Steven W Hardwick

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/2034119/publications.pdf

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28	1,566	394421 19	552781 26
papers	citations	h-index	g-index

35	35	35	2183
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Multiâ€scale ensemble properties of the Escherichia coli RNA degradosome. Molecular Microbiology, 2022, 117, 102-120.	2.5	7
2	Structural basis for the interaction of <scp>SARSâ€CoV</scp>â€2 virulence factor nsp1 with <scp>DNA</scp> polymerase Î±â€“primase. Protein Science, 2022, 31, 333-344.	7.6	23
3	Structural insights into inhibitor regulation of the DNA repair protein DNA-PKcs. Nature, 2022, 601, 643-648.	27.8	36
4	Mechanisms of inhibition and activation of extrasynaptic Î±Î² GABAA receptors. Nature, 2022, 602, 529-533.	27.8	31
5	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
6	Differential assembly diversifies GABAA receptor structures and signalling. Nature, 2022, 604, 190-194.	27.8	36
7	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
8	Cryo-EM of NHEJ supercomplexes provides insights into DNA repair. Molecular Cell, 2021, 81, 3400-3409.e3.	9.7	62
9	Using cryo-EM to understand antimycobacterial resistance in the catalase-peroxidase (KatG) from Mycobacterium tuberculosis. Structure, 2021, 29, 899-912.e4.	3.3	13
10	Protein Pulldown Assays to Monitor the Composition of the Bacterial RNA Degradosome. Methods in Molecular Biology, 2021, 2209, 425-432.	0.9	0
11	Single-particle cryo-EM at atomic resolution. Nature, 2020, 587, 152-156.	27.8	572
12	CryoEM structures of human CMGâ€“ATPÎ³Sâ€“DNA and CMGâ€“AND-1 complexes. Nucleic Acids Research, 2020, 48, 6980-6995.	14.5	56
13	Caulobacter crescentus 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
14	Structure of the Escherichia coli ProQ RNA-binding protein. Rna, 2017, 23, 696-711.	3.5	50
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	Viral interference of the bacterial RNA metabolism machinery. RNA Biology, 2017, 14, 6-10.	3.1	12
17	Structural insights into RapZ-mediated regulation of bacterial amino-sugar metabolism. Nucleic Acids Research, 2017, 45, 10845-10860.	14.5	30
18	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

#	Article	IF	Citations
19	Structural elucidation of a novel mechanism for the bacteriophage-based inhibition of the RNA degradosome. ELife, 2016, 5, .	6.0	47
20	Molecular recognition of RhlB and RNase D in the Caulobacter crescentus RNA degradosome. Nucleic Acids Research, 2014, 42, 13294-13305.	14.5	33
21	Nanopore-Based Identification of Individual Nucleotides for Direct RNA Sequencing. Nano Letters, 2013, 13, 6144-6150.	9.1	103
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	Rarely at rest. RNA Biology, 2013, 10, 56-70.	3.1	36
24	Crystal structure of Caulobacter crescentus polynucleotide phosphorylase reveals a mechanism of RNA substrate channelling and RNA degradosome assembly. Open Biology, 2012, 2, 120028.	3.6	52
25	An RNA degradosome assembly in Caulobacter crescentus. Nucleic Acids Research, 2011, 39, 1449-1459.	14.5	84
26	Role of RsbU in Controlling SigB Activity inStaphylococcus aureusfollowing Alkaline Stress. Journal of Bacteriology, 2009, 191, 2561-2573.	2.2	46
27	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
28	Functional and Structural Characterization of RsbU, a Stress Signaling Protein Phosphatase 2C. Journal of Biological Chemistry, 2004, 279, 40927-40937.	3.4	67