

# Sheena D'Arcy

## List of Publications by Year in descending order

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31  
papers

809  
citations

758635

12  
h-index

552369

26  
g-index

35  
all docs

35  
docs citations

35  
times ranked

1385  
citing authors

#	ARTICLE	IF	CITATIONS
1	Hydrogen-deuterium exchange mass spectrometry of Mtr4 with diverse RNAs reveals substrate-dependent dynamics and interfaces in the arch. <i>Nucleic Acids Research</i> , 2022, 50, 4042-4053.	6.5	5
2	Using hydrogen-deuterium exchange mass spectrometry to characterize Mtr4 interactions with RNA. <i>Methods in Enzymology</i> , 2022, , 475-516.	0.4	1
3	Leveraging intrinsic flexibility to engineer enhanced enzyme catalytic activity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	14
4	HD-eXplosion: visualization of hydrogen-deuterium exchange data as chiclet and volcano plots with statistical filtering. <i>Bioinformatics</i> , 2021, 37, 1926-1927.	1.8	19
5	Identification and physical characterization of a spontaneous mutation of the tobacco mosaic virus in the laboratory environment. <i>Scientific Reports</i> , 2021, 11, 15109.	1.6	5
6	An activity-based fluorescent sensor for the detection of the phenol sulfotransferase SULT1A1 in living cells. <i>RSC Chemical Biology</i> , 2021, 2, 830-834.	2.0	5
7	FACT caught in the act of manipulating the nucleosome. <i>Nature</i> , 2020, 577, 426-431.	13.7	160
8	Conformational Dynamics Contribute to Substrate Selectivity and Catalysis in Human Kynureninase. <i>ACS Chemical Biology</i> , 2020, 15, 3159-3166.	1.6	6
9	Proposed Allosteric Inhibitors Bind to the ATP Site of CK2±. <i>Journal of Medicinal Chemistry</i> , 2020, 63, 12786-12798.	2.9	12
10	Comprehensive analysis of histone-binding proteins with multi-angle light scattering. <i>Methods</i> , 2020, 184, 93-101.	1.9	8
11	Stoichiometry of Rtt109 complexes with Vps75 and histones H3-H4. <i>Life Science Alliance</i> , 2020, 3, e202000771.	1.3	3
12	IroT/MavN Is a <i>Legionella</i> Transmembrane Fe(II) Transporter: Metal Selectivity and Translocation Kinetics Revealed by <i>in Vitro</i> Real-Time Transport. <i>Biochemistry</i> , 2019, 58, 4337-4342.	1.2	14
13	Characterization of <i>Caenorhabditis elegans</i> Nucleosome Assembly Protein 1 Uncovers the Role of Acidic Tails in Histone Binding. <i>Biochemistry</i> , 2019, 58, 108-113.	1.2	11
14	Importin-9 wraps around the H2A-H2B core to act as nuclear importer and histone chaperone. <i>Elife</i> , 2019, 8, .	2.8	47
15	Regulating the Uptake of Viral Nanoparticles in Macrophage and Cancer Cells via a pH Switch. <i>Molecular Pharmaceutics</i> , 2018, 15, 2984-2990.	2.3	11
16	Stoichiometry of Multi-protein Complexes containing Rtt109, Vps75, and Histone H3-H4. <i>FASEB Journal</i> , 2018, 32, 524.13.	0.2	0
17	Dynamics of Kynureninase Orthologs during Catalysis. <i>FASEB Journal</i> , 2018, 32, 527.13.	0.2	0
18	Comparing the Solution Conformation and Activin-binding of Follistatin Isoforms. <i>FASEB Journal</i> , 2018, 32, 659.5.	0.2	0

#	ARTICLE	IF	CITATIONS
19	Thermoplasmonics: Molecular Hyperthermia: Spatiotemporal Protein Unfolding and Inactivation by Nanosecond Plasmonic Heating (Small 36/2017). Small, 2017, 13, .	5.2	0
20	Molecular Hyperthermia: Spatiotemporal Protein Unfolding and Inactivation by Nanosecond Plasmonic Heating. Small, 2017, 13, 1700841.	5.2	34
21	Fluorescent Functionalization across Quaternary Structure in a Virus-like Particle. Bioconjugate Chemistry, 2017, 28, 2277-2283.	1.8	17
22	Coordinated Action of Nap1 and RSC in Disassembly of Tandem Nucleosomes. Molecular and Cellular Biology, 2016, 36, 2262-2271.	1.1	13
23	Histone Chaperone Nap1 Is a Major Regulator of Histone H2A-H2B Dynamics at the Inducible GAL Locus. Molecular and Cellular Biology, 2016, 36, 1287-1296.	1.1	24
24	The right place at the right time: chaperoning core histone variants. EMBO Reports, 2015, 16, 1454-1466.	2.0	55
25	Chaperone Nap1 Shields Histone Surfaces Used in a Nucleosome and Can Put H2A-H2B in an Unconventional Tetrameric Form. Molecular Cell, 2013, 51, 662-677.	4.5	69
26	Fluorescence strategies for high-throughput quantification of protein interactions. Nucleic Acids Research, 2012, 40, e33-e33.	6.5	53
27	Towards a mechanism for histone chaperones. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2012, 1819, 211-221.	0.9	64
28	Understanding histone acetyltransferase Rtt109 structure and function: how many chaperones does it take?. Current Opinion in Structural Biology, 2011, 21, 728-734.	2.6	37
29	Defining the Molecular Basis of BubR1 Kinetochores Interactions and APC/C-CDC20 Inhibition. Journal of Biological Chemistry, 2010, 285, 14764-14776.	1.6	37
30	The Crystal Structure of the N-Terminal Region of BUB1 Provides Insight into the Mechanism of BUB1 Recruitment to Kinetochores. Structure, 2009, 17, 105-116.	1.6	45
31	A Positive Spin on the Centromere. Cell, 2009, 138, 22-24.	13.5	8