

Giancarlo Tria

List of Publications by Year in descending order

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Version: 2024-02-01

20
papers

2,515
citations

840119

11
h-index

839053

18
g-index

20
all docs

20
docs citations

20
times ranked

5662
citing authors

#	ARTICLE	IF	CITATIONS
1	Priming mycobacterial ESX-secreted protein B to form a channel-like structure. <i>Current Research in Structural Biology</i> , 2021, 3, 153-164.	1.1	15
2	Structural dynamics of the GluK3-kainate receptor neurotransmitter binding domains revealed by cryo-EM. <i>International Journal of Biological Macromolecules</i> , 2020, 149, 1051-1058.	3.6	11
3	Ensemble description of the intrinsically disordered N-terminal domain of the Nipah virus P/V protein from combined NMR and SAXS. <i>Scientific Reports</i> , 2020, 10, 19574.	1.6	13
4	Structure-specific recognition protein-1 (SSRP1) is an elongated homodimer that binds histones. <i>Journal of Biological Chemistry</i> , 2018, 293, 10071-10083.	1.6	9
5	A New Method for Determining Structure Ensemble: Application to a RNA Binding Di-Domain Protein. <i>Biophysical Journal</i> , 2016, 110, 1943-1956.	0.2	10
6	Casitas B-lineage lymphoma linker helix mutations found in myeloproliferative neoplasms affect conformation. <i>BMC Biology</i> , 2016, 14, 76.	1.7	16
7	Maturation of 6S regulatory RNA to a highly elongated structure. <i>FEBS Journal</i> , 2015, 282, 4548-4564.	2.2	4
8	Advanced ensemble modelling of flexible macromolecules using X-ray solution scattering. <i>IUCr</i> , 2015, 2, 207-217.	1.0	516
9	Structural insight and flexible features of NS5 proteins from all four serotypes of Dengue virus in solution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 2309-2327.	2.5	34
10	Structural Basis of a Kv7.1 Potassium Channel Gating Module: Studies of the Intracellular C-Terminal Domain in Complex with Calmodulin. <i>Structure</i> , 2014, 22, 1582-1594.	1.6	88
11	A conformational switch in collybistin determines the differentiation of inhibitory postsynapses. <i>EMBO Journal</i> , 2014, 33, 2113-2133.	3.5	75
12	The Salmonella enterica ZinT structure, zinc affinity and interaction with the high-affinity uptake protein ZnuA provide insight into the management of periplasmic zinc. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2014, 1840, 535-544.	1.1	46
13	The SH2 domain of Abl kinases regulates kinase autophosphorylation by controlling activation loop accessibility. <i>Nature Communications</i> , 2014, 5, 5470.	5.8	36
14	Analysis of macromolecular flexibility in solution by combining SAXS with MX. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2014, 70, C425-C425.	0.0	0
15	The SH2 Domain of BCR-ABL1 Regulates Kinase Autophosphorylation By Controlling Activation Loop Accessibility. <i>Blood</i> , 2014, 124, 2209-2209.	0.6	0
16	A structural model of PpoA derived from SAXS-analysis—Implications for substrate conversion. <i>Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids</i> , 2013, 1831, 1449-1457.	1.2	9
17	Structural characterization of gephyrin by AFM and SAXS reveals a mixture of compact and extended states. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 2050-2060.	2.5	43
18	Small Angle X-Ray Scattering Studies of Mitochondrial Glutaminase C Reveal Extended Flexible Regions, and Link Oligomeric State with Enzyme Activity. <i>PLoS ONE</i> , 2013, 8, e74783.	1.1	29

#	ARTICLE	IF	CITATIONS
19	New developments in the <i>ATSAS</i> program package for small-angle scattering data analysis. <i>Journal of Applied Crystallography</i> , 2012, 45, 342-350.	1.9	1,551
20	Finding New Genes for Non-Syndromic Hearing Loss through an In Silico Prioritization Study. <i>PLoS ONE</i> , 2010, 5, e12742.	1.1	10