

Thomas E Edwards

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2621771/publications.pdf>

Version: 2024-02-01

14
papers

480
citations

1306789

7
h-index

1199166

12
g-index

16
all docs

16
docs citations

16
times ranked

842
citing authors

#	ARTICLE	IF	CITATIONS
1	Cocrystal structure of a class I preQ1 riboswitch reveals a pseudoknot recognizing an essential hypermodified nucleobase. <i>Nature Structural and Molecular Biology</i> , 2009, 16, 343-344.	3.6	160
2	Increasing the structural coverage of tuberculosis drug targets. <i>Tuberculosis</i> , 2015, 95, 142-148.	0.8	103
3	High-throughput protein production and purification at the Seattle Structural Genomics Center for Infectious Disease. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 1010-1014.	0.7	75
4	SAD phasing using iodide ions in a high-throughput structural genomics environment. <i>Journal of Structural and Functional Genomics</i> , 2011, 12, 83-95.	1.2	68
5	Structure of an ADP-ribosylation factor, ARF1, from <i>Entamoeba histolytica</i> bound to Mg ²⁺ GDP. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 594-599.	0.4	27
6	<i>Mycobacterium thermoresistibile</i> as a source of thermostable orthologs of <i>Mycobacterium tuberculosis</i> proteins. <i>Protein Science</i> , 2012, 21, 1093-1096.	3.1	15
7	Aconitate decarboxylase 1 participates in the control of pulmonary <i>Brucella</i> infection in mice. <i>PLoS Pathogens</i> , 2021, 17, e1009887.	2.1	15
8	Crystal structures of <i>Mycobacterium</i> MeaB and MMAA-like GTPases. <i>Journal of Structural and Functional Genomics</i> , 2015, 16, 91-99.	1.2	7
9	Toward a structome of <i>Acinetobacter baumannii</i> drug targets. <i>Protein Science</i> , 2020, 29, 789-802.	3.1	4
10	Crystal structure of a hypothetical protein from <i>Giardia lamblia</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2022, 78, 59-65.	0.4	2
11	Ab initio structure solution of a proteolytic fragment using ARCIMBOLDO. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2018, 74, 530-535.	0.4	1
12	Crystal structure of betaine aldehyde dehydrogenase from <i>Burkholderia pseudomallei</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2022, 78, 45-51.	0.4	1
13	Crystal structures of FolM alternative dihydrofolate reductase 1 from <i>Brucella suis</i> and <i>Brucella canis</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2022, 78, 31-38.	0.4	0
14	Crystal structure of an inorganic pyrophosphatase from <i>Chlamydia trachomatis</i> D/UW-3/Cx. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2022, 78, 135-142.	0.4	0