

Matthew J Whitley

List of Publications by Year in descending order

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525
citing authors

#	ARTICLE	IF	CITATIONS
1	Cataract-associated P23T \hat{I}^3 D-crystallin retains a native-like fold in amorphous-looking aggregates formed at physiological pH. <i>Nature Communications</i> , 2017, 8, 15137.	12.8	69
2	Frameworks for Understanding Long-Range Intra-Protein Communication. <i>Current Protein and Peptide Science</i> , 2009, 10, 116-127.	1.4	64
3	<i>Burkholderia oklahomensis</i> agglutinin is a canonical two-domain OAA family lectin: structures, carbohydrate binding and anti-HIV activity. <i>FEBS Journal</i> , 2013, 280, 2056-2067.	4.7	33
4	Colocalization of Fast and Slow Timescale Dynamics in the Allosteric Signaling Protein CheY. <i>Journal of Molecular Biology</i> , 2013, 425, 2372-2381.	4.2	30
5	Integrating NMR, SAXS, and Atomistic Simulations: Structure and Dynamics of a Two-Domain Protein. <i>Biophysical Journal</i> , 2018, 114, 839-855.	0.5	20
6	Human \hat{I}^2 B2-Crystallin Forms a Face-en-Face Dimer in Solution: An Integrated NMR and SAXS Study. <i>Structure</i> , 2017, 25, 496-505.	3.3	19
7	Hydrophobic Core Mutations in Cl2 Globally Perturb Fast Side-Chain Dynamics Similarly without Regard to Position. <i>Biochemistry</i> , 2008, 47, 8566-8576.	2.5	18
8	A Combined NMR and SAXS Analysis of the Partially Folded Cataract-Associated V75D \hat{I}^3 D-Crystallin. <i>Biophysical Journal</i> , 2017, 112, 1135-1146.	0.5	15
9	Pyruvate dehydrogenase complex deficiency is linked to regulatory loop disorder in the \hat{I}^1 V138M variant of human pyruvate dehydrogenase. <i>Journal of Biological Chemistry</i> , 2018, 293, 13204-13213.	3.4	13
10	Structural Adaptation in Its Orphan Domain Engenders Betaglycan with an Alternate Mode of Growth Factor Binding Relative to Endoglin. <i>Structure</i> , 2019, 27, 1427-1442.e4.	3.3	12
11	Assessing the Structures and Interactions of \hat{I}^3 D-Crystallin Deamidation Variants. <i>Structure</i> , 2021, 29, 284-291.e3.	3.3	10
12	Nectar-feeding bats and birds show parallel molecular adaptations in sugar metabolism enzymes. <i>Current Biology</i> , 2021, 31, 4667-4674.e6.	3.9	7
13	Exploring the role of structure and dynamics in the function of chymotrypsin inhibitor 2. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 916-924.	2.6	6