Lars SkjÃ¦rven

List of Publications by Year
in descending order

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25 papers	1,404 citations	567281 15 h-index	610901 24 g-index
26 all docs	26 docs citations	26 times ranked	2169 citing authors

#	Article	IF	Citations
1	Integrating protein structural dynamics and evolutionary analysis with Bio3D. BMC Bioinformatics, 2014, 15, 399.	2.6	292
2	The <scp>Bio3D</scp> packages for structural bioinformatics. Protein Science, 2021, 30, 20-30.	7.6	200
3	The structure of the box C/D enzyme reveals regulation of RNA methylation. Nature, 2013, 502, 519-523.	27.8	154
4	Normal mode analysis for proteins. Computational and Theoretical Chemistry, 2009, 898, 42-48.	1.5	111
5	Principal component and normal mode analysis of proteins; a quantitative comparison using the GroEL subunit. Proteins: Structure, Function and Bioinformatics, 2011, 79, 232-243.	2.6	107
6	WEBnm@ v2.0: Web server and services for comparing protein flexibility. BMC Bioinformatics, 2014, 15, 427.	2.6	95
7	Dynamics, flexibility, and allostery in molecular chaperonins. FEBS Letters, 2015, 589, 2522-2532.	2.8	83
8	Dynamic Coupling and Allosteric Networks in the Î± Subunit of Heterotrimeric G Proteins. Journal of Biological Chemistry, 2016, 291, 4742-4753.	3.4	66
9	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.	7.1	44
10	Dynamics, flexibility and ligand-induced conformational changes in biological macromolecules: a computational approach. Future Medicinal Chemistry, 2011, 3, 2079-2100.	2.3	37
11	Deconstructing honeybee vitellogenin: novel 40 kDa fragment assigned to its N terminus. Journal of Experimental Biology, 2011, 214, 582-592.	1.7	37
12	Rapid Characterization of Allosteric Networks with Ensemble Normal Mode Analysis. Journal of Physical Chemistry B, 2016, 120, 8276-8288.	2.6	37
13	Online interactive analysis of protein structure ensembles with Bio3D-web. Bioinformatics, 2016, 32, 3510-3512.	4.1	37
14	Conformational Sampling and Nucleotide-Dependent Transitions of the GroEL Subunit Probed by Unbiased Molecular Dynamics Simulations. PLoS Computational Biology, 2011, 7, e1002004.	3.2	27
15	Accounting for Conformational Variability in Proteinâ€“Ligand Docking with NMR-Guided Rescoring. Journal of the American Chemical Society, 2013, 135, 5819-5827.	13.7	22
16	Discovery of a Specific Inhibitor of Pyomelanin Synthesis in Legionella pneumophila. Journal of Medicinal Chemistry, 2015, 58, 8402-8412.	6.4	15
17	The Peripheral Binding of 14-3-3Î³ to Membranes Involves Isoform-Specific Histidine Residues. PLoS ONE, 2012, 7, e49671.	2.5	15
18	A Pharmacological Chaperone Therapy for Acute Intermittent Porphyria. Molecular Therapy, 2020, 28, 677-689.	8.2	10

#	Article	IF	Citations
19	A dynamic model of longâ€range conformational adaptations triggered by nucleotide binding in GroELâ€GroES. Proteins: Structure, Function and Bioinformatics, 2012, 80, 2333-2346.	2.6	6
20	The Bio3D Project: Interactive Tools for Structural Bioinformatics. Biophysical Journal, 2016, 110, 379a.	0.5	3
21	TMM@: a web application for the analysis of transmembrane helix mobility. BMC Bioinformatics, 2007, 8, 232.	2.6	2
22	Investigating Protein Sequence-structure-dynamics Relationships with Bio3D-web. Journal of Visualized Experiments, 2017, , .	0.3	2
23	Identification of new hit scaffolds by INPHARMA-guided virtual screening. MedChemComm, 2015, 6, 1501-1507.	3.4	1
24	Dynamic Coupling and Allosteric Networks in the Alpha Subunit of Heterotrimeric G Proteins. Biophysical Journal, 2016, 110, 427a.	0.5	1
25	Characterizing Nucleotide Dependent Allostery in G-Proteins with Molecular Dynamics and Normal Mode Analysis. Biophysical Journal, 2015, 108, 59a.	0.5	0