

Vincent Frappier

List of Publications by Year in descending order

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Version: 2024-02-01

11
papers

435
citations

1040056

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h-index

1199594

12
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14
all docs

14
docs citations

14
times ranked

774
citing authors

#	ARTICLE	IF	CITATIONS
1	ENCoM server: exploring protein conformational space and the effect of mutations on protein function and stability. <i>Nucleic Acids Research</i> , 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. <i>PLoS Computational Biology</i> , 2014, 10, e1003569.	3.2	88
3	StAR-related lipid transfer domain protein 5 binds primary bile acids. <i>Journal of Lipid Research</i> , 2012, 53, 2677-2689.	4.2	33
4	PixelDB: Protein-peptide complexes annotated with structural conservation of the peptide binding mode. <i>Protein Science</i> , 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. <i>Structure</i> , 2019, 27, 606-617.e5.	3.3	29
6	Data-driven computational protein design. <i>Current Opinion in Structural Biology</i> , 2021, 69, 63-69.	5.7	28
7	Vibrational entropy differences between mesophile and thermophile proteins and their use in protein engineering. <i>Protein Science</i> , 2015, 24, 474-483.	7.6	21
8	The Mode of Action of Recombinant <i>Mycobacterium tuberculosis</i> Shikimate Kinase: Kinetics and Thermodynamics Analyses. <i>PLoS ONE</i> , 2013, 8, e61918.	2.5	15
9	New structural determinants for c-Myc specific heterodimerization with Max and development of a novel homodimeric c-Myc bHLH. <i>Journal of Molecular Recognition</i> , 2012, 25, 414-426.	2.1	12
10	Mutations that Allow SIR2 Orthologs to Function in a NAD ⁺ -Depleted Environment. <i>Cell Reports</i> , 2017, 18, 2310-2319.	6.4	9
11	Applications of Normal Mode Analysis Methods in Computational Protein Design. <i>Methods in Molecular Biology</i> , 2017, 1529, 203-214.	0.9	8