Indira Ghosh

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/1635273/publications.pdf

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28	484	840776 11	677142 22
papers	citations	h-index	g-index

30	30	30	593
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Hydration of chloride and bromide anions: determination of relative free energy by computer simulation. Journal of the American Chemical Society, 1985, 107, 7793-7794.	13.7	135
2	Analysis ofE.colipromoter structures using neural networks. Nucleic Acids Research, 1994, 22, 2158-2165.	14.5	51
3	Fractal symmetry of protein interior: what have we learned?. Cellular and Molecular Life Sciences, 2011, 68, 2711-2737.	5.4	33
4	Analysis of physico-chemical properties of substrates of ABC and MFS multidrug transporters of pathogenic Candida albicans. European Journal of Medicinal Chemistry, 2010, 45, 4813-4826.	5.5	31
5	Revisiting the Myths of Protein Interior: Studying Proteins with Mass-Fractal Hydrophobicity-Fractal and Polarizability-Fractal Dimensions. PLoS ONE, 2009, 4, e7361.	2.5	25
6	Developing an Antituberculosis Compounds Database and Data Mining in the Search of a Motif Responsible for the Activity of a Diverse Class of Antituberculosis Agents. Journal of Chemical Information and Modeling, 2006, 46, 17-23.	5.4	23
7	Modeling and Experimental Analyses Reveals Signaling Plasticity in a Bi-Modular Assembly of CD40 Receptor Activated Kinases. PLoS ONE, 2012, 7, e39898.	2.5	17
8	Modularity in protein structures: study on all-alpha proteins. Journal of Biomolecular Structure and Dynamics, 2015, 33, 2667-2681.	3.5	16
9	Characterization of Leishmania donovani Aquaporins Shows Presence of Subcellular Aquaporins Similar to Tonoplast Intrinsic Proteins of Plants. PLoS ONE, 2011, 6, e24820.	2.5	16
10	Determination of Phosphorylation Sites for NADP-specific Isocitrate Dehydrogenase fromMycobacterium tuberculosis. Journal of Biomolecular Structure and Dynamics, 2009, 26, 741-754.	3.5	15
11	Methylerythritol phosphate pathway to isoprenoids: Kinetic modeling and in silico enzyme inhibitions in Plasmodium falciparum. FEBS Letters, 2013, 587, 2806-2817.	2.8	15
12	Biochemical characterization of Plasmodium falciparum hypoxanthine-guanine-xanthine phosphorybosyltransferase: role of histidine residue in substrate selectivity. Molecular and Biochemical Parasitology, 2004, 137, 267-276.	1.1	11
13	A new computational model to study mass inhomogeneity and hydrophobicity inhomogeneity in proteins. European Biophysics Journal, 2009, 38, 577-587.	2.2	11
14	Structure and Dynamics of Double Helical DNA in Torsion Angle Hyperspace: A Molecular Mechanics Approach. Journal of Biomolecular Structure and Dynamics, 2010, 27, 695-712.	3.5	11
15	ILP-assisted de novo drug design. Machine Learning, 2016, 103, 309-341.	5.4	11
16	Molecular dynamics study of the binding of phenylalanine stereoisomers to thermolysin. Biophysical Chemistry, 1994, 50, 237-248.	2.8	8
17	Concepts on the protein folding problem. Journal of Biomolecular Structure and Dynamics, 2013, 31, 1020-1023.	3.5	8
18	A conformational approach to the study of the dynamics of enzyme inhibition: studies on thermolysin. International Journal of Biological Macromolecules, 1982, 4, 130-136.	7.5	7

#	Article	IF	Citations
19	Mapping Selectivity and Specificity of Active Site of Plasmepsins from Plasmodium falciparum Using Molecular Interaction Field Approach. Protein and Peptide Letters, 2007, 14, 569-574.	0.9	7
20	Hysteresis and Statistical Errors in Free Energy Perturbation L to D Amino Acid Conversion. Molecular Simulation, 1993, 10, 241-253.	2.0	6
21	Mathematical criteria to observe mesoscopic emergence of protein biochemical properties. Journal of Mathematical Chemistry, 2011, 49, 643-665.	1.5	5
22	In silico identification and characterization of stress and virulence associated repeats in Salmonella. Genomics, 2018, 110, 23-34.	2.9	5
23	Coupling Supervised Molecular Dynamics (SuMD) with Entropy Estimations To Shine Light on the Stability of Multiple Binding Sites. ACS Medicinal Chemistry Letters, 2019, 10, 444-449.	2.8	5
24	Simple sequence repeats in different genome sequences of Shigella and comparison with high GC and AT-rich genomes. DNA Sequence, 2008, 19, 167-176.	0.7	3
25	Effect of Configuration of the Inhibitors on the Mode of Binding to the Enzyme, Thermolysin. Journal of Biomolecular Structure and Dynamics, 1984, 2, 29-40.	3.5	2
26	Proteins will Fold Anyway!!. Journal of Biomolecular Structure and Dynamics, 2011, 28, 627-628.	3.5	2
27	Application and Comprehensive Analysis of Neighbor Approximated Information Theoretic Configurational Entropy Methods to Proteinâ€“Ligand Binding Cases. Journal of Chemical Theory and Computation, 2020, 16, 7581-7600.	5.3	2
28	PfalDB: An Integrated Drug Target and Chemical Database for Plasmodium flaciparum. Current Drug Targets, 2014, 15, 1089-1093.	2.1	1