

# Tom T Caradoc-Davies

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5792162/publications.pdf>

Version: 2024-02-01

30  
papers

2,222  
citations

361413

20  
h-index

477307

29  
g-index

30  
all docs

30  
docs citations

30  
times ranked

3469  
citing authors

#	ARTICLE	IF	CITATIONS
1	Crystal structure of posnjakite formed in the first crystal water-cooling line of the ANSTO Melbourne Australian Synchrotron MX1 Double Crystal Monochromator. <i>Acta Crystallographica Section E: Crystallographic Communications</i> , 2020, 76, 1136-1138.	0.5	0
2	Structure and Function Characterization of the a1a2 Motifs of Streptococcus pyogenes M Protein in Human Plasminogen Binding. <i>Journal of Molecular Biology</i> , 2019, 431, 3804-3813.	4.2	9
3	Structural studies of plasmin inhibition. <i>Biochemical Society Transactions</i> , 2019, 47, 541-557.	3.4	24
4	Tranexamic acid is an active site inhibitor of urokinase plasminogen activator. <i>Blood Advances</i> , 2019, 3, 729-733.	5.2	22
5	MX2: a high-flux undulator microfocus beamline serving both the chemical and macromolecular crystallography communities at the Australian Synchrotron. <i>Journal of Synchrotron Radiation</i> , 2018, 25, 885-891.	2.4	346
6	A Cyclic Peptide Inhibitor of the iNOSâ€“SPSB Proteinâ€“Protein Interaction as a Potential Anti-Infective Agent. <i>ACS Chemical Biology</i> , 2018, 13, 2930-2938.	3.4	17
7	The first transmembrane region of complement component-9 acts as a brake on its self-assembly. <i>Nature Communications</i> , 2018, 9, 3266.	12.8	56
8	Antibodies: From novel repertoires to defining and refining the structure of biologically important targets. <i>Methods</i> , 2017, 116, 12-22.	3.8	6
9	Structural basis of autoregulatory scaffolding by apoptosis signal-regulating kinase 1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E2096-E2105.	7.1	34
10	X-ray crystal structure of plasmin with tranexamic acidâ€“derived active site inhibitors. <i>Blood Advances</i> , 2017, 1, 766-771.	5.2	25
11	MX1: a bending-magnet crystallography beamline serving both chemical and macromolecular crystallography communities at the Australian Synchrotron. <i>Journal of Synchrotron Radiation</i> , 2015, 22, 187-190.	2.4	336
12	Conformational Changes during Pore Formation by the Perforin-Related Protein Pleurotolysin. <i>PLoS Biology</i> , 2015, 13, e1002049.	5.6	114
13	Operation of the Australian Store.Synchrotron for macromolecular crystallography. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 2510-2519.	2.5	21
14	Reconciling the Structural Attributes of Avian Antibodies. <i>Journal of Biological Chemistry</i> , 2014, 289, 15384-15392.	3.4	28
15	The structure of the caspase recruitment domain of BinCARD reveals that all three cysteines can be oxidized. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 774-784.	2.5	13
16	Fragment Screening for the Modelling Community: SPR, ITC, and Crystallography. <i>Australian Journal of Chemistry</i> , 2013, 66, 1507.	0.9	6
17	The X-ray Crystal Structure of Full-Length Human Plasminogen. <i>Cell Reports</i> , 2012, 1, 185-190.	6.4	189
18	Structural Basis for Hemoglobin Capture by Staphylococcus aureus Cell-surface Protein, IsdH. <i>Journal of Biological Chemistry</i> , 2011, 286, 38439-38447.	3.4	50

#	ARTICLE	IF	CITATIONS
19	The structural basis for membrane binding and pore formation by lymphocyte perforin. <i>Nature</i> , 2010, 468, 447-451.	27.8	364
20	Structure of the <i>Plasmodium falciparum</i> M17 aminopeptidase and significance for the design of drugs targeting the neutral exopeptidases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 2449-2454.	7.1	80
21	Crystal Structure of the Minor Pilin FctB Reveals Determinants of Group A Streptococcal Pilus Anchoring. <i>Journal of Biological Chemistry</i> , 2010, 285, 20381-20389.	3.4	61
22	Characterization of Tetra-aryl Benzene Isomers by Using Preparative Gas Chromatography with Mass Spectrometry, Nuclear Magnetic Resonance Spectroscopy, and X-ray Crystallographic Methods. <i>Analytical Chemistry</i> , 2010, 82, 4501-4509.	6.5	34
23	The X-Ray Crystal Structure of <i>Escherichia coli</i> Succinic Semialdehyde Dehydrogenase; Structural Insights into NADP+/Enzyme Interactions. <i>PLoS ONE</i> , 2010, 5, e9280.	2.5	31
24	The Laminin-Binding Protein Lbp from <i>Streptococcus pyogenes</i> Is a Zinc Receptor. <i>Journal of Bacteriology</i> , 2009, 191, 5814-5823.	2.2	56
25	Practical Aspects of the SAMPL Challenge: Providing an Extensive Experimental Data Set for the Modeling Community. <i>Journal of Biomolecular Screening</i> , 2009, 14, 1245-1250.	2.6	17
26	Structures of Glycinamide Ribonucleotide Transformylase (PurN) from <i>Mycobacterium tuberculosis</i> Reveal a Novel Dimer with Relevance to Drug Discovery. <i>Journal of Molecular Biology</i> , 2009, 389, 722-733.	4.2	15
27	Crystal Structures of the Staphylococcal Toxin SSL5 in Complex with Sialyl Lewis X Reveal a Conserved Binding Site that Shares Common Features with Viral and Bacterial Sialic Acid Binding Proteins. <i>Journal of Molecular Biology</i> , 2007, 374, 1298-1308.	4.2	62
28	Crystal structure of a substrate complex of myo-inositol oxygenase, a di-iron oxygenase with a key role in inositol metabolism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 15032-15037.	7.1	91
29	Crystal Structures of <i>Escherichia coli</i> Uridine Phosphorylase in Two Native and Three Complexed Forms Reveal Basis of Substrate Specificity, Induced Conformational Changes and Influence of Potassium. <i>Journal of Molecular Biology</i> , 2004, 337, 337-354.	4.2	59
30	Substrate Specificity of the Nonribosomal Peptide Synthetase PvdD from <i>Pseudomonas aeruginosa</i> . <i>Journal of Bacteriology</i> , 2003, 185, 2848-2855.	2.2	56