

# Debabani Ganguly

## List of Publications by Year in descending order

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Version: 2024-02-01

21  
papers

631  
citations

933447

10  
h-index

888059

17  
g-index

23  
all docs

23  
docs citations

23  
times ranked

663  
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural modulation of p53TAD1-TAZ2 complex upon mutations and post-translational modification. <i>Journal of Biomolecular Structure and Dynamics</i> , 2023, 41, 176-185.	3.5	0
2	Spike protein mutational landscape in India during the complete lockdown phase: Could Muller's ratchet be a future game-changer for COVID-19?. <i>Infection, Genetics and Evolution</i> , 2021, 92, 104874.	2.3	1
3	Single Amino Acid Based Self-Assembled Biomaterials with Potent Antimicrobial Activity. <i>Chemistry - A European Journal</i> , 2021, 27, 16744-16753.	3.3	9
4	Design, development and mechanistic insights into the enhanced antibacterial activity of mono and bis-phosphonium fluoresceinate ionic liquids. <i>Materials Today Communications</i> , 2021, 28, 102672.	1.9	6
5	C-terminal tail insertion of Bcl-xL in membrane occurs via partial unfolding and refolding cycle associating microsolvation. <i>Physical Chemistry Chemical Physics</i> , 2016, 18, 24095-24105.	2.8	4
6	Conformational Flexibility and pH Effects on Anisotropic Growth of Sheet-Like Assembly of Amphiphilic Peptides. <i>Journal of Nanoscience and Nanotechnology</i> , 2015, 15, 4470-4479.	0.9	4
7	Modulation of the Disordered Conformational Ensembles of the p53 Transactivation Domain by Cancer-Associated Mutations. <i>PLoS Computational Biology</i> , 2015, 11, e1004247.	3.2	32
8	Electrostatically Accelerated Encounter and Folding for Facile Recognition of Intrinsically Disordered Proteins. <i>PLoS Computational Biology</i> , 2013, 9, e1003363.	3.2	74
9	Electrostatically Accelerated Coupled Binding and Folding of Intrinsically Disordered Proteins. <i>Journal of Molecular Biology</i> , 2012, 422, 674-684.	4.2	71
10	Synergistic folding of two intrinsically disordered proteins: searching for conformational selection. <i>Molecular BioSystems</i> , 2012, 8, 198-209.	2.9	51
11	Residual Structures, Conformational Fluctuations, and Electrostatic Interactions in the Synergistic Folding of Two Intrinsically Disordered Proteins. <i>PLoS Computational Biology</i> , 2012, 8, e1002353.	3.2	78
12	Topology-based modeling of intrinsically disordered proteins: Balancing intrinsic folding and intermolecular interactions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 1251-1266.	2.6	67
13	Intrinsically Disordered Proteins in a Physics-Based World. <i>International Journal of Molecular Sciences</i> , 2010, 11, 5292-5309.	4.1	48
14	Concerted Involvement of Long-Range Electrostatic Interactions and Fly-Catching in Recognition of Intrinsically Disordered Proteins. <i>Biophysical Journal</i> , 2010, 98, 257a.	0.5	1
15	Structural Interpretation of Paramagnetic Relaxation Enhancement-Derived Distances for Disordered Protein States. <i>Journal of Molecular Biology</i> , 2009, 390, 467-477.	4.2	70
16	Molecular Dynamics Simulations of a Single 11-Residue Beta-Sheet Adhesive and its Assembly. <i>Biophysical Journal</i> , 2009, 96, 75a-76a.	0.5	0
17	Atomistic Details of the Disordered States of KID and pKID. Implications in Coupled Binding and Folding. <i>Journal of the American Chemical Society</i> , 2009, 131, 5214-5223.	13.7	88
18	Effects of Phosphorylation on the unbound states of an intrinsically disordered protein: A Computational Approach. <i>Biophysical Journal</i> , 2009, 96, 320a.	0.5	0

#	ARTICLE	IF	CITATIONS
19	Steered unfolding of ricin A and B chains. <i>Journal of Molecular Graphics and Modelling</i> , 2008, 27, 266-274.	2.4	0
20	Extended binding site of ricin B lectin for oligosaccharide recognition. <i>Biopolymers</i> , 2007, 86, 311-320.	2.4	4
21	Binding diversity of the two binding sites of ricin B lectin. <i>Biopolymers</i> , 2006, 83, 83-94.	2.4	18