

Bharath Srinivasan

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

30
papers

470
citations

13
h-index

21
g-index

44
ext. papers

597
ext. citations

5.2
avg, IF

4.52
L-index

#	Paper	IF	Citations
30	Coumarin-triazole hybrids: Design, microwave-assisted synthesis, crystal and molecular structure, theoretical and computational studies and screening for their anticancer potentials against PC-3 and DU-145. <i>Journal of Molecular Structure</i> , 2021 , 1230, 129899	3.4	4
29	Enrichment of Z ¹ Domains at cytoplasmic stress granules is due to their innate ability to bind to nucleic acids. <i>Journal of Cell Science</i> , 2021 , 134,	5.3	2
28	A guide to the Michaelis-Menten equation: steady state and beyond. <i>FEBS Journal</i> , 2021 ,	5.7	10
27	Explicit Treatment of Non-Michaelis-Menten and Atypical Kinetics in Early Drug Discovery*. <i>ChemMedChem</i> , 2021 , 16, 899-918	3.7	3
26	A Novel High-Throughput FLIPR Tetra-Based Method for Capturing Highly Confluent Kinetic Data for Structure-Kinetic Relationship Guided Early Drug Discovery. <i>SLAS Discovery</i> , 2021 , 26, 684-697	3.4	0
25	Design, synthesis, characterization, crystal structure, Hirshfeld surface analysis, DFT calculations, anticancer, angiogenic properties of new pyrazole carboxamide derivatives. <i>Journal of Molecular Structure</i> , 2021 , 1235, 130271	3.4	4
24	Structure and catalytic regulation of Plasmodium falciparum IMP specific nucleotidase. <i>Nature Communications</i> , 2020 , 11, 3228	17.4	0
23	Stable inheritance of CENP-A chromatin: Inner strength versus dynamic control. <i>Journal of Cell Biology</i> , 2020 , 219,	7.3	11
22	Resurrecting the phoenix: When an assay fails. <i>Medicinal Research Reviews</i> , 2020 , 40, 1776-1793	14.4	2
21	Chemical space of Escherichia coli dihydrofolate reductase inhibitors: New approaches for discovering novel drugs for old bugs. <i>Medicinal Research Reviews</i> , 2019 , 39, 684-705	14.4	16
20	Design and environmentally benign synthesis of novel thiophene appended pyrazole analogues as anti-inflammatory and radical scavenging agents: Crystallographic, in silico modeling, docking and SAR characterization. <i>Bioorganic Chemistry</i> , 2017 , 73, 109-120	5.1	29
19	Rational Design of Novel Allosteric Dihydrofolate Reductase Inhibitors Showing Antibacterial Effects on Drug-Resistant Escherichia coli Escape Variants. <i>ACS Chemical Biology</i> , 2017 , 12, 1848-1857	4.9	12
18	Design, synthesis of novel furan appended benzothiazepine derivatives and in vitro biological evaluation as potent VRV-PL-8a and H/K ATPase inhibitors. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2017 , 27, 3048-3054	2.9	13
17	Pocket detection and interaction-weighted ligand-similarity search yields novel high-affinity binders for Myocilin-OLF, a protein implicated in glaucoma. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2017 , 27, 4133-4139	2.9	2
16	Synthesis of novel 2-pyrazoline analogues with potent anti-inflammatory effect mediated by inhibition of phospholipase A2: Crystallographic, in silico docking and QSAR analysis. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2017 , 27, 3806-3811	2.9	23
15	On the importance of composite protein multiple ligand interactions in protein pockets. <i>Journal of Computational Chemistry</i> , 2017 , 38, 1252-1259	3.5	10
14	Catalytic and substrate promiscuity: distinct multiple chemistries catalysed by the phosphatase domain of receptor protein tyrosine phosphatase. <i>Biochemical Journal</i> , 2016 , 473, 2165-77	3.8	5

13	Synthesis of lignan conjugates via cyclopropanation: Antimicrobial and antioxidant studies. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2016 , 26, 3621-5	2.9	17
12	Synthesis of novel coumarin appended bis(formylpyrazole) derivatives: Studies on their antimicrobial and antioxidant activities. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2016 , 26, 690-694	2.9	84
11	Novel small molecule binders of human N-glycanase 1, a key player in the endoplasmic reticulum associated degradation pathway. <i>Bioorganic and Medicinal Chemistry</i> , 2016 , 24, 4750-4758	3.4	2
10	Repurposing FDA-approved drugs for anti-aging therapies. <i>Biogerontology</i> , 2016 , 17, 907-920	4.5	22
9	Implications of the small number of distinct ligand binding pockets in proteins for drug discovery, evolution and biochemical function. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2015 , 25, 1163-70	2.9	24
8	PoLi: A Virtual Screening Pipeline Based on Template Pocket and Ligand Similarity. <i>Journal of Chemical Information and Modeling</i> , 2015 , 55, 1757-70	6.1	30
7	Ligand binding studies, preliminary structure-activity relationship and detailed mechanistic characterization of 1-phenyl-6,6-dimethyl-1,3,5-triazine-2,4-diamine derivatives as inhibitors of Escherichia coli dihydrofolate reductase. <i>European Journal of Medicinal Chemistry</i> , 2015 , 103, 600-14	6.8	22
6	Insights into the slow-onset tight-binding inhibition of Escherichia coli dihydrofolate reductase: detailed mechanistic characterization of pyrrolo [3,2-f] quinazoline-1,3-diamine and its derivatives as novel tight-binding inhibitors. <i>FEBS Journal</i> , 2015 , 282, 1922-38	5.7	25
5	Prediction of substrate specificity and preliminary kinetic characterization of the hypothetical protein PVX_123945 from Plasmodium vivax. <i>Experimental Parasitology</i> , 2015 , 151-152, 56-63	2.1	6
4	Allosteric regulation and substrate activation in cytosolic nucleotidase II from Legionella pneumophila. <i>FEBS Journal</i> , 2014 , 281, 1613-1628	5.7	16
3	Experimental validation of FINDSITE(comb) virtual ligand screening results for eight proteins yields novel nanomolar and micromolar binders. <i>Journal of Cheminformatics</i> , 2014 , 6, 16	8.6	22
2	Elucidation of the substrate specificity, kinetic and catalytic mechanism of adenylosuccinate lyase from Plasmodium falciparum. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2009 , 1794, 642-54 [†]		34
1	ISN1 nucleotidases and HAD superfamily protein fold: in silico sequence and structure analysis. <i>In Silico Biology</i> , 2007 , 7, 187-93	2	8