Lars SkjÃ¦rven

List of Publications by Year
in descending order

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25	1,404	566801 15	610482 24
papers	citations	h-index	g-index

26	26	26	2169
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	The <scp>Bio3D</scp> packages for structural bioinformatics. Protein Science, 2021, 30, 20-30.	3.1	200
2	A Pharmacological Chaperone Therapy for Acute Intermittent Porphyria. Molecular Therapy, 2020, 28, 677-689.	3.7	10
3	Structure of full-length human phenylalanine hydroxylase in complex with tetrahydrobiopterin. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 11229-11234.	3.3	44
4	Investigating Protein Sequence-structure-dynamics Relationships with Bio3D-web. Journal of Visualized Experiments, 2017, , .	0.2	2
5	The Bio3D Project: Interactive Tools for Structural Bioinformatics. Biophysical Journal, 2016, 110, 379a.	0.2	3
6	Rapid Characterization of Allosteric Networks with Ensemble Normal Mode Analysis. Journal of Physical Chemistry B, 2016, 120, 8276-8288.	1.2	37
7	Online interactive analysis of protein structure ensembles with Bio3D-web. Bioinformatics, 2016, 32, 3510-3512.	1.8	37
8	Dynamic Coupling and Allosteric Networks in the Î± Subunit of Heterotrimeric G Proteins. Journal of Biological Chemistry, 2016, 291, 4742-4753.	1.6	66
9	Dynamic Coupling and Allosteric Networks in the Alpha Subunit of Heterotrimeric G Proteins. Biophysical Journal, 2016, 110, 427a.	0.2	1
10	Characterizing Nucleotide Dependent Allostery in G-Proteins with Molecular Dynamics and Normal Mode Analysis. Biophysical Journal, 2015, 108, 59a.	0.2	0
11	Identification of new hit scaffolds by INPHARMA-guided virtual screening. MedChemComm, 2015, 6, 1501-1507.	3.5	1
12	Dynamics, flexibility, and allostery in molecular chaperonins. FEBS Letters, 2015, 589, 2522-2532.	1.3	83
13	Discovery of a Specific Inhibitor of Pyomelanin Synthesis in Legionella pneumophila. Journal of Medicinal Chemistry, 2015, 58, 8402-8412.	2.9	15
14	Integrating protein structural dynamics and evolutionary analysis with Bio3D. BMC Bioinformatics, 2014, 15, 399.	1.2	292
15	WEBnm@ v2.0: Web server and services for comparing protein flexibility. BMC Bioinformatics, 2014, 15, 427.	1.2	95
16	The structure of the box C/D enzyme reveals regulation of RNA methylation. Nature, 2013, 502, 519-523.	13.7	154
17	Accounting for Conformational Variability in Proteinâ€“Ligand Docking with NMR-Guided Rescoring. Journal of the American Chemical Society, 2013, 135, 5819-5827.	6.6	22
18	A dynamic model of longâ€range conformational adaptations triggered by nucleotide binding in GroELâ€“GroES. Proteins: Structure, Function and Bioinformatics, 2012, 80, 2333-2346.	1.5	6

#	ARTICLE	IF	CITATIONS
19	The Peripheral Binding of 14-3-3Î³ to Membranes Involves Isoform-Specific Histidine Residues. PLoS ONE, 2012, 7, e49671.	1.1	15
20	Dynamics, flexibility and ligand-induced conformational changes in biological macromolecules: a computational approach. Future Medicinal Chemistry, 2011, 3, 2079-2100.	1.1	37
21	Principal component and normal mode analysis of proteins; a quantitative comparison using the GroEL subunit. Proteins: Structure, Function and Bioinformatics, 2011, 79, 232-243.	1.5	107
22	Deconstructing honeybee vitellogenin: novel 40 kDa fragment assigned to its N terminus. Journal of Experimental Biology, 2011, 214, 582-592.	0.8	37
23	Conformational Sampling and Nucleotide-Dependent Transitions of the GroEL Subunit Probed by Unbiased Molecular Dynamics Simulations. PLoS Computational Biology, 2011, 7, e1002004.	1.5	27
24	Normal mode analysis for proteins. Computational and Theoretical Chemistry, 2009, 898, 42-48.	1.5	111
25	TMM@: a web application for the analysis of transmembrane helix mobility. BMC Bioinformatics, 2007, 8, 232.	1.2	2