

# Adam Round

## List of Publications by Year in descending order

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35  
papers

1,726  
citations

361413

20  
h-index

377865

34  
g-index

37  
all docs

37  
docs citations

37  
times ranked

3226  
citing authors

#	ARTICLE	IF	CITATIONS
1	Co-flow injection for serial crystallography at X-ray free-electron lasers. <i>Journal of Applied Crystallography</i> , 2022, 55, 1-13.	4.5	12
2	3D printed devices and infrastructure for liquid sample delivery at the European XFEL. <i>Journal of Synchrotron Radiation</i> , 2022, 29, 331-346.	2.4	22
3	A multi-million image Serial Femtosecond Crystallography dataset collected at the European XFEL. <i>Scientific Data</i> , 2022, 9, 161.	5.3	5
4	Mechanisms of membrane protein crystallization in <i>â€ˆbicellesâ€™</i> . <i>Scientific Reports</i> , 2022, 12, .	3.3	17
5	K <sup>+</sup> vs. Na <sup>+</sup> Effects on the Self-Assembly of Guanosine 5â€™-Monophosphate: A Solution SAXS Structural Study. <i>Nanomaterials</i> , 2020, 10, 629.	4.1	3
6	Hierarchical Nanotube Self-Assembly of DNA Minor Groove-Binding Ligand DB921 via Alkali Halide Triggering. <i>Macromolecular Symposia</i> , 2019, 386, 1800243.	0.7	0
7	Small-angle neutron and X-ray scattering analysis of the supramolecular organization of rhodopsin in photoreceptor membrane. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2019, 1861, 183000.	2.6	8
8	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.	2.4	90
9	Dynamic self-assembly of DNA minor groove-binding ligand DB921 into nanotubes triggered by an alkali halide. <i>Nanoscale</i> , 2018, 10, 5550-5558.	5.6	6
10	Insc:LGN tetramers promote asymmetric divisions of mammary stem cells. <i>Nature Communications</i> , 2018, 9, 1025.	12.8	27
11	Megahertz serial crystallography. <i>Nature Communications</i> , 2018, 9, 4025.	12.8	147
12	SAXS Structural Studies of Dps from <i>Deinococcus radiodurans</i> Highlights the Conformation of the Mobile N-Terminal Extensions. <i>Journal of Molecular Biology</i> , 2017, 429, 667-687.	4.2	13
13	Coupling High Throughput Microfluidics and Small-Angle X-ray Scattering to Study Protein Crystallization from Solution. <i>Analytical Chemistry</i> , 2017, 89, 2282-2287.	6.5	49
14	Bacterial protease uses distinct thermodynamic signatures for substrate recognition. <i>Scientific Reports</i> , 2017, 7, 2848.	3.3	14
15	Binding of Myomesin to Obscurin-Like-1 at the Muscle M-Band Provides a Strategy for Isoform-Specific Mechanical Protection. <i>Structure</i> , 2017, 25, 107-120.	3.3	25
16	Development of tools to automate quantitative analysis of radiation damage in SAXS experiments. <i>Journal of Synchrotron Radiation</i> , 2017, 24, 63-72.	2.4	28
17	Architecture of TAF11/TAF13/TBP complex suggests novel regulation properties of general transcription factor TFIID. <i>ELife</i> , 2017, 6, .	6.0	29
18	Vaccinia Virus Immunomodulator A46: A Lipid and Protein-Binding Scaffold for Sequestering Host TIR-Domain Proteins. <i>PLoS Pathogens</i> , 2016, 12, e1006079.	4.7	19

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19	Online data analysis at the ESRF bioSAXS beamline, BM29. <i>Journal of Applied Crystallography</i> , 2016, 49, 203-212.	4.5	79
20	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.	3.3	36
21	The Use of Small-Angle Scattering for the Characterization of Multi Subunit Complexes. <i>Advances in Experimental Medicine and Biology</i> , 2016, 896, 329-350.	1.6	1
22	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.	3.4	74
23	Combined small angle X-ray solution scattering with atomic force microscopy for characterizing radiation damage on biological macromolecules. <i>BMC Structural Biology</i> , 2016, 16, 18.	2.3	13
24	Influenza Polymerase Can Adopt an Alternative Configuration Involving a Radical Repacking of PB2 Domains. <i>Molecular Cell</i> , 2016, 61, 125-137.	9.7	123
25	FANCM interacts with PCNA to promote replication traverse of DNA interstrand crosslinks. <i>Nucleic Acids Research</i> , 2016, 44, 3219-3232.	14.5	41
26	The Crystal Structure and Small-Angle X-Ray Analysis of CsdL/TcdA Reveal a New tRNA Binding Motif in the MoeB/E1 Superfamily. <i>PLoS ONE</i> , 2015, 10, e0118606.	2.5	10
27	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
28	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
29	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.	13.7	49
30	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.	3.6	58
31	A new calmodulin-binding motif for inositol 1,4,5-trisphosphate 3-kinase regulation. <i>Biochemical Journal</i> , 2014, 463, 319-328.	3.7	8
32	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.	14.5	40
33	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.	3.3	45
34	Upgraded ESRF BM29 beamline for SAXS on macromolecules in solution. <i>Journal of Synchrotron Radiation</i> , 2013, 20, 660-664.	2.4	359
35	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