

Shruthi Viswanath

List of Publications by Year in descending order

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Version: 2024-02-01

17
papers

678
citations

759233

12
h-index

940533

16
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22
all docs

22
docs citations

22
times ranked

1079
citing authors

#	ARTICLE	IF	CITATIONS
1	Prediction of homoprotein and heteroprotein complexes by protein docking and template-based modeling: A CASP-CAPRI experiment. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 323-348.	2.6	148
2	Integrative structure modeling with the Integrative Modeling Platform. <i>Protein Science</i> , 2018, 27, 245-258.	7.6	92
3	Architecture of the Human and Yeast General Transcription and DNA Repair Factor TFIIH. <i>Molecular Cell</i> , 2015, 59, 794-806.	9.7	91
4	Assessing Exhaustiveness of Stochastic Sampling for Integrative Modeling of Macromolecular Structures. <i>Biophysical Journal</i> , 2017, 113, 2344-2353.	0.5	68
5	Improving ranking of models for protein complexes with side chain modeling and atomic potentials. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 592-606.	2.6	54
6	The molecular architecture of the yeast spindle pole body core determined by Bayesian integrative modeling. <i>Molecular Biology of the Cell</i> , 2017, 28, 3298-3314.	2.1	44
7	Modeling Biological Complexes Using Integrative Modeling Platform. <i>Methods in Molecular Biology</i> , 2019, 2022, 353-377.	0.9	34
8	Using Integrative Modeling Platform to compute, validate, and archive a model of a protein complex structure. <i>Protein Science</i> , 2021, 30, 250-261.	7.6	31
9	DOCK/PIERR: Web Server for Structure Prediction of Protein-Protein Complexes. <i>Methods in Molecular Biology</i> , 2014, 1137, 199-207.	0.9	26
10	CM1-driven assembly and activation of yeast β -tubulin small complex underlies microtubule nucleation. <i>ELife</i> , 2021, 10, .	6.0	23
11	Analyzing milestone networks for molecular kinetics: Definitions, algorithms, and examples. <i>Journal of Chemical Physics</i> , 2013, 139, 174105.	3.0	20
12	Optimizing model representation for integrative structure determination of macromolecular assemblies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 540-545.	7.1	16
13	Extension of a protein docking algorithm to membranes and applications to amyloid precursor protein dimerization. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 2170-2185.	2.6	15
14	A Framework for Stochastic Optimization of Parameters for Integrative Modeling of Macromolecular Assemblies. <i>Life</i> , 2021, 11, 1183.	2.4	4
15	PrISM: precision for integrative structural models. <i>Bioinformatics</i> , 2022, 38, 3837-3839.	4.1	4
16	Color call improvement in next generation sequencing using multi-class support vector machines. <i>BMC Bioinformatics</i> , 2012, 13, .	2.6	2
17	A Bayesian Integrative Structure Model of the Yeast Centrosome. <i>Biophysical Journal</i> , 2018, 114, 35a.	0.5	0