Nicolas Panel

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/1812173/publications.pdf

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16	304	933447	996975
papers	citations	10 h-index	15 g-index

17	17	17	365
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Positive allosteric mechanisms of adenosine A1 receptor-mediated analgesia. Nature, 2021, 597, 571-576.	27.8	84
2	Ligand design by targeting a binding site water. Chemical Science, 2021, 12, 960-968.	7.4	34
3	Accurate PDZ/Peptide Binding Specificity with Additive and Polarizable Free Energy Simulations. Biophysical Journal, 2018, 114, 1091-1102.	0.5	30
4	Hotspot Mutations in KIT Receptor Differentially Modulate Its Allosterically Coupled Conformational Dynamics: Impact on Activation and Drug Sensitivity. PLoS Computational Biology, 2014, 10, e1003749.	3.2	27
5	Adaptive landscape flattening in amino acid sequence space for the computational design of protein:peptide binding. Journal of Chemical Physics, 2018, 149, 072302.	3.0	22
6	Protein side chain conformation predictions with an <scp>MMGBSA</scp> energy function. Proteins: Structure, Function and Bioinformatics, 2016, 84, 803-819.	2.6	21
7	Physics-Based Computational Protein Design: An Update. Journal of Physical Chemistry A, 2020, 124, 10637-10648.	2.5	16
8	Computational Design of the Tiam1 PDZ Domain and Its Ligand Binding. Journal of Chemical Theory and Computation, 2017, 13, 2271-2289.	5.3	12
9	Structureâ€Guided Design of Gâ€Proteinâ€Coupled Receptor Polypharmacology. Angewandte Chemie - International Edition, 2021, 60, 18022-18030.	13.8	12
10	Differential Effects of CSF-1R D802V and KIT D816V Homologous Mutations on Receptor Tertiary Structure and Allosteric Communication. PLoS ONE, 2014, 9, e97519.	2.5	11
11	A Simple PB/LIE Free Energy Function Accurately Predicts the Peptide Binding Specificity of the Tiam1 PDZ Domain. Frontiers in Molecular Biosciences, 2017, 4, 65.	3.5	10
12	Insight on Mutation-Induced Resistance from Molecular Dynamics Simulations of the Native and Mutated CSF-1R and KIT. PLoS ONE, 2016, 11, e0160165.	2.5	8
13	A physics-based energy function allows the computational redesign of a PDZ domain. Scientific Reports, 2020, 10, 11150.	3.3	7
14	Characterization of S628N. JAMA Dermatology, 2014, 150, 1345.	4.1	6
15	Computational Design of PDZ-Peptide Binding. Methods in Molecular Biology, 2021, 2256, 237-255.	0.9	3
16	Structureâ€Guided Design of Gâ€Proteinâ€Coupled Receptor Polypharmacology. Angewandte Chemie, 2021, 133, 18170-18178.	2.0	0