Kristoffer EnÃ¸e Johansson

List of Publications by Year
in descending order

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22 papers	433 citations	759233 12 h-index	794594 19 g-index
32 all docs	32 docs citations	32 times ranked	676 citing authors

#	Article	IF	Citations
1	Understanding the Origins of Loss of Protein Function by Analyzing the Effects of Thousands of Variants on Activity and Abundance. Molecular Biology and Evolution, 2021, 38, 3235-3246.	8.9	65
2	Structural heterogeneity and dynamics in protein evolution and design. Current Opinion in Structural Biology, 2018, 48, 157-163.	5.7	42
3	Beyond rotamers: a generative, probabilistic model of side chains in proteins. BMC Bioinformatics, 2010, 11, 306.	2.6	40
4	PHAISTOS: A framework for Markov chain Monte Carlo simulation and inference of protein structure. Journal of Computational Chemistry, 2013, 34, 1697-1705.	3.3	35
5	A Soluble, Folded Protein without Charged Amino Acid Residues. Biochemistry, 2016, 55, 3949-3956.	2.5	34
6	Tracking Dehydration Mechanisms in Crystalline Hydrates with Molecular Dynamics Simulations. Crystal Growth and Design, 2017, 17, 5017-5022.	3.0	25
7	Subtle Monte Carlo Updates in Dense Molecular Systems. Journal of Chemical Theory and Computation, 2012, 8, 695-702.	5.3	22
8	Computational Redesign of Thioredoxin Is Hypersensitive toward Minor Conformational Changes in the Backbone Template. Journal of Molecular Biology, 2016, 428, 4361-4377.	4.2	21
9	Global analysis of protein stability by temperature and chemical denaturation. Analytical Biochemistry, 2020, 605, 113863.	2.4	20
10	Distinguishing tautomerism in the crystal structure of (Z)-N-(5-ethyl-2,3-dihydro-1,3,4-thiadiazol-2-ylidene)-4-methylbenzenesulfonamide using DFT-D calculations and¹³C solid-state NMR. Acta Crystallographica Section C, Structural Chemistry, 2014, 70, 784-789.	0.5	17
11	Charge Interactions in a Highly Charge-Depleted Protein. Journal of the American Chemical Society, 2021, 143, 2500-2508.	13.7	15
12	Computational Dehydration of Crystalline Hydrates Using Molecular Dynamics Simulations. Journal of Pharmaceutical Sciences, 2017, 106, 348-355.	3.3	14
13	Local structure in the disordered solid solution ofcis- andtrans-perinones. Acta Crystallographica Section B: Structural Science, Crystal Engineering and Materials, 2016, 72, 416-433.	1.1	12
14	Revision of the Crystal Structure of the First Molecular Polymorph in History. Crystal Growth and Design, 2016, 16, 1366-1370.	3.0	12
15	A simple probabilistic model of multibody interactions in proteins. Proteins: Structure, Function and Bioinformatics, 2013, 81, 1340-1350.	2.6	8
16	Characterization of the Hydrodynamics in a Miniaturized Dissolution Apparatus. Journal of Pharmaceutical Sciences, 2018, 107, 1095-1103.	3.3	7
17	On the stacking disorder of DL-norleucine. Acta Crystallographica Section B: Structural Science, Crystal Engineering and Materials, 2017, 73, 1075-1084.	1.1	6
18	Improving folding properties of computationally designed proteins. Protein Engineering, Design and Selection, 2019, 32, 145-151.	2.1	5

#	Article	IF	Citations
19	Computational and Experimental Assessment of Backbone Templates for Computational Redesign of the Thioredoxin Fold. Journal of Physical Chemistry B, 2021, 125, 11141-11149.	2.6	5
20	Correction to Revision of the Crystal Structure of the First Molecular Polymorph in History. Crystal Growth and Design, 2016, 16, 3553-3553.	3.0	1
21	Substitutional landscape of a split fluorescent protein fragment using high-density peptide microarrays. PLoS ONE, 2021, 16, e0241461.	2.5	1
22	Hacking an enzyme. Nature Chemical Biology, 2018, 14, 202-204.	8.0	0