

# Scott W Nelson

## List of Publications by Year in descending order

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citations

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docs citations

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574  
citing authors

#	ARTICLE	IF	CITATIONS
1	Discovery of small molecule inhibitors of Plasmodium falciparum apicoplast DNA polymerase. Journal of Enzyme Inhibition and Medicinal Chemistry, 2022, 37, 1320-1326.	5.2	7
2	Functional evaluation of the C-terminal region of bacteriophage T4 Rad50. Biochemical and Biophysical Research Communications, 2020, 526, 485-490.	2.1	1
3	Kinetic Analysis of the Exonuclease Activity of the Bacteriophage T4 Mre11-Rad50 Complex. Methods in Enzymology, 2018, 600, 135-156.	1.0	4
4	Crystal Structure of the Apicoplast DNA Polymerase from Plasmodium falciparum: The First Look at a Plastidic A-Family DNA Polymerase. Journal of Molecular Biology, 2016, 428, 3920-3934.	4.2	10
5	A network of allosterically coupled residues in the bacteriophage T4 Mre11-Rad50 complex. Protein Science, 2016, 25, 2054-2065.	7.6	4
6	Replication and maintenance of the Plasmodium falciparum apicoplast genome. Molecular and Biochemical Parasitology, 2016, 208, 56-64.	1.1	17
7	Crystallization and preliminary X-ray analysis of the Plasmodium falciparum apicoplast DNA polymerase. Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 333-337.	0.8	2
8	Functional Analysis of the Bacteriophage T4 Rad50 Homolog (gp46) Coiled-coil Domain. Journal of Biological Chemistry, 2015, 290, 23905-23915.	3.4	14
9	A High-Throughput Assay to Identify Inhibitors of the Apicoplast DNA Polymerase from Plasmodium falciparum. Journal of Biomolecular Screening, 2014, 19, 966-972.	2.6	14
10	Catalytic Mechanism of Bacteriophage T4 Rad50 ATP Hydrolysis. Biochemistry, 2014, 53, 5647-5660.	2.5	11
11	Autoinhibition of Bacteriophage T4 Mre11 by Its C-terminal Domain. Journal of Biological Chemistry, 2014, 289, 26505-26513.	3.4	5
12	Fidelity, Mismatch Extension, and Proofreading Activity of the Plasmodium falciparum Apicoplast DNA Polymerase. Biochemistry, 2013, 52, 7723-7730.	2.5	13
13	Interaction of T4 UvsW Helicase and Single-Stranded DNA Binding Protein gp32 through Its Carboxy-Terminal Acidic Tail. Journal of Molecular Biology, 2013, 425, 2823-2839.	4.2	10
14	Coordination and Processing of DNA Ends During Double-Strand Break Repair: The Role of the Bacteriophage T4 Mre11/Rad50 (MR) Complex. Genetics, 2013, 195, 739-755.	2.9	11
15	Disruption of the Bacteriophage T4 Mre11 Dimer Interface Reveals a Two-state Mechanism for Exonuclease Activity. Journal of Biological Chemistry, 2012, 287, 31371-31381.	3.4	12
16	Functional Evaluation of Bacteriophage T4 Rad50 Signature Motif Residues. Biochemistry, 2011, 50, 6030-6040.	2.5	10
17	An Interaction between the Walker A and D-loop Motifs Is Critical to ATP Hydrolysis and Cooperativity in Bacteriophage T4 Rad50. Journal of Biological Chemistry, 2011, 286, 26258-26266.	3.4	24
18	Biochemical Characterization of Bacteriophage T4 Mre11-Rad50 Complex. Journal of Biological Chemistry, 2011, 286, 2382-2392.	3.4	48

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19	Response of the Bacteriophage T4 Replisome to Noncoding Lesions and Regression of a Stalled Replication Fork. <i>Journal of Molecular Biology</i> , 2010, 401, 743-756.	4.2	28
20	Processive and Unidirectional Translocation of Monomeric UvsW Helicase on Single-Stranded DNA. <i>Biochemistry</i> , 2009, 48, 1036-1046.	2.5	15
21	T4 Phage Replisome. , 2009, , 337-364.		6
22	Repetitive lagging strand DNA synthesis by the bacteriophage T4 replisome. <i>Molecular BioSystems</i> , 2008, 4, 1070.	2.9	11
23	RNA Primer Handoff in Bacteriophage T4 DNA Replication. <i>Journal of Biological Chemistry</i> , 2008, 283, 22838-22846.	3.4	28
24	The T4 Phage UvsW Protein Contains Both DNA Unwinding and Strand Annealing Activities. <i>Journal of Biological Chemistry</i> , 2007, 282, 407-416.	3.4	28
25	Environment of Tryptophan 57 in Porcine Fructose-1,6-bisphosphatase Studied by Time-resolved Fluorescence and Site-directed Mutagenesis. <i>Photochemistry and Photobiology</i> , 2007, 74, 679-685.	2.5	0
26	The Control Mechanism for Lagging Strand Polymerase Recycling during Bacteriophage T4 DNA Replication. <i>Molecular Cell</i> , 2006, 21, 153-164.	9.7	100
27	Site-directed Mutations of T4 Helicase Loading Protein (gp59) Reveal Multiple Modes of DNA Polymerase Inhibition and the Mechanism of Unlocking by gp41 Helicase. <i>Journal of Biological Chemistry</i> , 2006, 281, 8697-8706.	3.4	14
28	Mechanism of Action of Escherichia coli Phosphoribosylaminoimidazolesuccinocarboxamide Synthetase. <i>Biochemistry</i> , 2005, 44, 766-774.	2.5	18
29	Origin of Cooperativity in the Activation of Fructose-1,6-bisphosphatase by Mg <sup>2+</sup> . <i>Journal of Biological Chemistry</i> , 2004, 279, 18481-18487.	3.4	5
30	Inhibition of Fructose-1,6-bisphosphatase by a New Class of Allosteric Effectors. <i>Journal of Biological Chemistry</i> , 2003, 278, 51176-51183.	3.4	33
31	Interaction of TI <sup>+</sup> with Product Complexes of Fructose-1,6-bisphosphatase. <i>Journal of Biological Chemistry</i> , 2003, 278, 16008-16014.	3.4	9
32	Hybrid Tetramers of Porcine Liver Fructose-1,6-bisphosphatase Reveal Multiple Pathways of Allosteric Inhibition. <i>Journal of Biological Chemistry</i> , 2002, 277, 15539-15545.	3.4	22
33	Spontaneous subunit exchange in porcine liver fructose-1,6-bisphosphatase. <i>FEBS Letters</i> , 2001, 492, 254-258.	2.8	12
34	The N-terminal Segment of Recombinant Porcine Fructose-1,6-bisphosphatase Participates in the Allosteric Regulation of Catalysis. <i>Journal of Biological Chemistry</i> , 2001, 276, 6119-6124.	3.4	15
35	Environment of Tryptophan 57 in Porcine Fructose-1,6-bisphosphatase Studied by Time-resolved Fluorescence and Site-directed Mutagenesis. <i>Photochemistry and Photobiology</i> , 2001, 74, 679.	2.5	5
36	Mutations in the Hinge of a Dynamic Loop Broadly Influence Functional Properties of Fructose-1,6-bisphosphatase. <i>Journal of Biological Chemistry</i> , 2000, 275, 29986-29992.	3.4	24

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37	Tryptophan Fluorescence Reveals the Conformational State of a Dynamic Loop in Recombinant Porcine Fructose-1,6-bisphosphatase,. <i>Biochemistry</i> , 2000, 39, 11100-11106.	2.5	28