

Swarnendu Tripathi, S Tripathi

List of Publications by Year in descending order

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18
papers

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#	ARTICLE	IF	CITATIONS
1	Computational modeling reveals key molecular properties and dynamic behavior of disruptor of telomeric silencing 1â€ike (<i>DOT1L</i>) and partnering complexes involved in leukemogenesis. <i>Proteins: Structure, Function and Bioinformatics</i> , 2022, 90, 282-298.	2.6	3
2	Enhanced interpretation of 935 hotspot and non-hotspot RAS variants using evidence-based structural bioinformatics. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 117-127.	4.1	4
3	Structural bioinformatics enhances mechanistic interpretation of genomic variation, demonstrated through the analyses of 935 distinct RAS family mutations. <i>Bioinformatics</i> , 2021, 37, 1367-1375.	4.1	6
4	Molecular mechanics and dynamic simulations of well-known Kabuki syndrome-associated KDM6A variants reveal putative mechanisms of dysfunction. <i>Orphanet Journal of Rare Diseases</i> , 2021, 16, 66.	2.7	11
5	Pathogenic SPTBN1 variants cause an autosomal dominant neurodevelopmental syndrome. <i>Nature Genetics</i> , 2021, 53, 1006-1021.	21.4	44
6	Novel destabilizing Dynactin variant (DCTN1 p.Tyr78His) in patient with Perry syndrome. <i>Parkinsonism and Related Disorders</i> , 2020, 77, 110-113.	2.2	7
7	Novel <i>KLHL26</i> variant associated with a familial case of Ebsteinâ€™s anomaly and left ventricular noncompaction. <i>Molecular Genetics & Genomic Medicine</i> , 2020, 8, e1152.	1.2	11
8	Opposing Intermolecular Tuning of Ca ²⁺ Affinity for Calmodulin by Neurogranin and CaMKII Peptides. <i>Biophysical Journal</i> , 2017, 112, 1105-1119.	0.5	11
9	Correlation between Gene Variants, Signaling Pathways, and Efficacy of Chemotherapy Drugs against Colon Cancers. <i>Cancer Informatics</i> , 2016, 15, CIN.S34506.	1.9	13
10	Lessons in Protein Design from Combined Evolution and Conformational Dynamics. <i>Scientific Reports</i> , 2015, 5, 14259.	3.3	13
11	Conformational frustration in calmodulinâ€™target recognition. <i>Journal of Molecular Recognition</i> , 2015, 28, 74-86.	2.1	19
12	Alterations of Nonconserved Residues Affect Protein Stability and Folding Dynamics through Chargeâ€™Charge Interactions. <i>Journal of Physical Chemistry B</i> , 2015, 119, 13103-13112.	2.6	22
13	Protein recognition and selection through conformational and mutually induced fit. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 20545-20550.	7.1	50
14	Allostery and Folding of the N-terminal Receiver Domain of Protein NtrC. <i>Journal of Physical Chemistry B</i> , 2013, 117, 13182-13193.	2.6	5
15	Backtracking due to Residual Structure in the Unfolded State Changes the Folding of the Third Fibronectin Type III Domain from Tenascin-C. <i>Journal of Physical Chemistry B</i> , 2013, 117, 800-810.	2.6	12
16	Conformational flexibility and the mechanisms of allosteric transitions in topologically similar proteins. <i>Journal of Chemical Physics</i> , 2011, 135, 075104.	3.0	11
17	Inherent flexibility determines the transition mechanisms of the EF-hands of calmodulin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 2104-2109.	7.1	63
18	Inherent flexibility and protein function: The open/closed conformational transition in the N-terminal domain of calmodulin. <i>Journal of Chemical Physics</i> , 2008, 128, 205104.	3.0	22