Bogdan Lesyng

List of Publications by Year
in descending order

22	463	759233 12	794594 19
papers	citations	h-index	g-index

22	22	22	694
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Generalized Born Model:Â Analysis, Refinement, and Applications to Proteins. Journal of Physical Chemistry B, 2004, 108, 18368-18376.	2.6	115
2	Structural basis of oncogenic activation caused by point mutations in the kinase domain of the MET proto-oncogene: Modeling studies. Proteins: Structure, Function and Bioinformatics, 2001, 44, 32-43.	2.6	60
3	Class IV Charge Model for the Self-Consistent Charge Density-Functional Tight-Binding Method. Journal of Physical Chemistry A, 2004, 108, 2545-2549.	2.5	51
4	Structure-based sequence alignment for the Î²-trefoil subdomain of the clostridial neurotoxin family provides residue level information about the putative ganglioside binding site. FEBS Letters, 2000, 482, 119-124.	2.8	39
5	Surface markers of cancer stem-like cells of ovarian cancer and their clinical relevance. Wspolczesna Onkologia, 2018, 2018, 48-55.	1.4	30
6	A novel method to compare protein structures using local descriptors. BMC Bioinformatics, 2011, 12, 344.	2.6	25
7	Synthesis, structural and antimicrobial studies of type II topoisomerase-targeted copper(II) complexes of 1,3-disubstituted thiourea ligands. Journal of Inorganic Biochemistry, 2018, 182, 61-70.	3.5	25
8	Structural characterisation of inhibitory and non-inhibitory MMP-9â€“TIMP-1 complexes and implications for regulatory mechanisms of MMP-9. Scientific Reports, 2021, 11, 13376.	3.3	18
9	Lagrangian molecular dynamics using selected conformational degrees of freedom, with application to the pseudorotation dynamics of furanose rings. Biopolymers, 1994, 34, 383-392.	2.4	16
10	Effect of water on the tautomeric equilibrium of 2-oxopyridine. A Monte Carlo simulation study. International Journal of Quantum Chemistry, 1981, 20, 359-364.	2.0	15
11	The Tautomerism of Cytosine and Hydroxycytosine. A Quantum-Mechanical Study. Zeitschrift Fur Naturforschung - Section C Journal of Biosciences, 1982, 37, 937-941.	1.4	15
12	A Mezoscopic Model of Nucleic Acids. Part 1. Lagrangian and Quaternion Molecular Dynamics. Journal of Biomolecular Structure and Dynamics, 2000, 17, 1097-1108.	3.5	15
13	A Mezoscopic Model of Nucleic Acids. Part 2. An Effective Potential Energy Function for DNA. Journal of Biomolecular Structure and Dynamics, 2000, 17, 1109-1115.	3.5	11
14	ResiCon: a method for the identification of dynamic domains, hinges and interfacial regions in proteins. Bioinformatics, 2016, 32, 25-34.	4.1	10
15	Why isoguanine and isocytosine are not the components of the genetic code. International Journal of Quantum Chemistry, 1985, 28, 209-216.	2.0	6
16	Exploring Covalent Docking Mechanisms of Boron-Based Inhibitors to Class A, C and D Î²-Lactamases Using Time-dependent Hybrid QM/MM Simulations. Frontiers in Molecular Biosciences, 2021, 8, 633181.	3.5	4
17	Conformational Correlations in DNA. Molecular Dynamics Studies. Molecular Simulation, 1997, 19, 247-266.	2.0	3
18	DFT calculations and parameterization of the approximate valence bond method to describe the phosphoryl transfer reaction in a model system. International Journal of Quantum Chemistry, 2002, 90, 1129-1139.	2.0	3

#	Article	IF	Citations
19	DAMA: a method for computing multiple alignments of protein structures using local structure descriptors. Bioinformatics, 2021, , .	4.1	2
20	Parallelization of the quantum dynamics code for cluster architecture and its applications to the Gross-Pitaevskii equation. International Journal of Quantum Chemistry, 2006, 106, 664-669.	2.0	0
21	Toward the identification of molecular cogs. Journal of Computational Chemistry, 2016, 37, 848-860.	3.3	0
22	A novel formulation of an approximate valence bond model (AVB2) and its application to the tautomeric forms of porphyrin and porphycene. Journal of Molecular Modeling, 2019, 25, 155.	1.8	0