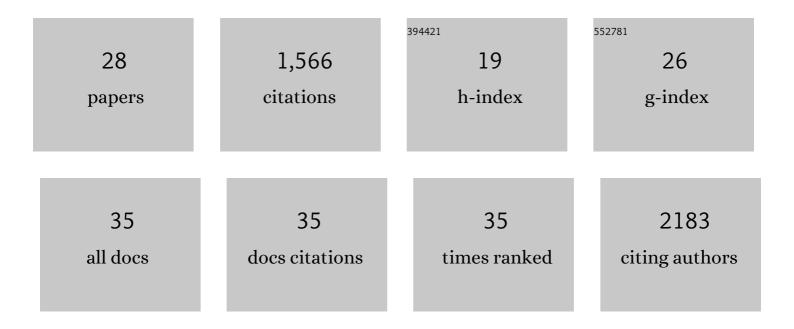
## Steven W Hardwick

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/2034119/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Single-particle cryo-EM at atomic resolution. Nature, 2020, 587, 152-156.	27.8	572
2	Nanopore-Based Identification of Individual Nucleotides for Direct RNA Sequencing. Nano Letters, 2013, 13, 6144-6150.	9.1	103
3	An RNA degradosome assembly in Caulobacter crescentus. Nucleic Acids Research, 2011, 39, 1449-1459.	14.5	84
4	Functional and Structural Characterization of RsbU, a Stress Signaling Protein Phosphatase 2C. Journal of Biological Chemistry, 2004, 279, 40927-40937.	3.4	67
5	Dimers of DNA-PK create a stage for DNA double-strand break repair. Nature Structural and Molecular Biology, 2021, 28, 13-19.	8.2	67
6	Cryo-EM of NHEJ supercomplexes provides insights into DNA repair. Molecular Cell, 2021, 81, 3400-3409.e3.	9.7	62
7	CryoEM structures of human CMG–ATPγS–DNA and CMG–AND-1 complexes. Nucleic Acids Research, 2020, 48, 6980-6995.	14.5	56
8	Crystal structure of <i>Caulobacter crescentus</i> polynucleotide phosphorylase reveals a mechanism of RNA substrate channelling and RNA degradosome assembly. Open Biology, 2012, 2, 120028.	3.6	52
9	Structure of the <i>Escherichia coli</i> ProQ RNA-binding protein. Rna, 2017, 23, 696-711.	3.5	50
10	Structural elucidation of a novel mechanism for the bacteriophage-based inhibition of the RNA degradosome. ELife, 2016, 5, .	6.0	47
11	Role of RsbU in Controlling SigB Activity in <i>Staphylococcus aureus</i> following Alkaline Stress. Journal of Bacteriology, 2009, 191, 2561-2573.	2.2	46
12	Rarely at rest. RNA Biology, 2013, 10, 56-70.	3.1	36
13	Structural insights into inhibitor regulation of the DNA repair protein DNA-PKcs. Nature, 2022, 601, 643-648.	27.8	36
14	Differential assembly diversifies GABAA receptor structures and signalling. Nature, 2022, 604, 190-194.	27.8	36
15	Association of the Cold Shock DEAD-Box RNA Helicase RhlE to the RNA Degradosome in Caulobacter crescentus. Journal of Bacteriology, 2017, 199, .	2.2	34
16	Molecular recognition of RhlB and RNase D in the Caulobacter crescentus RNA degradosome. Nucleic Acids Research, 2014, 42, 13294-13305.	14.5	33
17	Mechanisms of inhibition and activation of extrasynaptic $\hat{I} \pm \hat{I}^2$ GABAA receptors. Nature, 2022, 602, 529-533.	27.8	31
18	Structural insights into RapZ-mediated regulation of bacterial amino-sugar metabolism. Nucleic Acids Research, 2017, 45, 10845-10860.	14.5	30

STEVEN W HARDWICK

#	Article	IF	CITATIONS
19	Structural and Functional Characterization of Partner Switching Regulating the Environmental Stress Response in Bacillus subtilis. Journal of Biological Chemistry, 2007, 282, 11562-11572.	3.4	27
20	Structural basis for the interaction of <scp>SARSâ€CoV</scp> â€2 virulence factor nsp1 with <scp>DNA</scp> polymerase α–primase. Protein Science, 2022, 31, 333-344.	7.6	23
21	<i>Caulobacter crescentus</i> Hfq structure reveals a conserved mechanism of RNA annealing regulation. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 10978-10987.	7.1	20
22	Potential Regulatory Interactions of Escherichia coli RraA Protein with DEAD-box Helicases. Journal of Biological Chemistry, 2013, 288, 31919-31929.	3.4	13
23	Using cryo-EM to understand antimycobacterial resistance in the catalase-peroxidase (KatG) from Mycobacterium tuberculosis. Structure, 2021, 29, 899-912.e4.	3.3	13
24	Viral interference of the bacterial RNA metabolism machinery. RNA Biology, 2017, 14, 6-10.	3.1	12
25	Multiâ€scale ensemble properties of the <i>Escherichia coli</i> RNA degradosome. Molecular Microbiology, 2022, 117, 102-120.	2.5	7
26	Cryo-EM structures of staphylococcal IsdB bound to human hemoglobin reveal the process of heme extraction. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2116708119.	7.1	6
27	1.8â€Ã resolution crystal structure of the carbapenem intrinsic resistance protein CarF. Acta Crystallographica Section D: Structural Biology, 2017, 73, 549-556.	2.3	1
28	Protein Pulldown Assays to Monitor the Composition of the Bacterial RNA Degradosome. Methods in Molecular Biology, 2021, 2209, 425-432.	0.9	0