Aurijit Sarkar

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/8969471/publications.pdf

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19	506	840776 11	839539 18
papers	citations	h-index	g-index

24	24	24	793
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Challenges in Drug Discovery for Intracellular Bacteria. Pathogens, 2021, 10, 1172.	2.8	7
2	Enabling design of screening libraries for antibiotic discovery by modeling ChEMBL data. European Journal of Pharmaceutical Sciences, 2020, 143, 105166.	4.0	2
3	Resisting resistance: gearing up for war. MedChemComm, 2019, 10, 1512-1516.	3.4	5
4	Estimating glycosaminoglycanâ€“protein interaction affinity: water dominates the specific antithrombinâ€“heparin interaction. Glycobiology, 2016, 26, 1041-1047.	2.5	19
5	Understanding Water and Its Many Roles in Biological Structure: Ways to Exploit a Resource for Drug Discovery. Methods in Pharmacology and Toxicology, 2015, , 85-110.	0.2	0
6	Chemoenzymatically Prepared Heparan Sulfate Containing Rare 2-O-Sulfonated Glucuronic Acid Residues. ACS Chemical Biology, 2015, 10, 1485-1494.	3.4	16
7	Designing â€œHigh-Affinity, High-Specificityâ€•Glycosaminoglycan Sequences Through Computerized Modeling. Methods in Molecular Biology, 2015, 1229, 289-314.	0.9	16
8	To Hit or Not to Hit, That Is the Question â€“ Genome-wide Structure-Based Druggability Predictions for Pseudomonas aeruginosa Proteins. PLoS ONE, 2015, 10, e0137279.	2.5	9
9	A Simple Method for Discovering Druggable, Specific Glycosaminoglycan-Protein Systems. Elucidation of Key Principles from Heparin/Heparan Sulfate-Binding Proteins. PLoS ONE, 2015, 10, e0141127.	2.5	40
10	Allosteric Inhibition of Human Factor XIa: Discovery of Monosulfated Benzofurans as a Class of Promising Inhibitors. Journal of Medicinal Chemistry, 2014, 57, 3559-3569.	6.4	24
11	Specificity of glycosaminoglycanâ€protein interactions: the role of desolvation (1007.5). FASEB Journal, 2014, 28, 1007.5.	0.5	0
12	Allosteric Competitive Inhibitors of the Glucose-1-phosphate Thymidylyltransferase (RmlA) from Pseudomonas aeruginosa. ACS Chemical Biology, 2013, 8, 387-396.	3.4	39
13	Designing Allosteric Regulators of Thrombin. Exosite 2 Features Multiple Subsites That Can Be Targeted by Sulfated Small Molecules for Inducing Inhibition. Journal of Medicinal Chemistry, 2013, 56, 5059-5070.	6.4	48
14	Computational analysis of structure-based interactions and ligand properties can predict efflux effects on antibiotics. European Journal of Medicinal Chemistry, 2012, 52, 98-110.	5.5	10
15	DrugPred: A Structure-Based Approach To Predict Protein Druggability Developed Using an Extensive Nonredundant Data Set. Journal of Chemical Information and Modeling, 2011, 51, 2829-2842.	5.4	82
16	Editorial [Hot topic: Applying Induced Fit in Drug Discovery: Square Pegs and Round Holes? (Guest) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 Medicinal Chemistry, 2011, 11, 131-132.	2.1	2
17	Premature Activation of the Paramyxovirus Fusion Protein before Target Cell Attachment with Corruption of the Viral Fusion Machinery. Journal of Biological Chemistry, 2011, 286, 37945-37954.	3.4	34
18	Hydrophobicity - Shake Flasks, Protein Folding and Drug Discovery. Current Topics in Medicinal Chemistry, 2010, 10, 67-83.	2.1	111

#	Article	IF	Citations
19	Structureâ€“activity relationship (SAR) studies of 3-(2-amino-ethyl)-5-(4-ethoxy-benzylidene)-thiazolidine-2,4-dione: Development of potential substrate-specific ERK1/2 inhibitors. Bioorganic and Medicinal Chemistry Letters, 2009, 19, 6042-6046.	2.2	39