaction with the C-terminal Domain of Rev1. Journal of Biological Chemistry, 2016, 291, 8735-8744. | 3.4 | 44 |
| 25 | Structurally Distinct Ubiquitin- and Sumo-Modified PCNA: Implications for Their Distinct Roles in the DNA Damage Response. Structure, 2015, 23, 724-733. | 3.3 | 39 |
| 26 | Dead-End Elimination with a Polarizable Force Field Repacks PCNA Structures. Biophysical Journal, 2015, 109, 816-826. | 0.5 | 24 |
| 27 | Eukaryotic Y-Family Polymerases: A Biochemical and Structural Perspective. Nucleic Acids and Molecular Biology, 2014, , 85-108. | 0.2 | 16 |
| 28 | Structure and Functional Analysis of the BRCT Domain of Translesion Synthesis DNA Polymerase Rev1. Biochemistry, 2013, 52, 254-263. | 2.5 | 11 |
| 29 | PCNA trimer instability inhibits translesion synthesis by DNA polymerase δ and by DNA polymerase ϵ . DNA Repair, 2013, 12, 367-376. | 2.8 | 29 |
| 30 | Distinct Structural Alterations in Proliferating Cell Nuclear Antigen Block DNA Mismatch Repair. Biochemistry, 2013, 52, 5611-5619. | 2.5 | 19 |
| 31 | PCNA Structure and Function: Insights from Structures of PCNA Complexes and Post-translationally Modified PCNA. Sub-Cellular Biochemistry, 2012, 62, 281-299. | 2.4 | 76 |
| 32 | PCNA trimer stability and its impact on mutagenesis. FASEB Journal, 2012, 26, lb90. | 0.5 | 0 |
| 33 | Crystal Structure of SUMO-Modified Proliferating Cell Nuclear Antigen. Journal of Molecular Biology, 2011, 406, 9-17. | 4.2 | 29 |
| 34 | Pre-steady state kinetic studies show that an abasic site is a cognate lesion for the yeast Rev1 protein. DNA Repair, 2011, 10, 1138-1144. | 2.8 | 21 |
| 35 | Solution X-ray scattering combined with computational modeling reveals multiple conformations of covalently bound ubiquitin on PCNA. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 17672-17677. | 7.1 | 61 |
| 36 | Variations on a theme: Eukaryotic Y-family DNA polymerases. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2010, 1804, 1113-1123. | 2.3 | 75 |

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|----|---|------|-----------|
| 37 | 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 |
| 38 | Pre-Steady State Kinetic Studies of the Fidelity of Nucleotide Incorporation by Yeast DNA Polymerase ϵ . <i>Biochemistry</i> , 2010, 49, 7344-7350. | 2.5 | 31 |
| 39 | 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 |
| 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 | Substitution of a residue contacting the triphosphate moiety of the incoming nucleotide increases the fidelity of yeast DNA polymerase ϵ . <i>Nucleic Acids Research</i> , 2008, 36, 1731-1740. | 14.5 | 10 |
| 42 | 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 |
| 43 | 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 |
| 44 | Human DNA polymerase β 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 |
| 45 | Mechanism of Efficient and Accurate Nucleotide Incorporation Opposite 7,8-Dihydro-8-Oxoguanine by <i>Saccharomyces cerevisiae</i> DNA Polymerase ϵ . <i>Molecular and Cellular Biology</i> , 2005, 25, 2169-2176. | 2.3 | 67 |
| 46 | Evidence for a Watson-Crick Hydrogen Bonding Requirement in DNA Synthesis by Human DNA Polymerase ϵ . <i>Molecular and Cellular Biology</i> , 2005, 25, 7137-7143. | 2.3 | 53 |
| 47 | Human DNA Polymerase ϵ Utilizes Different Nucleotide Incorporation Mechanisms Dependent upon the Template Base. <i>Molecular and Cellular Biology</i> , 2004, 24, 936-943. | 2.3 | 57 |
| 48 | Efficient and Error-Free Replication past a Minor-Groove N 2 -Guanine Adduct by the Sequential Action of Yeast Rev1 and DNA Polymerase ϵ . <i>Molecular and Cellular Biology</i> , 2004, 24, 6900-6906. | 2.3 | 99 |
| 49 | Efficient and Error-Free Replication Past a Minor-Groove DNA Adduct by the Sequential Action of Human DNA Polymerases δ and ϵ . <i>Molecular and Cellular Biology</i> , 2004, 24, 5687-5693. | 2.3 | 114 |
| 50 | Translesion Synthesis past Acrolein-derived DNA Adduct, β -Hydroxypropanodeoxyguanosine, by Yeast and Human DNA Polymerase ϵ . <i>Journal of Biological Chemistry</i> , 2003, 278, 784-790. | 3.4 | 78 |
| 51 | Mechanism of nucleotide incorporation opposite a thymine-thymine dimer by yeast DNA polymerase β . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 12093-12098. | 7.1 | 78 |
| 52 | Yeast DNA polymerase β 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 |
| 53 | The Mechanism of Nucleotide Incorporation by Human DNA Polymerase ϵ Differs from That of the Yeast Enzyme. <i>Molecular and Cellular Biology</i> , 2003, 23, 8316-8322. | 2.3 | 43 |
| 54 | Requirement of Watson-Crick Hydrogen Bonding for DNA Synthesis by Yeast DNA Polymerase ϵ . <i>Molecular and Cellular Biology</i> , 2003, 23, 5107-5112. | 2.3 | 83 |

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|----|---|------|-----------|
| 55 | Human DNA polymerase β 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 |
| 56 | Human DINB1-encoded DNA polymerase β 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 |
| 57 | Yeast DNA Polymerase β Utilizes an Induced-Fit Mechanism of Nucleotide Incorporation. <i>Cell</i> , 2001, 107, 917-927. | 28.9 | 126 |
| 58 | Translesion DNA Synthesis by Yeast DNA Polymerase β 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 |
| 59 | Mismatch Extension Ability of Yeast and Human DNA Polymerase β . <i>Journal of Biological Chemistry</i> , 2001, 276, 2263-2266. | 3.4 | 51 |
| 60 | Accuracy of lesion bypass by yeast and human DNA polymerase β . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 8355-8360. | 7.1 | 72 |
| 61 | Inefficient Bypass of an Abasic Site by DNA Polymerase β . <i>Journal of Biological Chemistry</i> , 2001, 276, 6861-6866. | 3.4 | 105 |
| 62 | Acidic Residues Critical for the Activity and Biological Function of Yeast DNA Polymerase β . <i>Molecular and Cellular Biology</i> , 2001, 21, 2018-2025. | 2.3 | 44 |
| 63 | Fidelity and Damage Bypass Ability of <i>Schizosaccharomyces pombe</i> Eso1 Protein, Comprised of DNA Polymerase β and Sister Chromatid Cohesion Protein Ctf7. <i>Journal of Biological Chemistry</i> , 2001, 276, 42857-42862. | 3.4 | 24 |
| 64 | Eukaryotic polymerases β and β' act sequentially to bypass DNA lesions. <i>Nature</i> , 2000, 406, 1015-1019. | 27.8 | 622 |
| 65 | Fidelity of Human DNA Polymerase β . <i>Journal of Biological Chemistry</i> , 2000, 275, 7447-7450. | 3.4 | 365 |
| 66 | Accuracy of thymine-thymine dimer bypass by <i>Saccharomyces cerevisiae</i> DNA polymerase β . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 3094-3099. | 7.1 | 137 |
| 67 | Fidelity and Processivity of <i>Saccharomyces cerevisiae</i> DNA Polymerase β . <i>Journal of Biological Chemistry</i> , 1999, 274, 36835-36838. | 3.4 | 169 |
| 68 | 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 |
| 69 | Increased DNA Unwinding Efficiency of Bacteriophage T7 DNA Helicase Mutant Protein 4A/E348K. <i>Journal of Biological Chemistry</i> , 1998, 273, 7880-7887. | 3.4 | 12 |
| 70 | 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 |
| 71 | 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 |
| 72 | 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 |