Armin Madadkar-Sobhani

List of Publications by Citations

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31 613 15 24 g-index

32 650 3.2 3.29 ext. papers ext. citations avg, IF L-index

#	Paper	IF	Citations
31	An in vitro evaluation of human DNA topoisomerase I inhibition by Peganum harmala L. seeds extract and its beta-carboline alkaloids. <i>Journal of Pharmacy and Pharmaceutical Sciences</i> , 2002 , 5, 19-2.	3 ^{3,4}	79
30	Molecular interaction of human serum albumin with paracetamol: spectroscopic and molecular modeling studies. <i>International Journal of Biological Macromolecules</i> , 2009 , 45, 129-34	7.9	69
29	Design, synthesis and biological evaluation of novel anti-cytokine 1,2,4-triazine derivatives. <i>Bioorganic and Medicinal Chemistry</i> , 2013 , 21, 6708-17	3.4	56
28	Homology modeling of human CCR5 and analysis of its binding properties through molecular docking and molecular dynamics simulation. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2011 , 1808, 802-17	3.8	51
27	Phenylimino-2H-chromen-3-carboxamide derivatives as novel small molecule inhibitors of Elecretase (BACE1). <i>Bioorganic and Medicinal Chemistry</i> , 2013 , 21, 2396-2412	3.4	45
26	Application of an expert system based on Genetic Algorithm Adaptive Neuro-Fuzzy Inference System (GAANFIS) in QSAR of cathepsin K inhibitors. <i>Expert Systems With Applications</i> , 2012 , 39, 6182-6	1 3 .8	34
25	Application of partial least squares and radial basis function neural networks in multivariate imaging analysis-quantitative structure activity relationship: study of cyclin dependent kinase 4 inhibitors. <i>Journal of Molecular Graphics and Modelling</i> , 2010 , 29, 518-28	2.8	24
24	QSAR analysis for some diaryl-substituted pyrazoles as CCR2 inhibitors by GA-stepwise MLR. <i>Chemical Biology and Drug Design</i> , 2011 , 77, 75-85	2.9	22
23	Exploring a model of a chemokine receptor/ligand complex in an explicit membrane environment by molecular dynamics simulation: the human CCR1 receptor. <i>Journal of Chemical Information and Modeling</i> , 2011 , 51, 2717-30	6.1	21
22	Design, modeling, expression, and chemoselective PEGylation of a new nanosize cysteine analog of erythropoietin. <i>International Journal of Nanomedicine</i> , 2011 , 6, 1217-27	7.3	20
21	A theory of mode of action of azolylalkylquinolines as DNA binding agents using automated flexible ligand docking. <i>Journal of Molecular Graphics and Modelling</i> , 2006 , 25, 459-69	2.8	18
20	Nicotine inhibition of lycopene cyclase enhances accumulation of carotenoid intermediates by Dunaliella salina CCAP 19/18. <i>European Journal of Phycology</i> , 2009 , 44, 215-220	2.2	17
19	QSAR study of some CCR5 antagonists as anti-HIV agents using radial basis function neural network and general regression neural network on the basis of principal components. <i>Medicinal Chemistry Research</i> , 2012 , 21, 3246-3262	2.2	16
18	QSAR and docking analysis of A2B adenosine receptor antagonists based on non-xanthine scaffold. <i>Medicinal Chemistry Research</i> , 2015 , 24, 394-407	2.2	15
17	Characterization of adenosine receptor in its native environment: insights from molecular dynamics simulations of palmitoylated/glycosylated, membrane-integrated human A(2B) adenosine receptor. Journal of Molecular Modeling, 2012 , 18, 4309-24	2	15
16	Anti-tumor Activity of New Quinoline Derivatives in Human Breast Cancer T47D Cells. <i>International Journal of Cancer Research</i> , 2006 , 2, 102-108	0.2	15
15	Computational evaluation of some indenopyrazole derivatives as anticancer compounds; application of QSAR and docking methodologies. <i>Journal of Enzyme Inhibition and Medicinal Chemistry</i> , 2013 , 28, 16-32	5.6	14

LIST OF PUBLICATIONS

14	Insights into the human A1 adenosine receptor from molecular dynamics simulation: structural study in the presence of lipid membrane. <i>Medicinal Chemistry Research</i> , 2015 , 24, 3645-3659	2.2	13
13	Design, modeling, and expression of erythropoietin cysteine analogs in Pichia pastoris: improvement of mean residence times and in vivo activities through cysteine-specific PEGylation. <i>European Journal of Pharmaceutics and Biopharmaceutics</i> , 2012 , 80, 499-507	5.7	12
12	Novel imidazolyl derivatives of 1,8-acridinedione as potential DNA-intercalating agents. <i>Journal of the Iranian Chemical Society</i> , 2011 , 8, 1098-1112	2	12
11	Comparative quantitative structurelictivity relationship study of some 1-aminocyclopentyl-3-carboxyamides as CCR2 inhibitors using stepwise MLR, FA-MLR, and GA-PLS. <i>Medicinal Chemistry Research</i> , 2012 , 21, 100-115	2.2	9
10	Linear and nonlinear QSAR modeling of 1,3,8-substituted-9-deazaxanthines as potential selective A2BAR antagonists. <i>Medicinal Chemistry Research</i> , 2013 , 22, 4549-4567	2.2	8
9	Rubredoxin reductase from Alcanivorax borkumensis: expression and characterization. <i>Biotechnology Progress</i> , 2011 , 27, 1383-9	2.8	6
8	Prediction of the Human EP1 Receptor Binding Site by Homology Modeling and Molecular Dynamics Simulation. <i>Scientia Pharmaceutica</i> , 2011 , 79, 793-816	4.3	6
7	Protein-x of hepatitis B virus in interaction with CCAAT/enhancer-binding protein ﴿C/EBP∄-an in silico analysis approach. <i>Theoretical Biology and Medical Modelling</i> , 2011 , 8, 41	2.3	4
6	Computational and nonglycosylated systems: a simpler approach for development of nanosized PEGylated proteins. <i>Drug Design, Development and Therapy</i> , 2016 , 10, 1193-200	4.4	4
5	Immunological evaluation of predicted linear B-cell epitopes of human CD20 antigen. <i>Biotechnology and Applied Biochemistry</i> , 2012 , 59, 186-92	2.8	3
4	Biochemical characterization of two recombinant ferredoxin reductases from Alcanivorax borkumensis SK2. <i>Biotechnology and Applied Biochemistry</i> , 2012 , 59, 457-64	2.8	2
3	Structural Insight into Anaphase Promoting Complex 3 Structure and Docking with a Natural Inhibitory Compound. <i>Advanced Biomedical Research</i> , 2017 , 6, 26	1.2	2
2	Growth inhibition of MDA-MB-231 cell line by peptides designed based on uPA. <i>Acta Medica Iranica</i> , 2015 , 53, 403-7		1
1	Variability of the Cyclin-Dependent Kinase 2 Flexibility Without Significant Change in the Initial Conformation of the Protein or Its Environment; a Computational Study. <i>Iranian Journal of Biotechnology</i> 2016 14 1-12	1	O