

# Adam Round

## List of Publications by Year in descending order

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Version: 2024-02-01

35  
papers

1,726  
citations

361045

20  
h-index

377514

34  
g-index

37  
all docs

37  
docs citations

37  
times ranked

3226  
citing authors

#	ARTICLE	IF	CITATIONS
1	Upgraded ESRF BM29 beamline for SAXS on macromolecules in solution. <i>Journal of Synchrotron Radiation</i> , 2013, 20, 660-664.	1.0	359
2	BioSAXS Sample Changer: a robotic sample changer for rapid and reliable high-throughput X-ray solution scattering experiments. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 67-75.	2.5	181
3	Megahertz serial crystallography. <i>Nature Communications</i> , 2018, 9, 4025.	5.8	147
4	Influenza Polymerase Can Adopt an Alternative Configuration Involving a Radical Repacking of PB2 Domains. <i>Molecular Cell</i> , 2016, 61, 125-137.	4.5	123
5	The Single Particles, Clusters and Biomolecules and Serial Femtosecond Crystallography instrument of the European XFEL: initial installation. <i>Journal of Synchrotron Radiation</i> , 2019, 26, 660-676.	1.0	90
6	Online data analysis at the ESRF bioSAXS beamline, BM29. <i>Journal of Applied Crystallography</i> , 2016, 49, 203-212.	1.9	79
7	Structural Basis of Host Autophagy-related Protein 8 (ATG8) Binding by the Irish Potato Famine Pathogen Effector Protein PexRD54. <i>Journal of Biological Chemistry</i> , 2016, 291, 20270-20282.	1.6	74
8	Evolution of the Plant Reproduction Master Regulators LFY and the MADS Transcription Factors: The Role of Protein Structure in the Evolutionary Development of the Flower. <i>Frontiers in Plant Science</i> , 2015, 6, 1193.	1.7	58
9	ISPyB for BioSAXS, the gateway to user autonomy in solution scattering experiments. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 76-85.	2.5	56
10	Large-Scale Conformational Dynamics Control H5N1 Influenza Polymerase PB2 Binding to Importin $\beta$ . <i>Journal of the American Chemical Society</i> , 2015, 137, 15122-15134.	6.6	49
11	Coupling High Throughput Microfluidics and Small-Angle X-ray Scattering to Study Protein Crystallization from Solution. <i>Analytical Chemistry</i> , 2017, 89, 2282-2287.	3.2	49
12	Structure of the <i>C.Âelegans</i> ZYG-1 Cryptic Polo Box Suggests a Conserved Mechanism for Centriolar Docking of Plk4 Kinases. <i>Structure</i> , 2014, 22, 1090-1104.	1.6	45
13	FANCM interacts with PCNA to promote replication traverse of DNA interstrand crosslinks. <i>Nucleic Acids Research</i> , 2016, 44, 3219-3232.	6.5	41
14	The crystal structure of the Split End protein SHARP adds a new layer of complexity to proteins containing RNA recognition motifs. <i>Nucleic Acids Research</i> , 2014, 42, 6742-6752.	6.5	40
15	Determination of the GH3.12 protein conformation through HPLC-integrated SAXS measurements combined with X-ray crystallography. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 2072-2080.	2.5	37
16	The solution configurations of inactive and activated DntR have implications for the sliding dimer mechanism of LysR transcription factors. <i>Scientific Reports</i> , 2016, 6, 19988.	1.6	36
17	Architecture of TAF11/TAF13/TBP complex suggests novel regulation properties of general transcription factor TFIID. <i>ELife</i> , 2017, 6, .	2.8	29
18	Development of tools to automate quantitative analysis of radiation damage in SAXS experiments. <i>Journal of Synchrotron Radiation</i> , 2017, 24, 63-72.	1.0	28

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19	Insc:LGN tetramers promote asymmetric divisions of mammary stem cells. Nature Communications, 2018, 9, 1025.	5.8	27
20	Binding of Myomesin to Obscurin-Like-1 at the Muscle M-Band Provides a Strategy for Isoform-Specific Mechanical Protection. Structure, 2017, 25, 107-120.	1.6	25
21	3D printed devices and infrastructure for liquid sample delivery at the European XFEL. Journal of Synchrotron Radiation, 2022, 29, 331-346.	1.0	22
22	Vaccinia Virus Immunomodulator A46: A Lipid and Protein-Binding Scaffold for Sequestering Host TIR-Domain Proteins. PLoS Pathogens, 2016, 12, e1006079.	2.1	19
23	Mechanisms of membrane protein crystallization in $\alpha$ -bicelles <sup>TM</sup> . Scientific Reports, 2022, 12, .	1.6	17
24	Bacterial protease uses distinct thermodynamic signatures for substrate recognition. Scientific Reports, 2017, 7, 2848.	1.6	14
25	Combined small angle X-ray solution scattering with atomic force microscopy for characterizing radiation damage on biological macromolecules. BMC Structural Biology, 2016, 16, 18.	2.3	13
26	SAXS Structural Studies of Dps from Deinococcus radiodurans Highlights the Conformation of the Mobile N-Terminal Extensions. Journal of Molecular Biology, 2017, 429, 667-687.	2.0	13
27	Co-flow injection for serial crystallography at X-ray free-electron lasers. Journal of Applied Crystallography, 2022, 55, 1-13.	1.9	12
28	The Crystal Structure and Small-Angle X-Ray Analysis of CsdL/TcdA Reveal a New tRNA Binding Motif in the MoeB/E1 Superfamily. PLoS ONE, 2015, 10, e0118606.	1.1	10
29	A new calmodulin-binding motif for inositol 1,4,5-trisphosphate 3-kinase regulation. Biochemical Journal, 2014, 463, 319-328.	1.7	8
30	Small-angle neutron and X-ray scattering analysis of the supramolecular organization of rhodopsin in photoreceptor membrane. Biochimica Et Biophysica Acta - Biomembranes, 2019, 1861, 183000.	1.4	8
31	Dynamic self-assembly of DNA minor groove-binding ligand DB921 into nanotubes triggered by an alkali halide. Nanoscale, 2018, 10, 5550-5558.	2.8	6
32	A multi-million image Serial Femtosecond Crystallography dataset collected at the European XFEL. Scientific Data, 2022, 9, 161.	2.4	5
33	K <sup>+</sup> vs. Na <sup>+</sup> Effects on the Self-Assembly of Guanosine 5'-Monophosphate: A Solution SAXS Structural Study. Nanomaterials, 2020, 10, 629.	1.9	3
34	The Use of Small-Angle Scattering for the Characterization of Multi Subunit Complexes. Advances in Experimental Medicine and Biology, 2016, 896, 329-350.	0.8	1
35	Hierarchical Nanotube Self-Assembly of DNA Minor Groove-Binding Ligand DB921 via Alkali Halide Triggering. Macromolecular Symposia, 2019, 386, 1800243.	0.4	0