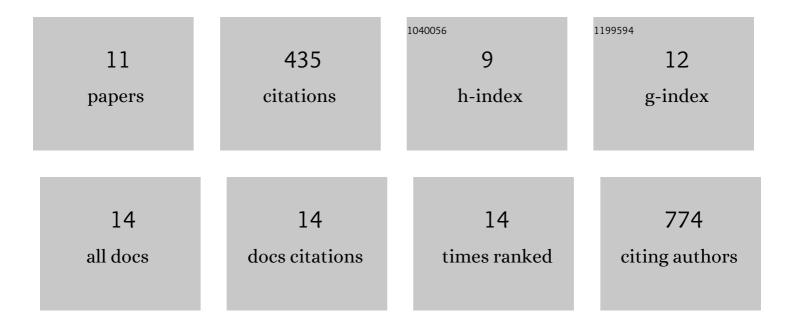
Vincent Frappier

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/4445550/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	ENCoM server: exploring protein conformational space and the effect of mutations on protein function and stability. Nucleic Acids Research, 2015, 43, W395-W400.	14.5	151
2	A Coarse-Grained Elastic Network Atom Contact Model and Its Use in the Simulation of Protein Dynamics and the Prediction of the Effect of Mutations. PLoS Computational Biology, 2014, 10, e1003569.	3.2	88
3	StAR-related lipid transfer domain protein 5 binds primary bile acids. Journal of Lipid Research, 2012, 53, 2677-2689.	4.2	33
4	PixelDB: Protein–peptide complexes annotated with structural conservation of the peptide binding mode. Protein Science, 2018, 27, 276-285.	7.6	31
5	Tertiary Structural Motif Sequence Statistics Enable Facile Prediction and Design of Peptides that Bind Anti-apoptotic Bfl-1 and Mcl-1. Structure, 2019, 27, 606-617.e5.	3.3	29
6	Data-driven computational protein design. Current Opinion in Structural Biology, 2021, 69, 63-69.	5.7	28
7	Vibrational entropy differences between mesophile and thermophile proteins and their use in protein engineering. Protein Science, 2015, 24, 474-483.	7.6	21
8	The Mode of Action of Recombinant Mycobacterium tuberculosis Shikimate Kinase: Kinetics and Thermodynamics Analyses. PLoS ONE, 2013, 8, e61918.	2.5	15
9	New structural determinants for câ€Myc specific heterodimerization with Max and development of a novel homodimeric câ€Myc bâ€HLH‣Z,. Journal of Molecular Recognition, 2012, 25, 414-426.	2.1	12
10	Mutations that Allow SIR2 Orthologs to Function in a NAD + -Depleted Environment. Cell Reports, 2017, 18, 2310-2319.	6.4	9
11	Applications of Normal Mode Analysis Methods in Computational Protein Design. Methods in Molecular Biology, 2017, 1529, 203-214.	0.9	8