

Kala Bharath Pilla

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6380265/publications.pdf>

Version: 2024-02-01

10
papers

4,316
citations

1162889

8
h-index

1372474

10
g-index

12
all docs

12
docs citations

12
times ranked

10317
citing authors

#	ARTICLE	IF	CITATIONS
1	Macromolecular modeling and design in Rosetta: recent methods and frameworks. <i>Nature Methods</i> , 2020, 17, 665-680.	9.0	513
2	A SARS-CoV-2 protein interaction map reveals targets for drug repurposing. <i>Nature</i> , 2020, 583, 459-468.	13.7	3,542
3	Protein Structure Determination by Assembling Super-Secondary Structure Motifs Using Pseudocontact Shifts. <i>Structure</i> , 2017, 25, 559-568.	1.6	17
4	3D Computational Modeling of Proteins Using Sparse Paramagnetic NMR Data. <i>Methods in Molecular Biology</i> , 2017, 1526, 3-21.	0.4	6
5	Molecular modeling of biomolecules by paramagnetic NMR and computational hybrid methods. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2017, 1865, 1654-1663.	1.1	9
6	Pseudocontact Shift-Driven Iterative Resampling for 3D Structure Determinations of Large Proteins. <i>Journal of Molecular Biology</i> , 2016, 428, 522-532.	2.0	26
7	Sensitive NMR Approach for Determining the Binding Mode of Tightly Binding Ligand Molecules to Protein Targets. <i>Journal of the American Chemical Society</i> , 2016, 138, 4539-4546.	6.6	53
8	Capturing Conformational States in Proteins Using Sparse Paramagnetic NMR Data. <i>PLoS ONE</i> , 2015, 10, e0127053.	1.1	29
9	Magic Angle Spinning NMR Structure Determination of Proteins from Pseudocontact Shifts. <i>Journal of the American Chemical Society</i> , 2013, 135, 8294-8303.	6.6	42
10	Three-Dimensional Protein Fold Determination from Backbone Amide Pseudocontact Shifts Generated by Lanthanide Tags at Multiple Sites. <i>Structure</i> , 2013, 21, 883-890.	1.6	77