# Indira Ghosh

List of Publications by Year
in descending order

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

Version: 2024-02-01

| 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 | 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 |
| 2 | 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 |
| 3 | In silico identification and characterization of stress and virulence associated repeats in Salmonella. Genomics, 2018, 110, 23-34. | 2.9 | 5 |
| 4 | ILP-assisted de novo drug design. Machine Learning, 2016, 103, 309-341. | 5.4 | 11 |
| 5 | Modularity in protein structures: study on all-alpha proteins. Journal of Biomolecular Structure and Dynamics, 2015, 33, 2667-2681. | 3.5 | 16 |
| 6 | PfalDB: An Integrated Drug Target and Chemical Database for Plasmodium flaciparum. Current Drug Targets, 2014, 15, 1089-1093. | 2.1 | 1 |
| 7 | Methylerythritol phosphate pathway to isoprenoids: Kinetic modeling and in silico enzyme inhibitions in Plasmodium falciparum. FEBS Letters, 2013, 587, 2806-2817. | 2.8 | 15 |
| 8 | Concepts on the protein folding problem. Journal of Biomolecular Structure and Dynamics, 2013, 31, 1020-1023. | 3.5 | 8 |
| 9 | 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 |
| 10 | Proteins will Fold Anyway!!. Journal of Biomolecular Structure and Dynamics, 2011, 28, 627-628. | 3.5 | 2 |
| 11 | Mathematical criteria to observe mesoscopic emergence of protein biochemical properties. Journal of Mathematical Chemistry, 2011, 49, 643-665. | 1.5 | 5 |
| 12 | Fractal symmetry of protein interior: what have we learned?. Cellular and Molecular Life Sciences, 2011, 68, 2711-2737. | 5.4 | 33 |
| 13 | 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 |
| 14 | 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 |
| 15 | 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 |
| 16 | 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 |
| 17 | A new computational model to study mass inhomogeneity and hydrophobicity inhomogeneity in proteins. European Biophysics Journal, 2009, 38, 577-587. | 2.2 | 11 |
| 18 | Determination of Phosphorylation Sites for NADP-specific Isocitrate Dehydrogenase fromMycobacterium tuberculosis. Journal of Biomolecular Structure and Dynamics, 2009, 26, 741-754. | 3.5 | 15 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | 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 |
| 20 | 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 |
| 21 | 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 |
| 22 | 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 |
| 23 | Analysis ofE.colipromoter structures using neural networks. Nucleic Acids Research, 1994, 22, 2158-2165. | 14.5 | 51 |
| 24 | Molecular dynamics study of the binding of phenylalanine stereoisomers to thermolysin. Biophysical Chemistry, 1994, 50, 237-248. | 2.8 | 8 |
| 25 | Hysteresis and Statistical Errors in Free Energy Perturbation L to D Amino Acid Conversion. Molecular Simulation, 1993, 10, 241-253. | 2.0 | 6 |
| 26 | 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 |
| 27 | 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 |
| 28 | 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 |