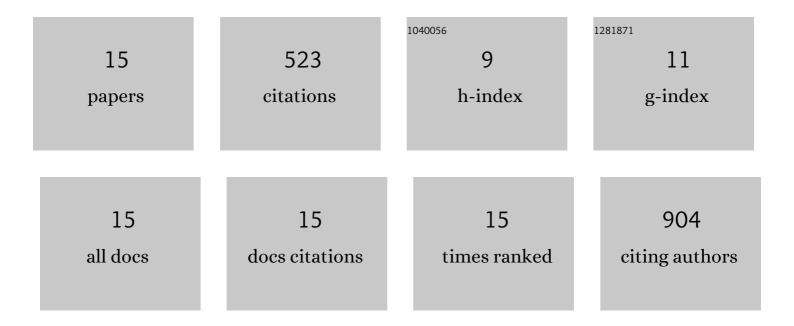
Edvin Fuglebakk

List of Publications by Year in descending order

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EDVIN FLICIERAKK

#	Article	IF	CITATIONS
1	Measuring and comparing structural fluctuation patterns in large protein datasets. Bioinformatics, 2012, 28, 2431-2440.	4.1	111
2	WEBnm@ v2.0: Web server and services for comparing protein flexibility. BMC Bioinformatics, 2014, 15, 427.	2.6	95
3	Comparing the intrinsic dynamics of multiple protein structures using elastic network models. Biochimica Et Biophysica Acta - General Subjects, 2015, 1850, 911-922.	2.4	68
4	Evaluation of Protein Elastic Network Models Based on an Analysis of Collective Motions. Journal of Chemical Theory and Computation, 2013, 9, 5618-5628.	5.3	65
5	The Interaction of Peripheral Proteins and Membranes Studied with α-Lactalbumin and Phospholipid Bilayers of Various Compositions. Journal of Biological Chemistry, 2003, 278, 21790-21797.	3.4	59
6	A Role for Weak Electrostatic Interactions in Peripheral Membrane Protein Binding. Biophysical Journal, 2016, 110, 1367-1378.	0.5	47
7	A model for hydrophobic protrusions on peripheral membrane proteins. PLoS Computational Biology, 2018, 14, e1006325.	3.2	26
8	Exploring the factors determining the dynamics of different protein folds. Protein Science, 2011, 20, 197-209.	7.6	25
9	StoX: An open source software for marine survey analyses. Methods in Ecology and Evolution, 2019, 10, 1523-1528.	5.2	12
10	Interactions stabilizing the C-terminal helix of human phospholipid scramblase 1 in lipid bilayers: A computational study. Biochimica Et Biophysica Acta - Biomembranes, 2017, 1859, 1200-1210.	2.6	8
11	A simulation approach to assessing bias in a fisheries self-sampling programme. ICES Journal of Marine Science, 2022, 79, 76-87.	2.5	7
12	Identification of minor metabolites of phospholipid signal molecules in [32 P]P i -labelled platelets. Platelets, 2002, 13, 279-284.	2.3	0
13	Comparing Normal Modes of Protein Structures using Webnm@ 2.0. Biophysical Journal, 2013, 104, 228a.	0.5	0
14	Benchmarking Collective Motion Predictions of Elastic Network Models. Biophysical Journal, 2014, 106, 462a.	0.5	0
15	Investigating the Interaction of the Putative Transmembrane Domain of Human Phospholipid Scramblase with Lipid Bilayers using Molecular Dynamics Simulations. Biophysical Journal, 2016, 110, 80a.	0.5	0