Edrisse Chermak

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/10542881/publications.pdf

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11	489	840776 11	1281871 11
papers	citations	h-index	g-index

11	11	11	836
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Occurrence and stability of lone pairâ€“Ï€ stacking interactions between ribose and nucleobases in functional RNAs. Nucleic Acids Research, 2017, 45, 11019-11032.	14.5	53
2	The D173G mutation in ADAMTS-13 causes a severe form of congenital thrombotic thrombocytopenic purpura. Thrombosis and Haemostasis, 2016, 115, 51-62.	3.4	14
3	Introducing a Clustering Step in a Consensus Approach for the Scoring of Protein-Protein Docking Models. PLoS ONE, 2016, 11, e0166460.	2.5	20
4	Prediction of homoprotein and heteroprotein complexes by protein docking and templateâ€based modeling: A CASPâ€CAPRI experiment. Proteins: Structure, Function and Bioinformatics, 2016, 84, 323-348.	2.6	148
5	Troubles in the Systematic Prediction of Transition Metal Thermochemistry with Contemporary Out-of-the-Box Methods. Journal of Chemical Theory and Computation, 2016, 12, 1542-1560.	5.3	42
6	Theoretical Characterization of the H-Bonding and Stacking Potential of Two Nonstandard Nucleobases Expanding the Genetic Alphabet. Journal of Physical Chemistry B, 2016, 120, 2216-2224.	2.6	22
7	Analysis and Ranking of Protein-Protein Docking Models Using Inter-Residue Contacts and Inter-Molecular Contact Maps. Molecules, 2015, 20, 12045-12060.	3.8	21
8	CONSRANK: a server for the analysis, comparison and ranking of docking models based on inter-residue contacts. Bioinformatics, 2015, 31, 1481-1483.	4.1	40
9	Accuracy of DLPNOâ€“CCSD(T) Method for Noncovalent Bond Dissociation Enthalpies from Coinage Metal Cation Complexes. Journal of Chemical Theory and Computation, 2015, 11, 4664-4676.	5.3	85
10	Molecular Dynamics Characterization of Five Pathogenic Factor X Mutants Associated with Decreased Catalytic Activity. Biochemistry, 2014, 53, 6992-7001.	2.5	15
11	MDcons: Intermolecular contact maps as a tool to analyze the interface of protein complexes from molecular dynamics trajectories. BMC Bioinformatics, 2014, 15, S1.	2.6	29